

DETECTION OF GENETIC POLYMORPHISMS

The present invention claims priority to Japanese Patent Application Ser. Nos. 2000-399,443 filed December 27, 2000, 2001-135,256 filed May 2, 2001, 2001-256,862
5 filed August 27, 2001, and 2001-(awaiting serial number) filed December 2001, each of
which was filed with the Commissioner of the Japanese Patent Office. Right of priority
under 35 U.S.C. 119 is claimed from these Japanese patent applications under the Paris
Convention for the Protection of Industrial Property. The present invention also claims
priority to PCT application (awaiting serial number) filed December 27, 2001 in the
10 Japanese receiving office. Each of these applications are herein incorporated by
reference in their entireties.

FIELD OF THE INVENTION

The present invention relates to genetic polymorphism data, compositions and
15 methods for detecting genetic polymorphisms, methods for evaluating drugs using
genetic polymorphisms and screening methods for drugs.

BACKGROUND

Human beings come in all shapes and sizes, and over three billion genetic codes
20 are located in somewhat different sites in each human being. Individual DNA sequence
variations in the human genome are known to directly cause specific diseases or
conditions, to predispose certain individuals to specific diseases or conditions, and to
affect responses of individuals to treatments such as drugs. Such variations also
modulate the severity or progression of many diseases. Additionally, DNA sequences
25 vary between populations. Therefore, determining DNA sequence variations in the
human genome is useful for making accurate diagnoses, for finding suitable therapies,
and for understanding the relationship between genome variations and environmental
factors in the pathogenesis of diseases, the prevalence of conditions and the efficacy of
therapies.

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
NDUFA9	18	(intron 4 1090)	atcattgctgttttaaagtt T/C aagtagtgtaatttcagta	6806
NDUFA9	19	(intron 4 1188)	aaccaatcctttttttttt A/T tcttcagaaactttgattt	6807
NDUFA9	20	(intron 5 161)	gggtgtgtgtgatgttttga C/T gttttgattgattgccttct	6808
NDUFA9	21	(intron 5 373)	ctttctcacccttgcaactg C/T agtgggtttgtgccactctt	6809
NDUFA9	22	(intron 5 457)	gccagggaagatgcctattc A/C cacagtgttatgtctccttt	6810
NDUFA9	23	(intron 5 3113)	gattttttctccttcttcaat G/A taagcttcccttaaaataaa	6811
NDUFA9	24	(intron 5 3339)	tctaaactcaaaacagggtt G/A tttggttattgtttaggctg	6812
NDUFA9	25	(intron 6 414)	tatagttttgccttttccag G/C atattacatatatggttaga	6813
NDUFA9	26	(intron 6 518)	ctttcattttcttttcatagc T/C tgatagctcattttcttata	6814
NDUFA9	27	(intron 7 974)	ggattatgcgtactctggaaa A/G tacttggtatagcgggtgatta	6815
NDUFA9	28	(intron 8 368)	acattaattttgatggagta T/G cacaatgcctccagaggctg	6816
NDUFA9	29	(intron 8 954)	gcatgcaatcagttatatag T/C ctgataagaattacaattc	6817
NDUFA9	30	(intron 8 1253)	tcctcttgaattgttagata G/T gtatctacacattttctcatc	6818
NDUFA9	31	(intron 8 11608)	gaaaagatagatgtataaat G/A accaaaaattcgtgaagaaa	6819
NDUFA9	32	(intron 8 11930)	ctacaaatatattctaaatg C/T gtaatcattgataagtagaaa	6820
NDUFA9	33	(intron 9 1998)	tggtttttcaagccttttaac G/A gctgtggaaccctgtgctca	6821
NDUFA9	34	(intron 9 2238)	ccagctactctggaggctga A/G gttggaggatcacttgagcc	6822
NDUFA9	35	(intron 9 2885)	acagcggtctgtcttctctgc A/G gttctcataggctagcttac	6823
NDUFA9	36	(intron 10 801)	tacactaaagtgtctctttac G/A tttatacttgagaaagtgtt	6824
NDUFA9	37	(intron 10 910)	tgcagactttcaggtgggta G/C gatgagggattgtctgtgct	6825
NDUFA9	38	(intron 10 1180)	aaaactgagtcagaacgccc G/A tgctcagaaaaacagggcgt	6826
NDUFA9	39	(3' flanking region 554)	gtgccagcacttaggaatta T/G gaccttctaataagattcttt	6827
NDUFA9	40	(5' flanking region (-1129) - (-1128))	taaacagtaggggcaagata (TC) gagtggaaacagccaagatt	6828
NDUFA9	40	(5' flanking region (-1129) - (-1128))	taaacagtaggggcaagata gagtggaaacagccaagatt	6829
NDUFA9	41	(5' flanking region -341)	tggtttct c/g tctccacttt T/Δ cccctgttcttctgtccc c/	6830
NDUFA9	42	(intron 4 594)	attcaactttttatcccccc T/Δ aatgattaacatagtgatt	6831
NDUFA9	43	(intron 10 356-375)	taacttctcttaacgtctct GAAGAACTGTTGACAGTT/Δ	6832
NDUFA9	44	(intron 10 379-381)	cttctctttttctttaacct	6833
NDUFA9	44	(intron 10 379-381)	gaaactgttgacagtttctt CCT/Δ tctttctttaacctactcca	6833
NDUFA9	45	(intron 10 384-387)	tggtgacagttttcttctctt TTC/Δ ttttaacctactccagtcagg	6834
NDUFA9	46	(intron 10 436-437)	ccattttctcccttaaaattg (TCTTTTAAATG) ctctttttcaaggt	6835
NDUFA9	46	(intron 10 436-437)	ccattttctcccttaaaattg ctctttttcaaggt	6836
NDUFA9	47	(intron 10 495-496)	gccacatccaatggtcagtt (TTCAGGCCTT) ctccagacctcagtc	6837
NDUFA9	47	(intron 10 495-496)	gccacatccaatggtcagtt ctccagacctcagtc	6838
NDUFA9	48	(intron 10 519-520)	gacctcatgtcatgtgctg (GGCCTG) tgcatttgcttctagggagg	6839
NDUFA9	48	(intron 10 519-520)	gacctcatgtcatgtgctg tgcatttgcttctagggagg	6840
NDUFA9	49	(intron 10 558-559)	gatgcaaaaataaaaataaaa (A) tactataccaataccacatc	6841
NDUFA9	49	(intron 10 558-559)	gatgcaaaaataaaaataaaa tactataccaataccacatc	6842
NDUFA10	1	(5' flanking region -1734)	tgcaccttgaactgtttact T/C tctgttaaccatttaccctt	6843
NDUFA10	2	(5' flanking region -1492)	aaaacatccacgcaaacagg T/C tgtgagaagttacgtctg	6844
NDUFA10	3	(intron 3 370)	aagactgtgcatgtgccaatg C/A agacagagatgtggatgcca	6845
NDUFA10	4	(intron 3 2485)	ttgttattttcttttctctg G/A aatgcagtgatcagttgaca	6846
NDUFA10	5	(intron 4 236)	ctgtgaaagcagattggagc C/T ctggacctcaaacacagca	6847
NDUFA10	6	(intron 4 1742)	tgtcgccatctgtctgagtg C/T tgcgtgaagtctgaggactgg	6848
NDUFA10	7	(intron 4 2090)	ggctgggggaaagcagatca T/C gttgctaaaggacaggtgg	6849
NDUFA10	8	(intron 4 3054)	cagctgattatactactgaa A/C cgggataaatg c/t agcttgat	6850
NDUFA10	9	(intron 4 3066)	ctactgaa a/c cgggataaatg C/T agcttgatgattttcagctg	6851
NDUFA10	10	(intron 4 3377)	gtcacagtttaaatgctgct G/A ttttactctgtgtaagtagc	6852
NDUFA10	11	(intron 5 46)	aagcatctctattttgaatg T/C agatcagcactaaaagccct	6853
NDUFA10	12	(intron 8 1465)	gcaacgcccagtttctgtgta C/T aggcctcataatccagctgc	6854
NDUFA10	13	(intron 8 1809)	cctggaggcacaaggtggc C/A ggggcactcaacttccctct	6855
NDUFA10	14	(intron 8 11226)	gttgtgtgactgtgtggggc A/G tctcaccctctcgggctgag	6856
NDUFA10	15	(intron 8 11319)	atcttgcccttccctctctgcc G/A tctgtttcaggcttgaacct	6857
NDUFA10	16	(intron 8 11386)	ccataatcctagcttgaacc C/T tcttttttccctgctgaccc	6858
NDUFA10	17	(intron 8 13361)	ccaggccactgattgttttc G/A cattttctagcattttctta	6859
NDUFA10	18	(intron 9 183)	ttctgtgtggaagctgat G/A aagtctcagatgacagccc	6860
NDUFA10	19	(intron 9 8028)	gaggacattccacagaactg G/A tgactattagagcagaaggt	6861
NDUFA10	20	(intron 9 10742)	ctggaggagaggggtggagc C/G agttcagccagcactggggt	6862
NDUFA10	21	(intron 9 13908)	cacattgttatgtaaccaag C/T ct g/t gaattgcagtgtaaga	6863
NDUFA10	22	(intron 9 13911)	attgttatgtaaccaag c/t ct G/T gaattgcagtgtaagaact	6864
NDUFA10	23	(intron 9 14064)	tcttgactattagaacctt A/G tcagataaatttttaaagac	6865
NDUFA10	24	(intron 9 14184)	tggtttgtgtgggaacagc G/A agagatacagaaccgaggt	6866
NDUFA10	25	(intron 9 16487)	cttgaagctgatcgttccct C/A cttgaagctgatcgttccct	6867
NDUFA10	26	(intron 9 16779)	gccagacgtgactgcttttag G/A ttctctcatgacattcagacc	6868
NDUFA10	27	(intron 9 17663)	ttccaaatcaccacagaact T/G tgcagtattttgaagctcct	6869
NDUFA10	28	(5' flanking region (-1668) - (-1659))	gtaaaattgttttaactaga (C) 9-11 ttcctaaaccaaggtataaa	6870

function. Analysis of genetic polymorphisms such as SNPs allows for the selection of drugs and the development of treatment protocols tailored to each individual patient (so-called "personalized" medical treatments). Instead of the using trial-and-error methods of matching patients with the right drugs, doctors may, for example, be able to analyze a patient's genetic profile and prescribe the best available drug therapy from the beginning. Not only would this take the guesswork out of finding the right drug, it would reduce the likelihood of adverse reactions, thus increasing safety.

SUMMARY OF THE INVENTION

The present invention identifies genetic polymorphisms relating to genes associated with drug metabolism. In some embodiments, the present invention provides methods for determining variations in sequences and genes associated with drug-metabolizing enzymes. In preferred embodiments, the present invention provides methods for collecting genetic polymorphism data for use in evaluating the effectiveness and safety of a drug based on the data, and screening drugs using the data. In some preferred embodiments, the polymorphisms of the present invention are used to evaluate a causal relationship between the genetic make-up of a patient and a response to an administered drug.

The present invention relates to genes encoding enzymes associated with drug metabolism (drug metabolizing enzymes, or DMEs). In particular, the present invention relates to sequence variations associated with variations in DMEs. In some embodiments, variations occur in coding regions of DMEs, such as may alter a function of the DMEs, (*e.g.*, by increasing or decreasing its level of activity, or shifting its activity to an alternative target or function). In other embodiments, the variations occur in non-coding regions of the genome, such as may alter expression of a DME (*e.g.*, increasing or decreasing the amount of an enzyme produced in a cell) or processing of an RNA transcript encoding a DME (*e.g.*, by altering splicing).

In some embodiments, the present invention provides methods for detecting DME-related sequence variations. In some preferred embodiments, the methods of the

present invention are used to create a profile of DME-related polymorphisms in a test subject.

In other embodiments, the present invention provides isolated nucleic acid sequences encoding variant DMEs. For example, the present invention provides a recombinant DNA vector comprising DNA having a nucleotide sequence encoding a variant DME, the nucleotide sequence comprising a sequence including, but not limited to, SEQ ID NOS:1-3360 and 3361-7669, and substantially similar sequences. In a preferred embodiment, the invention provides a host cell transformed with a recombinant DNA vector comprising DNA having a nucleotide sequence encoding a variant DME.

The invention is not limited by the nature of the host cell employed. The art is well aware of expression vectors suitable for the expression of nucleotide sequences encoding variant DMEs that can be expressed in a variety of prokaryotic and eukaryotic host cells. In some preferred embodiments, the host cell is a eukaryotic cell grown in culture, such as for use in *in vitro* drug screening (*e.g.*, by monitoring the expression of genes associated with the pathways targeted by a particular test drug). In other preferred embodiments, the host cell is *in vivo*.

The present invention provides systems and methods for detection of polymorphisms associated with genes encoding enzymes associated with drug metabolism. The present invention is not limited in the nature of the detection assay used for detection or identification of such polymorphisms. Such detection assays include, but are not limited to, hybridization methods and array technologies (*e.g.*, technologies available from Aclara BioSciences, Haywood, CA; Affymetrix, Santa Clara, CA; Agilent Technologies, Inc., Palo Alto, CA; Aviva Biosciences Corp., San Diego, CA; Caliper Technologies Corp., Palo Alto, CA; Celera, Rockville, MD; CuraGen Corp., New Haven, CT; Hyseq Inc., Sunnyvale, CA; Illumina, Inc., San Diego, CA; Incyte Genomics, Palo Alto, CA; Motorola BioChip Systems; Nanogen, San Diego, CA; Orchid BioSciences, Inc., Princeton, NJ; Applera Corp., Foster City, CA; Rosetta Inpharmatics, Kirkland, WA; and Sequenom, San Diego, CA); polymerase chain reaction-based methods (*e.g.*, TAQMAN, Applera Corp., GENECODE system, EraGen, Middleton, WI); branched hybridization methods; enzyme mismatch cleavage methods; NASBA;

sandwich hybridization methods; methods employing molecular beacons; ligase chain reactions, and the like.

Methods of the present invention find application in improving the drug discovery and approval processes. For example, the costs and risks of drug development may be reduced if only those persons capable of responding to a drug are selected for clinical trials. In addition, previously failed drug candidates may be revived as they are matched with more appropriate patient populations. Decreases in the number of adverse drug reactions, the number of failed drug trials, the time it takes to get a drug approved, the length of time patients are on medication, the number of medications patients must take to find an effective therapy, and an increase in the range of possible drug targets will promote a net decrease in the cost of health care.

Thus, in some embodiments, the present invention provides a method of identifying individuals having a polymorphism, comprising providing nucleic acid from a subject; and detecting the presence of at least one polymorphism in said nucleic acid, said at least one polymorphism including, but not limited to, polymorphisms found in SEQ ID Nos:1-3360 and 3361-7669. In some embodiments, the method further provides the step of providing a prognosis (e.g., a genotype relative risk or a population attributable risk) to the subject based on the presence or absence of the at least one polymorphism. In some embodiments, the detecting step is carried out using a detection assay including, but not limited to, a hybridization assay, a TAQMAN assay, an invasive cleavage assay, use of mass spectroscopy, a microarray, a polymerase chain reaction, a rolling circle extension assay, a sequencing assay, a hybridization assay employing a probe complementary to a polymorphism, a bead array assay, a primer extension assay, an enzyme mismatch cleavage assay, a branched hybridization assay, a NASBA assay, a molecular beacon assay, a cycling probe assay, a ligase chain reaction assay, and a sandwich hybridization assay.

The present invention also provides a nucleic acid (e.g., a gene, a probe, a primer, etc.) comprising a sequence selected from the group consisting of SEQ ID NO:1-3360 and 3361-7669 or complements thereof. In some embodiments, the nucleic acid molecule comprises a label. In some embodiments, the nucleic acid is attached to a solid

support (e.g., as part of a microarray). The present invention also provides vectors comprising the nucleic acid and host cell comprising the vector, as well as polypeptide encoded by the nucleic acid. Methods of producing and purifying polypeptides are well known in the art.

5 The present invention further provides kits for detecting a polymorphism, comprising at least one reagent that specifically detects a polymorphism in a sequence including, but not limited to, SEQ ID Nos:1-3360 and 3361-7669. In some embodiments, the kit further comprising instructions for determining whether the subject is at increased risk of having a drug metabolism disorder. In some embodiments, the at least one
10 reagent comprises a nucleic acid probe. The kits can be configured for a variety of uses including, but not limited to, use as an in vitro diagnostic detection assay, an analyte specific reagent detection assay, and a research-use-only detection assay.

 The present invention also provides a method for screening subjects for genetic markers associated with drug metabolizing enzyme(s), comprising: a) providing a
15 biological sample comprising a nucleic acid from a subject; b) testing the nucleic acid for a polymorphism in a genetic marker associated with a drug metabolizing enzyme, said genetic marker comprising one or more nucleotide polymorphisms designated by n, said n selected from a base substitution, an insertion, or a deletion found in a sequence selected from the group consisting of SEQ ID Nos:1-3360 and 3361-7669. The present
20 invention is not limited by the source of the nucleic acid. In some embodiments, the biological sample comprises blood, saliva, amniotic fluid, and tissue. In some embodiments, the subject is a human. In some preferred embodiments, the nucleic acid comprises DNA and/or RNA.

 The present invention further provides a composition comprising an array of
25 detection assays, said array comprising a plurality of drug metabolizing enzyme nucleotide polymorphism detection assays, one or more of said detection assays being capable of detecting one or more nucleotide polymorphisms designated by n in SEQ ID Nos:1-3360 and 3361-7669, wherein n represents a base substitution, insertion, or deletion compared to a wild-type sequence.

The present invention also provides a composition comprising a detection probe for determining the presence or absence of a single nucleotide polymorphism in a gene encoding a drug metabolizing enzyme, said gene comprising a sequence selected from the group consisting of SEQ ID Nos:1-3360 and 3361-7669.

5 The present invention further provides a method of determining the effectiveness of or side-effect of a drug or treatment protocol, comprising; a) administering a drug or treatment protocol to one or more subjects; b) obtaining nucleic acid from said one or more subjects; c) using a detection assay to detect the presence of at least one polymorphism in said nucleic acid from said one or more of subjects, said at least one
10 polymorphism selected from the group consisting of polymorphisms found in SEQ ID Nos:1-3360 and 3361-7669; and d) assigning an effectiveness rating, side-effect rating, or score for said drug or treatment protocol based upon a result of one or more said detection assays (*See e.g.*, Toxicology Testing Handbook: Principles, Applications, and Data Interpretation, ed. Jacobson-Kram and Keller, 2001, herein incorporated by
15 reference in its entirety).

The present invention also provides a method of prescribing a drug to or treatment protocol for a subject, comprising; providing nucleic acid from said subject; using a detection assay to detect the presence of at least one polymorphism in the nucleic acid, said at least one polymorphism selected from the group consisting of polymorphisms
20 found in SEQ ID Nos:1-3360 and 3361-7669; and, prescribing said drug or treatment protocol based upon the result of said detection assay.

The present invention further provides a method for generating assay data comprising: obtaining a sample from a subject containing nucleic acid; transferring said sample to a laboratory; and receiving data from said laboratory, wherein said data
25 corresponds to the presence of at least one polymorphism in said nucleic acid, said at least one polymorphism selected from the group consisting of polymorphisms found in SEQ ID Nos:1-3360 and 3361-7669. The present further provides data sets generated by this method.

DEFINITIONS

To facilitate an understanding of the present invention, a number of terms and phrases are defined below:

As used herein, the terms "complementary" or "complementarity" are used in reference to polynucleotides (*i.e.*, a sequence of nucleotides such as an oligonucleotide or a target nucleic acid) related by the base-pairing rules. For example, for the sequence "5'-A-G-T-3'," is complementary to the sequence "3'-T-C-A-5'." Complementarity may be "partial," in which only some of the nucleic acids' bases are matched according to the base pairing rules. Or, there may be "complete" or "total" complementarity between the nucleic acids. The degree of complementarity between nucleic acid strands has significant effects on the efficiency and strength of hybridization between nucleic acid strands. This is of particular importance in amplification reactions, as well as detection methods that depend upon binding between nucleic acids. Either term may also be used in reference to individual nucleotides, especially within the context of polynucleotides. For example, a particular nucleotide within an oligonucleotide may be noted for its complementarity, or lack thereof, to a nucleotide within another nucleic acid strand, in contrast or comparison to the complementarity between the rest of the oligonucleotide and the nucleic acid strand. Nucleotide analogs used to form non-standard base pairs, whether with another nucleotide analog (e.g., an IsoC/IsoG base pair), or with a naturally occurring nucleotide (e.g., as described in U.S. Patent 5,912,340, herein incorporated by reference in its entirety) are also considered to be complementary to a base pairing partner within the meaning this definition.

The term "homology" and "homologous" refers to a degree of identity. There may be partial homology or complete homology. A partially homologous sequence is one that is less than 100% identical to another sequence.

As used herein, the term "hybridization" is used in reference to the pairing of complementary nucleic acids. Hybridization and the strength of hybridization (*i.e.*, the strength of the association between the nucleic acids) is influenced by such factors as the degree of complementary between the nucleic acids, stringency of the conditions involved, and the T_m of the formed hybrid. "Hybridization" methods involve the

annealing of one nucleic acid to another, complementary nucleic acid, *i.e.*, a nucleic acid having a complementary nucleotide sequence. The ability of two polymers of nucleic acid containing complementary sequences to find each other and anneal through base pairing interaction is a well-recognized phenomenon. The initial observations of the "hybridization" process by Marmur and Lane, Proc. Natl. Acad. Sci. USA 46:453 (1960) and Doty et al., Proc. Natl. Acad. Sci. USA 46:461 (1960) have been followed by the refinement of this process into an essential tool of modern biology.

With regard to complementarity, it is important for some diagnostic applications to determine whether the hybridization represents complete or partial complementarity.

For example, where it is desired to detect simply the presence or absence of a foreign DNA sequence, it is only important that the hybridization method ensures hybridization when the relevant sequence is present; conditions can be selected where both partially complementary probes and completely complementary probes will hybridize. Other diagnostic applications, however, may require that the hybridization method distinguish between partial and complete complementarity. It may be of interest to detect genetic polymorphisms. For example, human hemoglobin is composed, in part, of four polypeptide chains. Two of these chains are identical chains of 141 amino acids (alpha chains) and two of these chains are identical chains of 146 amino acids (beta chains). The gene encoding the beta chain is known to exhibit polymorphism. The normal allele encodes a beta chain having glutamic acid at the sixth position. The mutant allele encodes a beta chain having valine at the sixth position. This difference in amino acids has a profound (most profound when the individual is homozygous for the mutant allele) physiological impact known clinically as sickle cell anemia. It is well known that the genetic basis of the amino acid change involves a single base difference between the normal allele DNA sequence and the mutant allele DNA sequence.

The complement of a nucleic acid sequence as used herein refers to an oligonucleotide which, when aligned with the nucleic acid sequence such that the 5' end of one sequence is paired with the 3' end of the other, is in "antiparallel association." Certain bases not commonly found in natural nucleic acids may be included in the nucleic acids of the present invention and include, for example, inosine and 7-deazaguanine.

Complementarity need not be perfect; stable duplexes may contain mismatched base pairs or unmatched bases. Those skilled in the art of nucleic acid technology can determine duplex stability empirically considering a number of variables including, for example, the length of the oligonucleotide, base composition and sequence of the oligonucleotide, ionic strength and incidence of mismatched base pairs.

As used herein, the term " T_m " is used in reference to the "melting temperature." The melting temperature is the temperature at which a population of double-stranded nucleic acid molecules becomes half dissociated into single strands. Several equations for calculating the T_m of nucleic acids are well known in the art. As indicated by standard references, a simple estimate of the T_m value may be calculated by the equation: $T_m = 81.5 + 0.41(\% G + C)$, when a nucleic acid is in aqueous solution at 1 M NaCl (*see e.g.*, Anderson and Young, Quantitative Filter Hybridization, in Nucleic Acid Hybridization (1985). Other references (*e.g.*, Allawi, H.T. & SantaLucia, J., Jr. Thermodynamics and NMR of internal G.T mismatches in DNA. Biochemistry 36, 10581-94 (1997) include more sophisticated computations which take structural and environmental, as well as sequence characteristics into account for the calculation of T_m .

As used herein the term "stringency" is used in reference to the conditions of temperature, ionic strength, and the presence of other compounds, under which nucleic acid hybridizations are conducted. With "high stringency" conditions, nucleic acid base pairing will occur only between nucleic acid fragments that have a high frequency of complementary base sequences. Thus, conditions of "weak" or "low" stringency are often required when it is desired that nucleic acids that are not completely complementary to one another be hybridized or annealed together.

"High stringency conditions" when used in reference to nucleic acid hybridization comprise conditions equivalent to binding or hybridization at 42 C in a solution consisting of 5X SSPE (43.8 g/l NaCl, 6.9 g/l NaH_2PO_4 H_2O and 1.85 g/l EDTA, pH adjusted to 7.4 with NaOH), 0.5% SDS, 5X Denhardt's reagent and 100 $\mu\text{g/ml}$ denatured salmon sperm DNA followed by washing in a solution comprising 0.1X SSPE, 1.0% SDS at 42 C when a probe of about 500 nucleotides in length is employed.

"Medium stringency conditions" when used in reference to nucleic acid hybridization comprise conditions equivalent to binding or hybridization at 42 C in a solution consisting of 5X SSPE (43.8 g/l NaCl, 6.9 g/l NaH₂PO₄ H₂O and 1.85 g/l EDTA, pH adjusted to 7.4 with NaOH), 0.5% SDS, 5X Denhardt's reagent and 100 µg/ml denatured salmon sperm DNA followed by washing in a solution comprising 1.0X SSPE, 1.0% SDS at 42 C when a probe of about 500 nucleotides in length is employed.

"Low stringency conditions" comprise conditions equivalent to binding or hybridization at 42 C in a solution consisting of 5X SSPE (43.8 g/l NaCl, 6.9 g/l NaH₂PO₄ H₂O and 1.85 g/l EDTA, pH adjusted to 7.4 with NaOH), 0.1% SDS, 5X

Denhardt's reagent [50X Denhardt's contains per 500 ml: 5 g Ficoll (Type 400, Pharmacia), 5 g BSA (Fraction V; Sigma)] and 100 g/ml denatured salmon sperm DNA followed by washing in a solution comprising 5X SSPE, 0.1% SDS at 42 C when a probe of about 500 nucleotides in length is employed.

The term "gene" refers to a DNA sequence that comprises control and coding sequences necessary for the production of an RNA having a non-coding function (*e.g.*, a ribosomal or transfer RNA), a polypeptide or a precursor. The RNA or polypeptide can be encoded by a full-length coding sequence or by any portion of the coding sequence so long as the desired activity or function is retained.

The term "wild-type" refers to a gene or a gene product that has the characteristics of that gene or gene product when isolated from a naturally occurring source. A wild-type gene is that which is most frequently observed in a population and is thus arbitrarily designated the "normal" or "wild-type" form of the gene. In contrast, the term "modified," "mutant," or "polymorphic" refers to a gene or gene product that displays modifications in sequence and or functional properties (*i.e.*, altered characteristics) when compared to the wild-type gene or gene product. It is noted that naturally-occurring mutants can be isolated; these are identified by the fact that they have altered characteristics when compared to the wild-type gene or gene product.

The term "oligonucleotide" as used herein is defined as a molecule comprising two or more deoxyribonucleotides or ribonucleotides, preferably at least 5 nucleotides, more preferably at least about 10-15 nucleotides and more preferably at least about 15 to

30 nucleotides. The exact size will depend on many factors, which in turn depend on the ultimate function or use of the oligonucleotide. The oligonucleotide may be generated in any manner, including chemical synthesis, DNA replication, reverse transcription, PCR, or a combination thereof.

5 Because mononucleotides are reacted to make oligonucleotides in a manner such that the 5' phosphate of one mononucleotide pentose ring is attached to the 3' oxygen of its neighbor in one direction via a phosphodiester linkage, an end of an oligonucleotide is referred to as the "5' end" if its 5' phosphate is not linked to the 3' oxygen of a mononucleotide pentose ring and as the "3' end" if its 3' oxygen is not linked to a 5' phosphate of a subsequent mononucleotide pentose ring. As used herein, a nucleic acid sequence, even if internal to a larger oligonucleotide, also may be said to have 5' and 3' ends. A first region along a nucleic acid strand is said to be upstream of another region if the 3' end of the first region is before the 5' end of the second region when moving along a strand of nucleic acid in a 5' to 3' direction.

10 15 When two different, non-overlapping oligonucleotides anneal to different regions of the same linear complementary nucleic acid sequence, and the 3' end of one oligonucleotide points towards the 5' end of the other, the former may be called the "upstream" oligonucleotide and the latter the "downstream" oligonucleotide. Similarly, when two overlapping oligonucleotides are hybridized to the same linear complementary nucleic acid sequence, with the first oligonucleotide positioned such that its 5' end is upstream of the 5' end of the second oligonucleotide, and the 3' end of the first oligonucleotide is upstream of the 3' end of the second oligonucleotide, the first oligonucleotide may be called the "upstream" oligonucleotide and the second oligonucleotide may be called the "downstream" oligonucleotide.

20 25 The term "primer" refers to an oligonucleotide that is capable of acting as a point of initiation of synthesis when placed under conditions in which primer extension is initiated. An oligonucleotide "primer" may occur naturally, as in a purified restriction digest or may be produced synthetically.

30 A primer is selected to be "substantially" complementary to a strand of specific sequence of the template. A primer must be sufficiently complementary to hybridize

with a template strand for primer elongation to occur. A primer sequence need not reflect the exact sequence of the template. For example, a non-complementary nucleotide fragment may be attached to the 5' end of the primer, with the remainder of the primer sequence being substantially complementary to the strand. Non-complementary bases or longer sequences can be interspersed into the primer, provided that the primer sequence has sufficient complementarity with the sequence of the template to hybridize and thereby form a template primer complex for synthesis of the extension product of the primer.

The term "label" as used herein refers to any atom or molecule that can be used to provide a detectable (preferably quantifiable) effect, and that can be attached to a nucleic acid or protein. Labels include but are not limited to dyes; radiolabels such as ^{32}P ; binding moieties such as biotin; haptens such as digoxigenin; luminogenic, phosphorescent or fluorogenic moieties; and fluorescent dyes alone or in combination with moieties that can suppress or shift emission spectra by fluorescence resonance energy transfer (FRET). Labels may provide signals detectable by fluorescence, radioactivity, colorimetry, gravimetry, X-ray diffraction or absorption, magnetism, enzymatic activity, and the like. A label may be a charged moiety (positive or negative charge) or alternatively, may be charge neutral. Labels can include or consist of nucleic acid or protein sequence, so long as the sequence comprising the label is detectable.

The term "signal" as used herein refers to any detectable effect, such as would be caused or provided by a label or an assay reaction.

As used herein, the term "detector" refers to a system or component of a system, e.g., an instrument (e.g. a camera, fluorimeter, charge-coupled device, scintillation counter, etc.) or a reactive medium (X-ray or camera film, pH indicator, etc.), that can convey to a user or to another component of a system (e.g., a computer or controller) the presence of a signal or effect. A detector can be a photometric or spectrophotometric system, which can detect ultraviolet, visible or infrared light, including fluorescence or chemiluminescence; a radiation detection system; a spectroscopic system such as nuclear magnetic resonance spectroscopy, mass spectrometry or surface enhanced Raman

spectrometry; a system such as gel or capillary electrophoresis or gel exclusion chromatography; or other detection systems known in the art, or combinations thereof.

The term "sequence variation" as used herein refers to differences in nucleic acid sequence between two nucleic acids. For example, a wild-type structural gene and a mutant form of this wild-type structural gene may vary in sequence by the presence of single base substitutions and/or deletions or insertions of one or more nucleotides. These two forms of the structural gene are said to vary in sequence from one another. A second mutant form of the structural gene may exist. This second mutant form is said to vary in sequence from both the wild-type gene and the first mutant form of the gene.

The term "nucleotide analog" as used herein refers to modified or non-naturally occurring nucleotides such as 7-deaza purines (*i.e.*, 7-deaza-dATP and 7-deaza-dGTP). Nucleotide analogs include base analogs and comprise modified forms of deoxyribonucleotides as well as ribonucleotides.

The term "polymorphism" refers to the coexistence of more than one form of a gene or portion thereof. A portion of a gene of which there are at least two different forms, *i.e.*, two different nucleotide sequences, is referred to as a "polymorphic region of a gene". A polymorphic region can be a single nucleotide, the identity of which differs in different alleles. A polymorphic region can also be several nucleotides long.

A "polymorphic gene" refers to a gene having at least one polymorphic region.

The term "polymorphic locus" is a locus present in a population that shows variation between members of the population (*e.g.*, the most common allele has a frequency of less than 0.95). In contrast, a "monomorphic locus" is a genetic locus at little or no variations seen between members of the population (generally taken to be a locus at which the most common allele exceeds a frequency of 0.95 in the gene pool of the population).

A "non-human animal" of the invention can include mammals such as rodents, non-human primates, sheep, goats, horses, dogs, cows, chickens, amphibians, reptiles, etc. Preferred non-human animals are selected from the rodent family including rat and mouse, most preferably mouse, though transgenic amphibians, such as members of the *Xenopus* genus, and transgenic chickens can also provide important tools for

understanding and identifying drugs that can affect processes, *e.g.*, embryogenesis and tissue formation.

The term "operably linked" is intended to mean that the promoter is associated with the nucleic acid in such a manner as to facilitate transcription of the nucleic acid from the promoter.

The terms "protein", "polypeptide" and "peptide" are used interchangeably herein when referring to a gene product.

The term "recombinant protein" refers to a polypeptide which is produced by recombinant DNA techniques, wherein generally, DNA encoding the polypeptide is inserted into a suitable expression vector which is in turn used to transform a host cell to produce the heterologous protein.

A "regulatory element", also termed herein "regulatory sequence" is intended to include elements which are capable of modulating transcription from a basic promoter and include elements such as enhancers and silencers. The term "enhancer", also referred to herein as "enhancer element", is intended to include regulatory elements capable of increasing, stimulating, or enhancing transcription from a basic promoter. The term "silencer", also referred to herein as "silencer element" is intended to include regulatory elements capable of decreasing, inhibiting, or repressing transcription from a basic promoter. Regulatory elements are typically present in 5' flanking regions of genes.

However, regulatory elements have also been shown to be present in other regions of a gene, in particular in introns. Regulatory elements may also be present downstream of coding regions. Thus, it is possible that DME genes have regulatory elements located in introns, exons, coding regions, and 3' flanking sequences. Such regulatory elements are also intended to be encompassed by the present invention and polymorphisms in such elements can be identified by any of the assays that can be used to identify polymorphisms in regulatory elements in 5' flanking regions of genes.

The term "regulatory element" further encompasses "tissue specific" regulatory elements, *i.e.*, regulatory elements that affect expression of a DME gene preferentially in specific cells (*e.g.*, cells of a specific tissue). Gene expression occurs preferentially in a specific cell if expression in this cell type is significantly higher than expression in other

cell types. The term "regulatory element" also encompasses non-tissue specific regulatory elements, i.e., regulatory elements that are active in most cell types. Furthermore, a regulatory element can be a constitutive regulatory element, i.e., a regulatory element that constitutively regulates transcription, as opposed to a regulatory element that is inducible, i.e., a regulatory element which is active primarily in response to a stimulus. A stimulus can be, e.g., a molecule, such as a hormone, cytokine, heavy metal, phorbol ester, cyclic AMP (cAMP), or retinoic acid.

As used herein, the term "transfection" means the introduction of a nucleic acid, e.g., an expression vector, into a recipient cell by nucleic acid-mediated gene transfer.

The term "transduction" is generally used herein when the transfection with a nucleic acid is by viral delivery of the nucleic acid. "Transformation", as used herein, refers to a process in which a cell's genotype is changed as a result of the cellular uptake of exogenous DNA or RNA, and, for example, the transformed cell expresses a recombinant form of a polypeptide or, in the case of anti-sense expression from the transferred gene, the expression of a naturally-occurring form of the recombinant protein is disrupted.

As used herein, the term "transgene" refers to a nucleic acid sequence that has been introduced into a cell. Daughter cells deriving from a cell in which a transgene has been introduced are also said to contain the transgene (unless it has been deleted). A transgene can encode, e.g., a polypeptide, or an antisense transcript, partly or entirely heterologous, i.e., foreign, to the transgenic animal or cell into which it is introduced, or, is homologous to an endogenous gene of the transgenic animal or cell into which it is introduced, but which is designed to be inserted, or is inserted, into the animal's genome in such a way as to alter the genome of the cell into which it is inserted (e.g., it is inserted at a location which differs from that of the natural gene or its insertion results in a knockout). Alternatively, a transgene can also be present in an episome. A transgene can include one or more transcriptional regulatory sequence and any other nucleic acid, (e.g. intron), that may be necessary for optimal expression of a selected nucleic acid.

A "transgenic animal" refers to any animal, preferably a non-human animal, e.g. a mammal, bird or an amphibian, in which one or more of the cells of the animal contain heterologous nucleic acid introduced by way of human intervention, such as by

transgenic techniques well known in the art. The nucleic acid is introduced into the cell, directly or indirectly by introduction into a precursor of the cell, by way of deliberate genetic manipulation, such as by microinjection or by infection with a recombinant virus. The term genetic manipulation does not include classical cross-breeding, or in vitro fertilization, but rather is directed to the introduction of a recombinant DNA molecule. This molecule may be integrated within a chromosome, or it may be extrachromosomally replicating DNA. In the typical transgenic animals described herein, the transgene causes cells to express a recombinant form of one of a protein, e.g. either agonistic or antagonistic forms. However, transgenic animals in which the recombinant gene is silent are also contemplated. Moreover, "transgenic animal" also includes those recombinant animals in which gene disruption of one or more genes is caused by human intervention, including both recombination and antisense techniques.

The term "treating" as used herein is intended to encompass curing as well as ameliorating at least one symptom of the condition or disease.

The term "sample" in the present specification and claims is used in its broadest sense. On the one hand it is meant to include a biological (*e.g.*, human) specimen. On the other hand, a sample may include a specimen of synthetic origin.

Biological samples may be animal, including human, fluid, solid (*e.g.*, stool) or tissue, as well as liquid and solid food and feed products and ingredients such as dairy items, vegetables, meat and meat by-products, and waste. Biological samples may be obtained from all of the various families of domestic animals, as well as feral or wild animals, including, but not limited to, such animals as ungulates, bear, fish, lagamorphs, rodents, etc.

The term "source of target nucleic acid" refers to any sample that contains or is suspected to contain nucleic acids (RNA or DNA). Particularly preferred sources of target nucleic acids are biological samples including, but not limited to blood, saliva, cerebral spinal fluid, pleural fluid, milk, lymph, sputum and semen.

The term "polymerization means" or "polymerization agent" refers to any agent capable of facilitating the addition of nucleoside triphosphates to an oligonucleotide.

Preferred polymerization means comprise DNA and RNA polymerases.

The term "ligation means" or "ligation agent" refers to any agent capable of facilitating the ligation (i.e., the formation of a phosphodiester bond between a 3'-OH and a 5' P located at the termini of two strands of nucleic acid). Preferred ligation means comprise DNA ligases and RNA ligases.

5 The term "reactant" is used herein in its broadest sense. The reactant can comprise, for example, an enzymatic reactant, a chemical reactant or light (e.g., ultraviolet light, particularly short wavelength ultraviolet light is known to break oligonucleotide chains). Any agent capable of reacting with an oligonucleotide to either shorten (i.e., cleave) or elongate the oligonucleotide is encompassed within the term
10 "reactant."

The term "nucleic acid sequence" as used herein refers to an oligonucleotide, nucleotide or polynucleotide, and fragments or portions thereof, and to DNA or RNA of genomic or synthetic origin that may be single or double stranded, and represent the sense or antisense strand. Similarly, "amino acid sequence" as used herein refers to
15 peptide or protein sequence.

The term "peptide nucleic acid" ("PNA") as used herein refers to a molecule comprising bases or base analogs such as would be found in natural nucleic acid, but attached to a peptide backbone rather than the sugar-phosphate backbone typical of nucleic acids. The attachment of the bases to the peptide is such as to allow the bases to
20 base pair with complementary bases of nucleic acid in a manner similar to that of an oligonucleotide. These small molecules, also designated anti gene agents, stop transcript elongation by binding to their complementary strand of nucleic acid (Nielsen, *et al.* Anticancer Drug Des. 8:53 63 [1993]).

As used herein, the terms "purified" or "substantially purified" refer to
25 molecules, either nucleic or amino acid sequences, that are removed from their natural environment, isolated or separated, and are at least 60% free, preferably 75% free, and most preferably 90% free from other components with which they are naturally associated. An "isolated polynucleotide" or "isolated oligonucleotide" is therefore a substantially purified polynucleotide.

population, the percentage likelihood of an allele being present in an individual having one or more particular characteristics, etc.

The term "cleavage structure" as used herein, refers to a structure that is formed by the interaction of at least one probe oligonucleotide and a target nucleic acid, forming a structure comprising a duplex, the resulting structure being cleavable by a cleavage agent, including but not limited to an enzyme. The cleavage structure is a substrate for specific cleavage by the cleavage means in contrast to a nucleic acid molecule that is a substrate for non-specific cleavage by agents such as phosphodiesterases that cleave nucleic acid molecules without regard to secondary structure (*i.e.*, no formation of a duplexed structure is required).

DESCRIPTION OF THE DRAWINGS

Figure 1 shows sample embodiments of TAQMAN probes.

Figure 2 represents one embodiment of the TAQMAN PCR method.

Figure 3 shows examples of probes labeled with fluorescent dyes.

Figure 4 shows a sample embodiment of an invasive cleavage structure, *e.g.*, for an INVADER assay.

Figure 5 shows one embodiment of a FRET probe, *e.g.*, for an INVADER assay.

Figure 6 shows one embodiment of an INVADER assay.

Figure 7 shows a diagram of an INVADER assay probe in which the allele does not match the probe.

Figure 8 shows one embodiment of allele identification using a ligation reaction.

Figure 9 shows a drawing of the structure of and SNP position in the ATP-binding cassette subfamily B member 2 (ABCB2) gene.

Figure 10 shows a drawing of the structure of and SNP position in the ATP-binding cassette subfamily B member 4 (ABCB4) gene.

Figure 11 shows a drawing of the structure of and SNP position in the microsomal epoxide hydrogenase 1 (EPHX1) gene.

Figure 12 shows a drawing of the structure of and SNP position in the cytoplasmic epoxide hydrogenase 2 (EPHX2) gene.

Figure 13 shows a drawing of the structure of and SNP position in the guanidinoacetate-N-methyltransferase (GAMT) gene.

Figure 14 shows a drawing of the structure of and SNP position in the nicotinamide-N-methyltransferase (NNMT) gene.

5 Figure 15 shows a drawing of the structure of and SNP position in the phenylethanolamine-N-methyltransferase (PNMT) gene.

Figure 16 shows a drawing of the structure of and SNP position in the phosphatidylethanolamine-N-methyltransferase (PEMT) gene.

10 Figure 17 shows a drawing of the structure of and SNP position in the glutathione-S-methyltransferase 3 (GSTM3) gene.

Figure 18 shows a drawing of the structure of and SNP position in the aldehyde dehydrogenase 5 (ALDH5) gene.

Figure 19 shows a drawing of the structure of and SNP position in the transglutaminase (TGM1) gene.

15 Figure 20 shows a drawing of the structure of and SNP position in the gamma glutamyltransferase (GGT1) gene.

Figure 21 shows a drawing of the structure of and SNP position in the NAD(P)H: quinone oxidettransferase (NQ01) gene.

20 Figure 22 shows a drawing of the structure of and SNP position in the p53-induced gene 3 (PIG3) of a quinone oxide transferase homologue.

Figure 23 shows a drawing of the structure of and SNP position in the NRH: quinone oxide transferase 2 (NQ02) gene.

Figure 24 shows a drawing of the structure of and SNP position in the sulfotransferase 1A1 (SULT1A1/STP1) gene.

25 Figure 25 shows a drawing of the structure of and SNP position in the sulfotransferase 1A2 (SULT1A2/STP2) gene.

Figure 26 shows a drawing of the structure of and SNP position in the sulfotransferase-related protein 3 (SULTX3) gene.

30 Figure 27 shows a drawing of the structure of and SNP position in the tyrosyl protein sulfotransferase (TPST1) gene.

Figure 28 shows a drawing of the structure of and SNP position in the tyrosyl protein sulfotransferase (TPST2) gene.

Figure 29 shows a drawing of the structure of and SNP position in the sulfotransferase 1A3 (SULT1A3/ STM/HAST) gene.

5 Figure 30 shows a drawing of the structure of and SNP position in the cerebroside transferase (CST) gene.

Figure 31 shows a drawing of the structure of and SNP position in the sulfotransferase 1C1 (SULT1C1) gene.

10 Figure 32 shows a drawing of the structure of and SNP position in the sulfotransferase 1C2 (SULT1C2) gene.

Figure 33 shows a drawing of the structure of and SNP position in the thyroid hormone sulfotransferase (ST1B2) gene.

Figure 34 shows a drawing of the structure of and SNP position in the hydrocarbon sulfotransferase 2 (CHST2) gene.

15 Figure 35 shows a drawing of the structure of and SNP position in the sulfotransferase 2A1 (SULT2A1) gene.

Figure 36 shows a drawing of the structure of and SNP position in the sulfotransferase 2B1 (SULT2B1) gene.

20 Figure 37 shows a drawing of the structure of and SNP position in the hydrocarbon sulfotransferase 4 (CHST4) gene.

Figure 38 shows a drawing of the structure of and SNP position in the hydrocarbon sulfotransferase 5 (CHST5) gene.

Figure 39 shows a drawing of the structure of and SNP position in the HNK-sulfotransferase (NHK-1ST) gene.

25 Figure 40 shows a drawing of the structure of and SNP position in the estrogen sulfotransferase (STE) gene.

Figure 41 shows a drawing of the structure of and SNP position in the alcohol dehydrogenase 1 (ADH1) gene.

30 Figure 42 shows a drawing of the structure of and SNP position in the alcohol dehydrogenase 2 (ADH2) gene.

Figure 43 shows a drawing of the structure of and SNP position in the alcohol dehydrogenase 3 (ADH3) gene.

Figure 44 shows a drawing of the structure of and SNP position in the alcohol dehydrogenase 6 (ADH6) gene.

5 Figure 45 shows a drawing of the structure of and SNP position in the alcohol dehydrogenase 7 (ADH7) gene.

Figure 46 shows a drawing of the structure of and SNP position in the short-chained alcohol dehydrogenase family (HEP27) gene.

10 Figure 47 shows a drawing of the structure of and SNP position in the L1 intracellular adhesion molecule (L1CAM) gene.

Figure 48 shows a drawing of the structure of and SNP position in the arylalkylamine-N-acetyltransferase (AANAT) gene.

Figure 49 shows a drawing of the structure of and SNP position in the N-actyltransferase homologue (ARD1) gene of *Saccharomyces cerevisiae*.

15 Figure 50 shows a drawing of the structure of and SNP position in the N-actyltransferase 1 (NAT1) gene.

Figure 51 shows a drawing of the structure of and SNP position in the N-actyltransferase 2 (NAT2) gene.

20 Figure 52 shows a drawing of the structure of and SNP position in the granzyme A (GZMA) gene.

Figure 53 shows a drawing of the structure of and SNP position in the granzyme B (GZMB) gene.

Figure 54 shows a drawing of the structure of and SNP position in the esterase D-formylglutathione hydrolase (ESD) gene.

25 Figure 55 shows a drawing of the structure of and SNP position in the dolichyl-diphosphooligosaccharide-protein glycosyltransferase (DDOST) gene.

Figure 56 shows a drawing of the structure of and SNP position in the microsomal glutathione-S-transferase (MGST1) gene.

30 Figure 57 shows a drawing of the structure of and SNP position in the alcohol dehydrogenase 5 (ADH5) gene.

Figure 58 shows a drawing of the structure of and SNP position in the glutathione-S-transferase M1 (GSTM1) gene.

Figure 59 shows a drawing of the structure of and SNP position in the glutathione-S-transferase M2 (GSTM2) gene.

5 Figure 60 shows a drawing of the structure of and SNP position in the glutathione-S-transferase M4 (GSTM4) gene.

Figure 61 shows a drawing of the structure of and SNP position in the glutathione-S-transferase Z1 (GSTZ1) gene.

10 Figure 62 shows a drawing of the structure of and SNP position in the glutathione-S-transferase P (GSTZPi) gene.

Figure 63 shows a drawing of the structure of and SNP position in the glutathione-S-transferase q1 (GSTT1) gene.

Figure 64 shows a drawing of the structure of and SNP position in the microsomal glutathione-S-transferase 1L1 (MGST1L1) gene.

15 Figure 65 shows a drawing of the structure of and SNP position in the microsomal glutathione-S-transferase 2 (MGST2) gene.

Figure 66 shows a drawing of the structure of and SNP position in the microsomal glutathione-S-transferase 3 (MGST3) gene.

20 Figure 67 shows a drawing of the structure of and SNP position in the glutathione-S-transferase A1 (GSTA1) gene.

Figure 68 shows a drawing of the structure of and SNP position in the glutathione-S-transferase A4 (GSTA4) gene.

Figure 69 shows a drawing of the structure of and SNP position in the NADH-ubiquinone oxide reductase 1a subcomplex 1 (NDUFA1) gene.

25 Figure 70 shows a drawing of the structure of and SNP position in the NADH-ubiquinone oxide reductase 1a subcomplex 2 (NDUFA2) gene.

Figure 71 shows a drawing of the structure of and SNP position in the NADH-ubiquinone oxide reductase 1a subcomplex 3 (NDUFA3) gene.

30 Figure 72 shows a drawing of the structure of and SNP position in the NADH-ubiquinone oxide reductase 1a subcomplex 5 (NDUFA5) gene.

Figure 73 shows a drawing of the structure of and SNP position in the NADH-ubiquinone oxidoreductase 1a subcomplex 6 (NDUFA6) gene.

Figure 74 shows a drawing of the structure of and SNP position in the NADH-ubiquinone oxidoreductase 1a subcomplex 7 (NDUFA7) gene.

5 Figure 75 shows a drawing of the structure of and SNP position in the NADH-ubiquinone oxidoreductase 1a subcomplex 8 (NDUFA8) gene.

Figure 76 shows a drawing of the structure of and SNP position in the NADH-ubiquinone oxidoreductase 1a/b subcomplex 1 (NDUFAB1) gene.

10 Figure 77 shows a drawing of the structure of and SNP position in the NADH-ubiquinone oxidoreductase 1a subcomplex 9 (NDUFA9) gene.

Figure 78 shows a drawing of the structure of and SNP position in the NADH-ubiquinone oxidoreductase Fe-S protein 1 (NDUFS1) gene.

Figure 79 shows a drawing of the structure of and SNP position in the NADH-ubiquinone oxidoreductase Fe-S protein 3 (NDUFS3) gene.

15 Figure 80 shows a drawing of the structure of and SNP position in the NADH-ubiquinone oxidoreductase Fe-S protein 4 (NDUFS4) gene.

Figure 81 shows a drawing of the structure of and SNP position in the NADH-ubiquinone oxidoreductase Fe-S protein 5 (NDUFS5) gene.

20 Figure 82 shows a drawing of the structure of and SNP position in the NADH-ubiquinone oxidoreductase Fe-S protein 6 (NDUFS6) gene.

Figure 83 shows a drawing of the structure of and SNP position in the NADH-ubiquinone oxidoreductase Fe-S protein 8 (NDUFS8) gene.

Figure 84 shows a drawing of the structure of and SNP position in the NADH-ubiquinone oxidoreductase 1b subcomplex 3 (NDUFB3) gene.

25 Figure 85 shows a drawing of the structure of and SNP position in the NADH-ubiquinone oxidoreductase 1b subcomplex 5 (NDUFB5) gene.

Figure 86 shows a drawing of the structure of and SNP position in the NADH-ubiquinone oxidoreductase 1b subcomplex 7 (NDUFB7) gene.

30 Figure 87 shows a drawing of the structure of and SNP position in the ATP-binding cassette subfamily A member 1 (ABCA1) gene.

Figure 88 shows a drawing of the structure of and SNP position in the catechol-O-methyltransferase (COMT) gene.

Figure 89 shows a drawing of the structure of and SNP position in the vitamin-N-transferase (HNMT) gene.

5 Figure 90 shows a drawing of the structure of and SNP position in the cytochrome P450 subfamily 1 (aromatic compound-induced) polypeptide 1 (CYP1A1) gene.

Figure 91 shows a drawing of the structure of and SNP position in the cytochrome P450 subfamily 1 (aromatic compound-induced) polypeptide 2 (CYP1A2) gene.

10 Figure 92 shows a drawing of the structure of and SNP position in the cytochrome P450 subfamily 1 (dioxin-induced) polypeptide 1 (CYP1B1) gene.

Figure 93 shows a drawing of the structure of and SNP position in the arylacetamide deacylase (AADAC) gene.

Figure 94 shows a drawing of the structure of and SNP position in the neuropathy target esterase (NTE) gene.

15 Figure 95 shows a drawing of the structure of and SNP position in the ATP-binding cassette subfamily C (CFTR/MRP) member 2 (MRP2) gene.

Figure 96 shows a drawing of the structure of and SNP position in the ATP-binding cassette subfamily B member 1 (ABCB1) gene.

20 Figure 97 shows a drawing of the structure of and SNP position in the ATP-binding cassette subfamily B member 3 (ABCB3) gene.

Figure 98 shows a drawing of the structure of and SNP position in the ATP-binding cassette subfamily B member 7 (ABCB7) gene.

Figure 99 shows a drawing of the structure of and SNP position in the ATP-binding cassette subfamily B member 8 (ABCB8) gene.

25 Figure 100 shows a drawing of the structure of and SNP position in the ATP-binding cassette subfamily B member 9 (ABCB9) gene.

Figure 101 shows a drawing of the structure of and SNP position in the ATP-binding cassette subfamily B member 10 (ABCB10) gene.

30 Figure 102 shows a drawing of the structure of and SNP position in the ATP-binding cassette subfamily B member 11 (ABCB11) gene.

Figure 103 shows a drawing of the structure of and SNP position in the cytochrome P450 subfamily IVB polypeptide 1 (CYP4B1) gene.

Figure 104 shows a drawing of the structure of and SNP position in the cytochrome P450 subfamily XXVIIA polypeptide 1 (CYP27A1) gene.

5 Figure 105 shows a drawing of the structure of and SNP position in the cytochrome P450 subfamily IVF polypeptide 1 (CYP4F2) gene.

Figure 106 shows a drawing of the structure of and SNP position in the cytochrome P450 subfamily 4F polypeptide 3 (CYP4F3) gene.

10 Figure 107 shows a drawing of the structure of and SNP position in the cytochrome P450 subfamily 4F polypeptide 8 (CYP4F8) gene.

Figure 108 shows a drawing of the structure of and SNP position in the aldehyde dehydrogenase 1 (ALDH1) gene.

Figure 109 shows a drawing of the structure of and SNP position in the aldehyde dehydrogenase 2 (ALDH2) gene.

15 Figure 110 shows a drawing of the structure of and SNP position in the aldehyde dehydrogenase 7 (ALDH7) gene.

Figure 111 shows a drawing of the structure of and SNP position in the aldehyde dehydrogenase 8 (ALDH8) gene.

20 Figure 112 shows a drawing of the structure of and SNP position in the aldehyde dehydrogenase 9 (ALDH9) gene.

Figure 113 shows a drawing of the structure of and SNP position in the aldehyde dehydrogenase 10 (ALDH10) gene.

Figure 114 shows a drawing of the structure of and SNP position in the ATP-binding cassette subfamily C member 7 (ABCC7) gene.

25 Figure 115 shows a drawing of the structure of and SNP position in the ATP-binding cassette subfamily C member 8 (ABCC8) gene.

Figure 116 shows a drawing of the structure of and SNP position in the ATP-binding cassette subfamily C member 9 (ABCC9) gene.

30 Figure 117 shows a drawing of the structure of and SNP position in the carboxylesterase 1 (CES1) gene.

Figure 118 shows a drawing of the structure of and SNP position in the ATP-binding cassette subfamily A member 4 (ABCC4) gene.

Figure 119 shows a drawing of the structure of and SNP position in the ATP-binding cassette subfamily A member 7 (ABCC7) gene.

5 Figure 120 shows a drawing of the structure of and SNP position in the ATP-binding cassette subfamily G member 1 (ABCG1) gene.

Figure 121 shows a drawing of the structure of and SNP position in the ATP-binding cassette subfamily G member 2 (ABCG2) gene.

10 Figure 122 shows a drawing of the structure of and SNP position in the ATP-binding cassette subfamily G member 4 (ABCG4) gene.

Figure 123 shows a drawing of the structure of and SNP position in the ATP-binding cassette subfamily E member 1 (ABCE1) gene.

Figure 124 shows a drawing of the structure of and SNP position in the carbohydrate sulfotransferase 1 (CHST1) gene.

15 Figure 125 shows a drawing of the structure of and SNP position in the carbohydrate sulfotransferase 3 (CHST3) gene.

Figure 126 shows a drawing of the structure of and SNP position in the NADH: ubiquinone dehydrogenase flavoprotein 1 (NDUFV1) gene.

20 Figure 127 shows a drawing of the structure of and SNP position in the NADH: ubiquinone dehydrogenase flavoprotein 2 (NDUFV2) gene.

Figure 128 shows a drawing of the structure of and SNP position in the NADH: ubiquinone dehydrogenase flavoprotein 3 (NDUFV3) gene.

Figure 129 shows a drawing of the structure of and SNP position in the NADH: ubiquinone oxide reductase A10 (NDUFA10) gene.

25 Figure 130 shows a drawing of the structure of and SNP position in the high-mobility group protein 17-like 1 (HMG17L1) gene.

Figure 131 shows a drawing of the structure of and SNP position in the UDP glycoxyl transferase 2 family polypeptide A1 (UGT2A1) gene.

30 Figure 132 shows a drawing of the structure of and SNP position in the human organic anion transporter polypeptide 1 (hOATP1) gene.

Figure 133 shows a drawing of the structure of and SNP position in the human organic anion transporter polypeptide 2 (hOATP2) gene.

Figure 134 shows a drawing of the structure of and SNP position in the human organic anion transporter polypeptide 8 (hOATP8) gene.

5 Figure 135 shows a drawing of the structure of and SNP position in the human organic anion transporter 1 (hOAT1) gene.

Figure 136 shows a drawing of the structure of and SNP position in the human organic anion transporter 2 (hOAT2) gene.

10 Figure 137 shows a drawing of the structure of and SNP position in the human organic anion transporter 3 (hOAT3) gene.

Figure 138 shows a drawing of the structure of and SNP position in the aldehyde dehydrogenase 1 family member A2 (ALDH1A2) gene.

Figure 139 shows a drawing of the structure of and SNP position in the aldehyde dehydrogenase 1 family member A3 (ALDH1A3) gene.

15 Figure 140 shows a drawing of the structure of and SNP position in the formyltetrahydroforate dehydrogenase (FTHFD/ALDH1L1) gene.

Figure 141 shows a drawing of the structure of and SNP position in the cytochrome P450 subfamily IIIA (aromatic compound-induced) polypeptide 4 (CYP3A4) gene.

20 Figure 142 shows graph of the results of typing performed on two different groups of subjects using the INVADER assay method.

Figure 143 shows a summary of genetic information.

Figure 144A shows a structure of ATP-binding cassette subfamily A member 1 (ABCA1) gene and the SNP location therein.

25 Accession No.: AF275948.1 and AL359846.11

Figure 144B shows a structure of ATP-binding cassette subfamily A member 1 (ABCA1) gene and the SNP location therein. (continuation of Figure 144A)

Accession No.: AF275948.1 and AL359846.11

30 Figure 145 shows a structure of ATP-binding cassette subfamily A member 4 (ABCA4) gene and the SNP location therein.

Accession No.: NT_019258.1

Figure 146 shows a structure of ATP-binding cassette subfamily A member 7 (ABCA7) gene and the SNP location therein.

Accession No.: NT_025194.1

5 Figure 147 shows a structure of ATP-binding cassette subfamily A member 8 (ABCA8) gene and the SNP location therein.

Accession No.: AC005922.1 and AC015844.5

Figure 148 shows a structure of ATP-binding cassette subfamily B member 1 (ABCB1) gene and the SNP location therein.

10 Accession No.: AC002457.1 and AC005068.1

Figure 149 shows a structure of ATP-binding cassette subfamily B member 4 (ABCB4) gene and the SNP location therein.

Accession No.: AC079591.1, AC079303.3 and AC005045.2

15 Figure 150 shows a structure of ATP-binding cassette subfamily B member 7 (ABCB7) gene and the SNP location therein.

Accession No.: AL360179.3 and AC002417.1

Figure 151 shows a structure of ATP-binding cassette subfamily B member 8 (ABCB8) gene and the SNP location therein.

Accession No.: AC010973.4

20 Figure 152 shows a structure of ATP-binding cassette subfamily B member 9 (ABCB9) gene and the SNP location therein.

Accession No.: AC026362.9 and AC073857.10

Figure 153 shows a structure of ATP-binding cassette subfamily B member 10 (ABCB10) gene and the SNP location therein.

25 Accession No.: AL121990.9

Figure 154 shows a structure of ATP-binding cassette subfamily B member 11 (ABCB11) gene and the SNP location therein.

Accession No.: AC008177.3 and AC069137.3

30 Figure 155 shows a structure of ATP-binding cassette subfamily C member 1 (ABCC1) gene and the SNP location therein.

Accession No.: AC026452.5 and AC025778.4

Figure 156 shows a structure of ATP-binding cassette subfamily C member 2 (ABCC2) gene and the SNP location therein.

Accession No.: AL392107.4

5 Figure 157 shows a structure of ATP-binding cassette subfamily C member 3 (ABCC3) gene and the SNP location therein.

Accession No.: AC004590.1 and AC005921.3

Figure 158A shows a structure of ATP-binding cassette subfamily C member 4 (ABCC4) gene and the SNP location therein.

10 Accession No.: AL356257.11, AL157818.12 and AL139381.12

Figure 158B shows a structure of ATP-binding cassette subfamily C member 4 (ABCC4) gene and the SNP location therein. (continuation of Figure 158A)

Accession No.: AL356257.11, AL157818.12, and AL139381.12

15 Figure 159 shows a structure of ATP-binding cassette subfamily C member 5 (ABCC5) gene and the SNP location therein.

Accession No.: AC068644.5

Figure 160 shows a structure of ATP-binding cassette subfamily C member 7 (ABCC7) gene and the SNP location therein.

Accession No.: AC000111.1 and AC000061.1

20 Figure 161 shows a structure of ATP-binding cassette subfamily C member 8 (ABCC8) gene and the SNP location therein.

Accession No.: AC000406.1

Figure 162 shows a structure of ATP-binding cassette subfamily C member 9 (ABCC9) gene and the SNP location therein.

25 Accession No.: AC084806.9 and AC008250.23

Figure 163 shows a structure of ATP-binding cassette subfamily D member 1 (ABCD1) gene and the SNP location therein.

Accession No.: U52111.2

30 Figure 164 shows a structure of ATP-binding cassette subfamily D member 3 (ABCD3) gene and the SNP location therein.

Accession No.: NT_019284.3

Figure 165 shows a structure of ATP-binding cassette subfamily D member 4 (ABCD4) gene and the SNP location therein.

Accession No.: AC005519.3

5 Figure 166 shows a structure of ATP-binding cassette subfamily G member 1 (ABCG1) gene and the SNP location therein.

Accession No.: AP001746.1

Figure 167 shows a structure of ATP-binding cassette subfamily G member 2 (ABCG2) gene and the SNP location therein.

10 Accession No.: NT_022959.2

Figure 168 shows a structure of ATP-binding cassette subfamily G member 4 (ABCG4) gene and the SNP location therein.

Accession No.: AP001315.3

15 Figure 169 shows a structure of ATP-binding cassette subfamily G member 5 (ABCG5) gene and the SNP location therein.

Accession No.: AC084265.2 and AC011242.8

Figure 170 shows a structure of ATP-binding cassette subfamily G member 8 (ABCG8) gene and the SNP location therein.

Accession No.: AC084265.2

20 Figure 171 shows a structure of ATP-binding cassette subfamily E member 1 (ABCE1) gene and the SNP location therein.

Accession No.: NT_006296.2

Figure 172 shows a structure of ATP-binding cassette subfamily F member 1 (ABCF1) gene and the SNP location therein.

25 Accession No.: NT_007592.3

Figure 173 shows a structure of organic anion transporter 1 (OAT1) gene and the SNP location therein.

Accession No.: AP001858.3, AJ249369.1, and AP000438.4

30 Figure 174 shows a structure of organic anion transporter 2 (OAT2) gene and the SNP location therein.

Accession No.: AC26532.3

Figure 175 shows a structure of organic anion transporter 3 (OAT3) gene and the SNP location therein.

Accession No.: AP001858.3

5 Figure 176 shows a structure of organic anion transporter polypeptide 1 (OATP1) gene and the SNP location therein.

Accession No.: AC022224.22

Figure 177 shows a structure of organic anion transporter polypeptide 2 (OATP2) gene and the SNP location therein.

10 Accession No.: NT_024399.2

Figure 178 shows a structure of organic anion transporter polypeptide 8 (OATP8) gene and the SNP location therein.

Accession No.: NT_024399.2

15 Figure 179 shows a structure of transporter 1 ATP-binding cassette subfamily B (TAP1) gene and the SNP location therein.

Accession No.: X66401.1

Figure 180 shows a structure of transporter 2 ATP-binding cassette subfamily B (TAP2) gene and the SNP location therein.

Accession No.: X66401.1

20 Figure 181 shows a structure of SLC22A4 solute carrier family 22 (organic cation transporter) member 4 (OCTN1) gene and the SNP location therein.

Accession No.: AC008599.6

Figure 182 shows a structure of SLC22A5 solute carrier family 22 (organic cation transporter) member 5 (OCTN2) gene and the SNP location therein.

25 Accession No.: AC023861.3

Figure 183 shows a structure of SLC22A1 solute carrier family 22 (organic cation transporter) member 1 (OCT1) gene and the SNP location therein.

Accession No.: AL35625.5

30 Figure 184 shows a structure of SLC22A2 solute carrier family 22 (organic cation transporter) member 2 (OCT2) gene and the SNP location therein.

Accession No.: AL162582.18

Figure 185 shows a structure of SLC10A2 solute carrier family 10 (sodium/bile acid cotransporter family) member 2 (NTCP) gene and the SNP location therein.

Accession No.: AL157789.6

5 Figure 186 shows a structure of SLC15A1 solute carrier family 15 (oligopeptide transporter) member 1 (PEPT1) gene and the SNP location therein.

Accession No.: AL353574.8 and AL391670.6

Figure 187 shows a structure of microsomal epoxide hydrolase 1 (EPHX1) gene and the SNP location therein.

10 Accession No.: AC058782.8

Figure 188 shows a structure of cytoplasmic epoxide hydrolase (EPHX2) gene and the SNP location therein.

Accession No.: AC010856.3

15 Figure 189 shows a structure of catechol-O-methyl transferase (COMT) gene and the SNP location therein.

Accession No.: AC000080.2

Figure 190 shows a structure of guanidinoacetate N-methyl transferase (GAMT) gene and the SNP location therein.

Accession No.: NT_000879.1

20 Figure 191 shows a structure of phenyl ethanolamine N-methyl transferase (PNMT) gene and the SNP location therein.

Accession No.: AC040933.3

Figure 192 shows a structure of histamine N-methyl transferase (HNMT) gene and the SNP location therein.

25 Accession No.: AC019304.3

Figure 193 shows a structure of nicotinamide N-methyl transferase (NNMT) gene and the SNP location therein.

Accession No.: AC019290.3

30 Figure 194 shows a structure of phosphatidylethanolamine N-methyl transferase (PEMT) gene and the SNP location therein.

Accession No.: AC020558.3

Figure 195 shows a structure of aldehyde dehydrogenase 1 family member A1 (ALDH1A1) gene and the SNP location therein.

Accession No.: AC009284.2 and AL162416.3

5 Figure 196 shows a structure of aldehyde dehydrogenase 1 family member A2 (ALDH1A2) gene and the SNP location therein.

Accession No.: AC025431.7 and AC012653.8

Figure 197 shows a structure of aldehyde dehydrogenase 1 family member A3 (ALDH1A3) gene and the SNP location therein.

10 Accession No.: AC015712.7

Figure 198 shows a structure of aldehyde dehydrogenase 1 family member B1 (ALDH1B1) gene and the SNP location therein.

Accession No.: AL135785.9

15 Figure 199A shows a structure of formyl tetrahydrofolate dehydrogenase (ALDH1L1) gene and the SNP location therein.

Accession No.: AC079848.6

Figure 199B shows a structure of formyl tetrahydrofolate dehydrogenase (ALDH1L1) gene and the SNP location therein. (continuation of Figure 199A)

Accession No.: AC079848.6

20 Figure 200 shows a structure of aldehyde dehydrogenase 2 (ALDH2) gene and the SNP location therein.

Accession No.: AC002996.1 and AC003029.2

Figure 201 shows a structure of aldehyde dehydrogenase 3 family member A1 (ALDH3A1) gene and the SNP location therein.

25 Accession No.: AC005722.1

Figure 202 shows a structure of aldehyde dehydrogenase 3 family member A2 (ALDH3A2) gene and the SNP location therein.

Accession No.: AC005722.1

30 Figure 203 shows a structure of aldehyde dehydrogenase 3 family member B1 (ALDH3B1) gene and the SNP location therein.

Accession No.: AC004923.2

Figure 204 shows a structure of aldehyde dehydrogenase 3 family member B2 (ALDH3B2) gene and the SNP location therein.

Accession No.: AC021987.3

5 Figure 205 shows a structure of aldehyde dehydrogenase 5 family member A1 (ALDH5A1) gene and the SNP location therein.

Accession No.: AL031230.1

Figure 206 shows a structure of aldehyde dehydrogenase 6 family member A1 (ALDH6A1) gene and the SNP location therein.

10 Accession No.: AC005484.2

Figure 207 shows a structure of aldehyde dehydrogenase 8 family member A1 (ALDH8A1) gene and the SNP location therein.

Accession No.: AL445190.9 and AL021939.1

15 Figure 208 shows a structure of aldehyde dehydrogenase 9 family member A1 (ALDH9A1) gene and the SNP location therein.

Accession No.: AL451074.4

Figure 209 shows a structure of alcohol dehydrogenase 1 (ADH1) gene and the SNP location therein.

Accession No.: AP002027.1

20 Figure 210 shows a structure of alcohol dehydrogenase 2 (ADH2) gene and the SNP location therein.

Accession No.: AP002027.1

Figure 211 shows a structure of alcohol dehydrogenase 3 (ADH3) gene and the SNP location therein.

25 Accession No.: AP002027.1

Figure 212 shows a structure of alcohol dehydrogenase 4 (ADH4) gene and the SNP location therein.

Accession No.: AP002026.1

30 Figure 213 shows a structure of alcohol dehydrogenase 5 (ADH5) gene and the SNP location therein.

Accession No.: AC019131.4

Figure 214 shows a structure of alcohol dehydrogenase 6 (ADH6) gene and the SNP location therein.

Accession No.: AP002026.1

5 Figure 215 shows a structure of alcohol dehydrogenase 7 (ADH7) gene and the SNP location therein.

Accession No.: AC027065.3

Figure 216 shows a structure of short-chain alcohol dehydrogenase family gene (HEP27) and the SNP location therein.

10 Accession No.: AL135999.3

Figure 217 shows a structure of UDP glycosyltransferase 1 family polypeptide A1 (UGT1A1) and the SNP location therein.

Accession No.: AC006985.2

15 Figure 218 shows a structure of UDP glycosyltransferase 2 family polypeptide A1 (UGT2A1) and the SNP location therein.

Accession No.: AC011254.3

Figure 219 shows a structure of UDP glycosyltransferase 2 family polypeptide B15 (UGT2B15) and the SNP location therein.

Accession No.: AC019173.4

20 Figure 220 shows a structure of UDP glycosyltransferase 8 (UGT8) and the SNP location therein.

Accession No.: U31353.1

Figure 221 shows a structure of glutathione S transferase A1 (GSTA1) gene and the SNP location therein.

25 Accession No.: AC021133.4

Figure 222 shows a structure of glutathione S transferase A4 (GSTA4) gene and the SNP location therein.

Accession No.: AC025085.4

30 Figure 223 shows a structure of glutathione S transferase M1 (GSTM1) gene and the SNP location therein.

Accession No.: AC000032.7

Figure 224 shows a structure of glutathione S transferase M2 (GSTM2) gene and the SNP location therein.

Accession No.: AC000031.5

5 Figure 225 shows a structure of glutathione S transferase Z1 (GSTZ1) gene and the SNP location therein.

Accession No.: AC007954.7

Figure 226 shows a structure of glutathione S transferase Pi (GSTPi) gene and the SNP location therein.

10 Accession No.: X08058.1 and M24485.1

Figure 227 shows a structure of glutathione S transferase T1 (GSTT1) gene and the SNP location therein.

Accession No.: AF240786.1 and AP000351.3

15 Figure 228 shows a structure of microsomal glutathione S transferase 1 (MGST1) gene and the SNP location therein.

Accession No.: AC007528.5

Figure 229 shows a structure of microsomal glutathione S transferase 1-like 1 (MGST1L1) gene and the SNP location therein.

Accession No.: AC007936.2

20 Figure 230 shows a structure of microsomal glutathione S transferase T2 (MGST2) gene and the SNP location therein.

Accession No.: AC019049.4

Figure 231 shows a structure of microsomal glutathione S transferase T3 (MGST3) gene and the SNP location therein.

25 Accession No.: AC064827.2

Figure 232 shows a structure of sulfotransferase 1A1 (SULT1A1/STP1) gene and the SNP location therein.

Accession No.: U52852.2

30 Figure 233 shows a structure of sulfotransferase 1A2 (SULT1A2/STP2) gene and the SNP location therein.

Accession No.: U33886.1, U34804.1 and AC020765.5

Figure 234 shows a structure of sulfotransferase 1A3 (SULT1A3/STM/HAST) gene and the SNP location therein

Accession No.: L34160.1 and AC012645.4

5 Figure 235 shows a structure of sulfotransferase 1C1 (SULT1C1) gene and the SNP location therein.

Accession No.: AC019100.4

Figure 236 shows a structure of sulfotransferase 1C2 (SULT1C2) gene and the SNP location therein.

10 Accession No.: AF186263.1

Figure 237 shows a structure of sulfotransferase 2A1 (SULT2A1) gene and the SNP location therein.

Accession No.: AC024582.4, AC008745.5, NT_011190.1, and AC024582.4

15 Figure 238 shows a structure of sulfotransferase 2B1 (SULT2B1) gene and the SNP location therein.

Accession No.: AC040922.2 and AC008403.6

Figure 239 shows a structure of sulfotransferase-associated protein 3 (SULTX3) gene and the SNP location therein.

Accession No.: Z97055.1

20 Figure 240 shows a structure of tyrosyl protein sulfotransferase 1 (TPST1) gene and the SNP location therein.

Accession No.: AC026281.5

Figure 241 shows a structure of tyrosyl protein sulfotransferase 2 (TPST2) gene and the SNP location therein.

25 Accession No.: Z95115.1

Figure 242 shows a structure of cerebroside sulfotransferase (CST) gene and the SNP location therein.

Accession No.: AC005006.2

30 Figure 243 shows a structure of thyroid hormone sulfotransferase (ST1B2) gene and the SNP location therein.

Accession No.: AC027059.2

Figure 244 shows a structure of carbohydrate sulfotransferase 1 (CHST1) gene and the SNP location therein.

Accession No.: NT_008982.1

5 Figure 245 shows a structure of carbohydrate sulfotransferase 2 (CHST2) gene and the SNP location therein.

Accession No.: AC055737.10

Figure 246 shows a structure of carbohydrate sulfotransferase 3 (CHST3) gene and the SNP location therein.

10 Accession No.: AC073370.3

Figure 247 shows a structure of carbohydrate sulfotransferase 4 (CHST4) gene and the SNP location therein.

Accession No.: AC010547.5

15 Figure 248 shows a structure of carbohydrate sulfotransferase 5 (CHST5) gene and the SNP location therein.

Accession No.: AC025287.3

Figure 249 shows a structure of HNK-sulfotransferase (HNK-1ST) gene and the SNP location therein.

Accession No.: AC012493.4

20 Figure 250 shows a structure of estrogen sulfotransferase (STE) gene and the SNP location therein.

Accession No.: AC074273.1

Figure 251 shows a structure of NAD (P)H: quinone oxidoreductase 1 (NQO1) gene and the SNP location therein.

25 Accession No.: M81596.1

Figure 252 shows a structure of NRH: quinone oxidoreductase 2 (NQO2) gene and the SNP location therein.

Accession No.: AB050248.1

30 Figure 253 shows a structure of p53-inducible gene 3 (PIG3) in a quinone oxidoreductase homolog and the SNP location therein.

Accession No.: AC008073.3

Figure 254 shows a structure of NADH-dehydrogenase(ubiquinone)1 α -subcomplex 1 (NDUFA1) gene and the SNP location therein.

Accession No.: AC002477.1

5 Figure 255 shows a structure of NADH-dehydrogenase(ubiquinone)1 α -subcomplex 2 (NDUFA2) gene and the SNP location therein.

Accession No.: AB054976.1

Figure 256 shows a structure of NADH-dehydrogenase(ubiquinone)1 α -subcomplex 3 (NDUFA3) gene and the SNP location therein.

10 Accession No.: AC009968.6

Figure 257 shows a structure of NADH-dehydrogenase(ubiquinone)1 α -subcomplex 5 (NDUFA5) gene and the SNP location therein.

Accession No.: AC073323.5

15 Figure 258 shows a structure of NADH-dehydrogenase(ubiquinone)1 α -subcomplex 6 (NDUFA6) gene and the SNP location therein.

Accession No.: AL021878.1

Figure 259 shows a structure of NADH-dehydrogenase(ubiquinone)1 α -subcomplex 7 (NDUFA7) gene and the SNP location therein.

Accession No.: AC010323.6

20 Figure 260 shows a structure of NADH-dehydrogenase(ubiquinone)1 α -subcomplex 8 (NDUFA8) gene and the SNP location therein.

Accession No.: AL162423.10

Figure 261 shows a structure of NADH-dehydrogenase(ubiquinone)1 α -subcomplex 9 (NDUFA9) gene and the SNP location therein.

25 Accession No.: AC005832.1

Figure 262 shows a structure of NADH-dehydrogenase(ubiquinone)1 α -subcomplex 10 (NDUFA10) gene and the SNP location therein.

Accession No.: AC013469.8

30 Figure 263 shows a structure of NADH-dehydrogenase(ubiquinone)1 α / β -subcomplex 1 (NDUFAB1) gene and the SNP location therein.

Accession No.: AC008870.6

Figure 264 shows a structure of NADH-dehydrogenase(ubiquinone)1 β -subcomplex 3 (NDUFB3) gene and the SNP location therein.

Accession No.: AC007272.3

5 Figure 265 shows a structure of NADH-dehydrogenase(ubiquinone)1 β -subcomplex 5 (NDUFB5) gene and the SNP location therein.

Accession No.: AC068361.2

Figure 266 shows a structure of NADH-dehydrogenase(ubiquinone)1 β -subcomplex 7 (NDUFB7) gene and the SNP location therein.

10 Accession No.: AC010527.4

Figure 267 shows a structure of NADH-dehydrogenase(ubiquinone)Fe-S protein 1 (NDUFS1) gene and the SNP location therein.

Accession No.: AC007383.4

15 Figure 268 shows a structure of NADH-dehydrogenase(ubiquinone)Fe-S protein 3 (NDUFS3) gene and the SNP location therein.

Accession No.: AC067943.4

Figure 269 shows a structure of NADH-dehydrogenase(ubiquinone)Fe-S protein 4 (NDUFS4) gene and the SNP location therein.

Accession No.: AC024569.3

20 Figure 270 shows a structure of NADH-dehydrogenase(ubiquinone)Fe-S protein 5 (NDUFS5) gene and the SNP location therein.

Accession No.: AL139015.5

Figure 271 shows a structure of NADH-dehydrogenase(ubiquinone)Fe-S protein 6 (NDUFS6) gene and the SNP location therein.

25 Accession No.: AC026443.2

Figure 272 shows a structure of NADH-dehydrogenase(ubiquinone)Fe-S protein 8 (NDUFS8) gene and the SNP location therein.

Accession No.: AC034259.2

30 Figure 273 shows a structure of NADH-dehydrogenase(ubiquinone)flavoprotein 1 (NDUFV1) gene and the SNP location therein.

Accession No.: NT_009304.2

Figure 274 shows a structure of NADH-dehydrogenase(ubiquinone)flavoprotein 2 (NDUFV2) gene and the SNP location therein.

Accession No.: NT_011024.2

5 Figure 275 shows a structure of NADH-dehydrogenase(ubiquinone)flavoprotein 3 (NDUFV3) gene and the SNP location therein.

Accession No.: AP001748.1

Figure 276 shows a structure of gamma-glutamyl transferase 1 (GGT1) gene and the SNP location therein.

10 Accession No.: D87002.1

Figure 277 shows a structure of transglutaminase 1 (TGM1) gene and the SNP location therein.

Accession No.: M98447.1

15 Figure 278 shows a structure of cytochrome P450 subfamily 1 (aromatic compound-inducible) polypeptide 1 (CYP1A1) gene and the SNP location therein.

Accession No.: X04300.1 and AC020705.4

Figure 279 shows a structure of cytochrome P450 subfamily 1 (aromatic compound-inducible) polypeptide 2 (CYP1A2) gene and the SNP location therein.

Accession No.: AC020705.4

20 Figure 280 shows a structure of cytochrome P450 subfamily 1 (dioxin-inducible) polypeptide 1 (CYP1B1) gene and the SNP location therein.

Accession No.: AC009229.4

Figure 281 shows a structure of cytochrome P450 subfamily 3A (aromatic compound-inducible) polypeptide 4 (CYP3A4) gene and the SNP location therein.

25 Accession No.: AF280107.1

Figure 282 shows a structure of cytochrome P450 subfamily 3A (aromatic compound-inducible) polypeptide 5 (CYP3A5) gene and the SNP location therein.

Accession No.: AC005020.5

30 Figure 283 shows a structure of cytochrome P450 subfamily 3A polypeptide 7 (CYP3A7) gene and the SNP location therein.

Accession No.: AF280107.1

Figure 284 shows a structure of cytochrome P450 polypeptide 43 (CYP3A43) gene and the SNP location therein.

Accession No.: AC011904.3

5 Figure 285 shows a structure of cytochrome P450 subfamily IVB polypeptide 1 (CYP4B1) gene and the SNP location therein.

Accession No.: AL356793.10

Figure 286 shows a structure of cytochrome P450 subfamily IVF polypeptide 2 (CYP4F2) gene and the SNP location therein.

10 Accession No.: AC005336.1

Figure 287 shows a structure of cytochrome P450 subfamily IVF polypeptide 3 (CYP4F3) gene and the SNP location therein.

Accession No.: AD000685.1

15 Figure 288 shows a structure of cytochrome P450 subfamily IVF polypeptide 8 (CYP4F8) gene and the SNP location therein.

Accession No.: AC068845.3

Figure 289 shows a structure of cytochrome P450 subfamily XXVIA polypeptide 1 (CYP27A1) gene and the SNP location therein.

Accession No.: AC009974.7

20 Figure 290 shows a structure of cytochrome P450 subfamily XXVIIB polypeptide 1 (CYP27B1) gene and the SNP location therein.

Accession No.: AC025165.27

Figure 291 shows a structure of allylacetamide deacetylase (AADAC) gene and the SNP location therein.

25 Accession No.: AC068647.4

Figure 292 shows a structure of carboxyl esterase 1 (CES1) gene and the SNP location therein

Accession No.: AC007602.4

30 Figure 293 shows a structure of carboxyl esterase 2 (CES2) gene and the SNP location therein

Accession No.: AC027131.4

Figure 294 shows a structure of granzyme A (GZMA) gene and the SNP location therein.

Accession No.: AC091977.1

5 Figure 295 shows a structure of granzyme B (GZMB) gene and the SNP location therein.

Accession No.: AL136018.3

Figure 296 shows a structure of esterase D/formylglutathione hydrolase (ESD) gene and the SNP location therein.

10 Accession No.: AL136958.9

Figure 297A shows a structure of carboxyl ester lipase (bile salt-stimulated lipase) (CEL) gene and the SNP location therein.

Accession No.: AL138750.8, AL162417.20 and AF072711.1

15 Figure 297B shows a structure of carboxyl ester lipase (bile salt-stimulated lipase) (CEL) gene and the SNP location therein. (continuation of Figure 297A)

Accession No.: AL138750. , AL162417.20 and AF072711.1

Figure 298 shows a structure of interleukin 17 (cytotoxic T lymphocyte-associated serine esterase 8) (IL17) gene and the SNP location therein.

Accession No.: AL355513.11

20 Figure 299 shows a structure of ubiquitin carboxyl terminal esterase L3 (ubiquitin thiol esterase) (UCHL3) gene and the SNP location therein.

Accession No.: AL137244.28

Figure 300 shows a structure of dolichyl-diphosphooligosaccharide-protein glycosyltransferase (DDOST) gene and the SNP location therein.

25 Accession No.: D89060

Figure 301 shows a structure of neuropathy target esterase (NTE) gene and the SNP location therein.

Accession No.: AC021153

30 Figure 302 shows a structure of L1 cell adhesion molecule (L1CAM) gene and the SNP location therein.

Accession No.: U52112

Figure 303 shows a structure of arylalkylamine N-acetyltransferase (AANAT) gene and the SNP location therein.

Accession No.: U40391

5 Figure 304 shows a structure of N-acetyltransferase homolog (ARD1) gene of *Saccharomyces cerevisiae* and the SNP location therein.

Accession No.: U52112

Figure 305 shows a structure of N-acetyltransferase (NAT1) gene and the SNP location therein.

10 Accession No.: X17059

Figure 306 shows a structure of N-acetyltransferase 2 (NAT2) gene and the SNP location therein.

Accession No.: D10870

15 Figure 307 shows a structure of ATP-binding cassette subfamily B member 2 (ABCB2) gene and the SNP location therein.

Accession No.: X66401

Figure 308 shows a structure of ATP-binding cassette subfamily B member 3 (ABCB3) gene and the SNP location therein.

Accession No.: X66401

20 Figure 309 shows a structure of glutathione S transferase M3 (GSTM3) gene and the SNP location therein.

Accession No.: AF043105.1

Figure 310 shows a structure of glutathione S transferase M4 (GSTM4) gene and the SNP location therein.

25 Accession No.: M96233.1

Figure 311 shows a structure of aldehyde dehydrogenase 7 (ALDH7) gene and the SNP location therein.

Accession No.: AC004923

30 Figure 312 shows a structure of high-mobility group protein 17-like 1 (HMG17L1) gene and the SNP location therein.

Accession No.: Z97055.1

Figure 313 shows a printed representation of submissions from Laboratory for Genotyping, The SNP Research Center, The Institute of Physical and Chemical Research (RIKEN) on the IMS-JST JSNP database website

5

GENERAL DESCRIPTION OF THE INVENTION

The present invention provides a method of analysis of drug metabolizing enzymes by analysis of SNPs associated with their encoding genes. In some embodiments, the method of the present invention can be used in the selection of drugs based on, *e.g.*, particular characteristics of an individual patient or on characteristics of a target disease.

In some embodiments, the present invention provides a method for detecting a genetic polymorphism associated with a DME, wherein an oligonucleotide probe and/or oligonucleotide primer is created so as to include the genetic polymorphism site from genetic polymorphism data in a gene for encoding a drug metabolizing enzyme or so as to include the genetic polymorphism site in an amplified fragment when the gene encoding the drug metabolizing enzyme has been amplified, and wherein at least one genetic polymorphism in a gene for encoding the target drug metabolizing enzyme is detected using the oligonucleotide probe and/or oligonucleotide primer thus obtained.

The present invention further provides methods for evaluating a drug, wherein the effectiveness and safety of a drug metabolized by the drug metabolizing enzyme are evaluated based on the results obtained by the detection method.

In some embodiments, the present invention provides a method for screening a drug, wherein the drug to be used is selected based on the results obtained in the evaluation method. In other embodiments, the present invention provides a method for screening a drug, wherein the genetic polymorphism data associated with the gene encoding a DME in a control subject is compared to the genetic polymorphism data associated with the same gene in a test subject, and wherein a drug to be used is selected from the results of an analysis of the effectiveness and/or safety of the drugs metabolized by the drug metabolizing enzyme.

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
PEMT	80	intron 5 - 6636	ttttctctctcaccttttg T/C gttcagaggcagaggtgtgc	5515
PEMT	81	intron 5 - 6448	gttggggccaggtctctgacag G/A accctcgggaccagctcctg	5516
PEMT	82	intron 5 - 5218	ggagccctggctgaagaagc C/G ttacgaccaaggcctggagg	5517
PEMT	83	intron 5 - 4824	ggacaggccgggggttgagc G/A gctgcatgaaggaggagg	5518
PEMT	84	intron 5 - 4249	tcaccagagtgatttctctcg C/A ggcaggtgcctggggtagcc	5519
PEMT	85	intron 5 - 4230	gaggcaggtgcctggggtag C/T cactgggagggtccatgag	5520
PEMT	86	intron 5 - 4182	ggagagtaagggtgggggg G/A cacttaggacagggaagctg	5521
PEMT	87	intron 5 - 3369	ccaggtggggcggtgtgcct G/C tggcctggtgtgtggccag	5522
PEMT	88	intron 5 - 2625	cagggaagctgggcccgtaa C/T gagctgggcttttggccac	5523
PEMT	89	intron 5 - 1200	attattgtgagcatgggaag A/T gcacatttgggtcacacatgt	5524
PEMT	90	intron 6 + 606	gcctggctagacgccaccca A/G tgaccctgatgatggcagca	5525
PEMT	91	intron 6 + 1229	tttggtccaggaagggggac G/A gcagccaggagcgtctggt	5526
PEMT	92	intron 7 + 716	atggagatgtgctcccccg C/G gggtcagaggacctgcggtc	5527
PEMT	93	intron 7 + 1537	ctctgggggagcgataagcc G/A cctccagaggacatcagcca	5528
PEMT	94	intron 7 + 1718	gggcttcacagtgcttgagc T/C ccccgcatgtaggaccca	5529
PEMT	95	intron 7 + 2695	ggctttgggggacctggac C/T catttctagaaacagcctt	5530
PEMT	96	intron 8 + 140	ccagggtctccaggtcagag C/T ggccatggttagcttacaatg	5531
PEMT	97	3'flanking + 179	tacttaggagcgctcagggg C/T tcacctggccatggccatgg	5532
PEMT	98	3'flanking + 394	gatgacactgtcattcctaa A/G tgaatggcctgtgtgctgacc	5533
ALDH1A1	1	intron 1 + 564	cattattttctcagccaagt T/C tgttgccattggagcagatg	5534
ALDH1A1	2	intron 1 + 710	gttctgagagtaactctgaa C/T tttgctgtttcacactgct	5535
ALDH1A1	3	intron 1 - 3868	ccctttttatccagaata C/G agcctaaactcttctctg	5536
ALDH1A1	4	intron 2 + 2933	taagtatgctatactatatt T/C gatagatactatactata	5537
ALDH1A1	5	intron 2 - 1646	caatgtgattaaactgaatgc C/T gcaaatatgcactgtatatg	5538
ALDH1A1	6	exon 3 + 54	caggcttttcagattggatc C/T cgtggcgctactatggatgc	5539
ALDH1A1	7	intron 3 + 157	taggccccttaacattgaac T/G attctcaaatagtaactctgc	5540
ALDH1A1	8	intron 3 + 339	tgagtctcctagatgatat G/A ttaggttttattcaagcattt	5541
ALDH1A1	9	intron 3 + 655	agcagtttagatgagtcagag C/A ataatatagttggggagg	5542
ALDH1A1	10	intron 3 + 735	gaagccaatttaacataaac C/A aataccaagatcaggtttca	5543
ALDH1A1	11	intron 3 + 863	gcaagtatggttaatacaag G/A accattttactcaaatat	5544
ALDH1A1	12	intron 3 + 1757	agatgacaagatttcttcta T/A ttcaaaaattccctagcaca	5545
ALDH1A1	13	intron 5 + 90	ttctctaaacagatggatg C/A ttatgtatttgttaaatgtg	5546
ALDH1A1	14	intron 6 + 213	caggaagccaacacaaagg T/C ttgggtgcaaacagtcact	5547
ALDH1A1	15	intron 6 + 1323	ttttgaattaaattcttata C/T tgaacttttaaacctttta	5548
ALDH1A1	16	intron 7 + 638	gcaaaagaaagtgttggaag C/A atactgtaccatgcacaaaa	5549
ALDH1A1	17	intron 9 + (1462-1463)	aatggaattctatgtttttt (T) gttgtgattattttatctatc	5550
ALDH1A1	17	intron 9 + (1462-1463)	aatggaattctatgtttttt gttgtgattattttatctatc	5551
ALDH1A1	18	intron 9 + 1757	tgatctagaatttagtttct A/G taaatgaatagaatccagtg	5552
ALDH1A1	19	intron 12 - 1383	aatccacttattactctcc T/G gagagcttcaagtcctata	5553
ALDH1A1	20	3'flanking + 40	ttttaagtacaagttttggt T/C acagtgattttcttctgtca	5554
ALDH1A2	1	5'flanking - 716	cagggtatctctattctgagc C/G cgaggcgaggggactcgca	5555
ALDH1A2	2	intron 1 + 314	cggtcccgactgcgcgggg G/Δ aaggcgctcggaacccgttag	5556
ALDH1A2	3	intron 1 + (664-675)	ttttgaactgaagaacttac (T)11-13 ataacgaactgtgacatctt	5557
ALDH1A2	4	intron 1 + 1370	gcattgcagcttagaagtttt A/G ttttatgaggggtctctaac	5558
ALDH1A2	5	intron 1 + 1557	ggtagcttttttcagaattta A/Δ ttgggaagctcttccagttc	5559
ALDH1A2	6	intron 1 + 1934	tcagctcttttagtgagactt C/G taaattttctaaagacaagca	5560
ALDH1A2	7	intron 1 + (1971-1980)	agcatgtgggacaagcagta (T)9-11 aaactgtgaagagcagaagct	5561
ALDH1A2	8	intron 1 + 2295	tactgtaagacaatatgtta T/C tgtttttgtcttgcataac	5562
ALDH1A2	9	intron 1 + 2387	ttgggacccacatagagta C/T tacttaaaataaatgaccag	5563
ALDH1A2	10	intron 1 + 2841	aggaatgtgcttttttaaac T/Δ agatggtgttagtcaaggag	5564
ALDH1A2	11	intron 1 + 3035	gacttttataattttgtata A/G ctgatattataggaatacac	5565
ALDH1A2	12	intron 1 + 3319	aaagagttatgtttttttt T/Δ ctgcatctgatattatattg	5566
ALDH1A2	13	intron 1 + 3474	ttgtctttttattttatcat T/C taaacttctgttttctgggg	5567
ALDH1A2	14	intron 1 + 4186	ccctccaaaccttttaactaa G/C attgtctgttttgggtcataa	5568
ALDH1A2	15	intron 1 + 4222	cataaattgtcagtcacaa C/G catgttaatagaggacttca	5569
ALDH1A2	16	intron 1 + 4254	aggacttcagggtttttttt T/Δ aaatacttttccataactat	5570
ALDH1A2	17	intron 1 + 4397	cccttccactacatgggct A/G tgttaccatgtggaattatc	5571
ALDH1A2	18	intron 1 + 5935	aaactccaggttgcacataga T/C gtttctggtatttttaagtag	5572
ALDH1A2	19	intron 1 + 6206	ttttgaaagccctctagca T/G ttctttaatttctttattga	5573
ALDH1A2	20	intron 1 + 9559	agataaattgatgaattatt C/T actctgtgctgctgatagat	5574
ALDH1A2	21	intron 1 + (9631-9632)	taaaaagaattttctaaaaga (AAGA) ccttttttttgaataactct	5575
ALDH1A2	21	intron 1 + (9631-9632)	taaaaagaattttctaaaaga ccttttttttgaataactct	5576
ALDH1A2	22	intron 1 + 12731	ctgaaatagaaacctttcag T/A gtacctgacagagcagtgaa	5577
ALDH1A2	23	intron 1 + 13442	cagtgctcataaagatccagc G/A gaaatcaaatgtttcatat	5578
ALDH1A2	24	intron 1 + (14173-14176)	tctaaaaaaataaataaaaa AAAA/Δ gagaaaattaagtttaagat	5579
ALDH1A2	25	intron 1 + 14586	actcatttatttggttcaaac C/G cttcttcaaccttaggatag	5580
ALDH1A2	26	intron 1 + 14595	ttgggttcaagaccttcttca A/G ccttaggatatgcattgagg	5581
ALDH1A2	27	intron 1 + 14711	gtttgagacattaacttcta A/G ttaactgaagatgctagtt	5582
ALDH1A2	28	intron 1 + (15327-15337)	gaagagcacagtagaagac (T)9-11 aacctagcaataactattga	5583
ALDH1A2	29	intron 1 + 17258	atcagtcacatgtgttgggc A/G tacaacacttaatttaaat	5584

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ABCB2	1	5'flanking - 673	agctaaagatcaaaagcacc G/C cttttccaccagcctcg	1
ABCB2	2	5'flanking - 646	ccaccagcctcgctgctg T/G tcccttcacggacactctag	2
ABCB2	3	5'flanking - 563	ttgcaagcgttgctgctac A/C ggcgaacctccctgcctccc	3
ABCB2	4	5'flanking - 236	gctttgcgcgcggcctaac G/T tggtagggcgatctgccc	4
ABCB2	5	Intron3 + 408	aaggaaactgaggccaagac C/T ctaaatgctgaactgcaca	5
ABCB2	6	Exon4 + 153	cctccaccatggcaccctg A/G tcaccctgcctctgcttttc	6
ABCB2	7	Intron4 + 289	gtattcttttagcatcaag G/T ggcatagctgtgtcttttc	7
ABCB2	8	Intron4 + 291	attcttttagcatcaagg G/C catagctgtgtctcttttc	8
ABCB2	9	Intron5 - 63	ttccttcaggttaactgct C/T ggttctttgtgtccctcca	9
ABCB2	10	Intron7 - 185	gtctctgccttgctttgc G/T gcttcttctatctctactcc	10
ABCB2	11	3'flanking + 71	agcgcacttttcagctgcgg G/A tgcctctctttttatcatcc	11
ABCB2	12	3'flanking + 129	aaatgcatacaattttccct T/C aagcttttgaattctatga	12
ABCB2	13	3'flanking + 459	cattcagggagggccagg G/A tggagctgcacagtgtgtg	13
ABCB4	1	exon3 + 3	aacacccttattttatagat C/T caatgactgagtcagaatt	14
ABCB4	2	intron3 + 45	cagcatctctactatacca T/C gctctgcttttaaggttctct	15
ABCB4	3	intron3 + 498	actcaaatgggtgtaggag C/T agagacaattcaatcacagac	16
ABCB4	4	intron3 + 515	gagcagagacaattcaatac A/G gacagaagctttagatgaga	17
ABCB4	5	intron6 + 1030	tagttttgccatgtagaatt G/C aaaaagtgatagatggtgt	18
ABCB4	6	intron6 + 1437	tttaagcctgcttcacaa G/A ttgatttattcttcttctta	19
ABCB4	7	intron6 + 2449	ttgacttgcgacactgta G/A cactcttcttcttctgtgt	20
ABCB4	8	intron7 + 451	ccttgctgcacctgtgtgt A/C taagtttgcttattatagt	21
ABCB4	9	intron7 + 530	agtagagacagctgctgct G/C acaccggagcagagatlaactg	22
ABCB4	10	intron7 - 152	aacgaatcatgaatttaag T/C tgttaatgattgaagccct	23
ABCB4	11	exon8 + 40	aggataaattgtttatgtc G/T ctgggtaccatcatggccat	24
ABCB4	12	intron8 + 130	ctggttgactccagatatac T/C agaagggttgtaaaattct	25
ABCB4	13	intron8 + 248	aatacacagggaagctttaa A/G taagtaggaagtcactct	26
ABCB4	14	intron8 + 531	ctaaaggtgaatggattca A/G tacgtcccttggaactcacc	27
ABCB4	15	intron8 + 4240	ctgaggttccagcttattctc T/A tagagctgtttactagtct	28
ABCB4	16	intron8 + 4343	tgtagaagaaaaaaaggtt C/T atattacagagggtctgac	29
ABCB4	17	intron8 + 4677	cccaagatattctcataact G/C tccatagtgcttgggtgcc	30
ABCB4	18	intron9 + 113	tttaccagcttcaactatt A/G ttatcatttttgcctccaaa	31
ABCB4	19	intron9 + 982	tgctctatacagttttgtt T/A taagtttagtaaatgatta	32
ABCB4	20	intron11 + 457	tcacgttgggtgacagagt A/G agactctatctcaaaaaaa	33
ABCB4	21	intron11 + 1337	tactcttggggagcctatca G/C caggttgggtcagatagc	34
ABCB4	22	exon12 + 3	tggttttttctgtccagat A/T ctctcggcatttagtgcac	35
ABCB4	23	intron12 + 1288	cagaccacctaaccctcag T/C tggacctcagggtgtcagt	36
ABCB4	24	intron13 + 206	tgtagaagaaaaatagcat G/A tggtagaccattgtgaaa	37
ABCB4	25	intron13 + 988	cogtorgtttggagcttgc T/G acccttcttctactctcca	38
ABCB4	26	intron13 + (1413-1414)	ttatcttctacttattgttt (T) ctacgttaagttatgtat	39
ABCB4	26	intron13 + (1413-1414)	ttatcttctacttattgttt ctacgttaagttatgtat	40
ABCB4	27	intron13 + 1931	cttgcaaatgttgccttcc A/G caaaaaaaaggaaggat	41
ABCB4	28	intron23 + 784	aglatctctaaactcttgc T/C atgcaggaataattttta	42
ABCB4	29	intron25 + 158	gaatatattactgtattaa T/C gctcagaacttaataaag	43
ABCB4	30	intron25 + 2920	ctgagcttctctatcatct T/A ttccattctcggatgtgt	44
ABCB4	31	intron29 + 411	cttctctacctgaattct A/C ggcctcgaactttgacttt	45
ABCB4	32	intron32 + 458	agaaatgaattgcctac T/C gagctaacctgaagcaca	46
EPHX1	1	intron1 + 110	tgcaaatgtgtctactag C/T ttctagtgcataaatattg	47
EPHX1	2	intron1 + 143	aaatattgttgagctcttc G/A ctgtcgtggcagtcacca	48
EPHX1	3	intron1 + 1097	aatccagagaggagataga T/G tggaggtcaagggtggaca	49
EPHX1	4	intron1 + 1717	ttccaagcagagcagggg T/C gctcgtgggcgtgtgttc	50
EPHX1	5	intron1 + 1772	aaactcgtcttctctctcc G/T tctggctcctaactcagtg	51
EPHX1	6	intron1 + 2054	gaatgttaacaggcaact A/G tggacacagaagtagatta	52
EPHX1	7	intron2 + 1414	atttccaaatctgtttgg G/T gtaactgaacacttggaaa	53
EPHX1	8	exon3 + 174	taccctcaactcaagactaa G/A attgaaggtatgttgcaaa	54
EPHX1	9	intron3 + 6583	ctgtcaatacatgaagg G/C ggcggggcactaaagggtg	55
EPHX1	10	intron4 + 34	agaggttccataactgccc G/A tctctgccaaagggtggccc	56
EPHX1	11	intron4 + 63	aaggttgggcccgtgttcc C/T aacaggtctctctccggcg	57
EPHX1	12	intron5 + 154	gcagtgctgagggcagttg G/A ctggatctctctgtctga	58
EPHX1	13	intron5 + 276	tgctgaccaaagctctggga T/C agcctgagcagaactcccc	59
EPHX1	14	exon6 + 130	gctgtgaagctgctgtccc C/T gtcaggagaggtattcta	60

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
EPHX1	15	intron8 + 206	ggcgccctgctccggggcgg C/A cctcagtcacgctccccagt	61
EPHX1	16	intron8 + 353	tggccctcccgaaagaga A/G gggccctcagtgagggagag	62
EPHX1	17	3'flanking + 708	aggtgcagactcatgcactc A/G gccctgaagagtgagagag	63
EPHX2	1	5'flanking - (523-522)	aaagtcactggatagcccc (C) tccccgcccccaacacgg	64
EPHX2	1	5'flanking - (523-522)	aaagtcactggatagcccc tccccgcccccaacacgg	65
EPHX2	2	5'flanking - 522	aaagtcactggatagcccc T/C cccccgcccccaacacgg	66
EPHX2	3	5'flanking - 521	aagtcactggatagcccc G/T cccccgcccccaacacgg	67
EPHX2	4	5'flanking - 516	actggatagcccccccc G/C ccccccaacacggcttatg	68
EPHX2	5	5'flanking - 515	ctggatagcccccccc G/C ccccccaacacggcttatg	69
EPHX2	6	Intron1 - 74	tggctgcttccatgaata T/C gaacagtgtctgttccatg	70
EPHX2	7	Intron3 + 72	ggcattaggatcagaatcca T/C tgaagtgaagcttgagatca	71
EPHX2	8	Intron4 + 473	gtgtgtctctactttatct A/G caaaagtgagtgatggag	72
EPHX2	9	Intron5 + 276	caagagtgagtgatccaagg C/T catctgacctcactttga	73
EPHX2	10	Intron8 + 8	tcgtctctcccggtgggtg T/C gctgtcttgacgctgttta	74
EPHX2	11	Intron9 + 1573	atgtctgaagactgatga C/T gatggacggctgacgtctc	75
EPHX2	12	Intron10 + 207	gaacaggatggagatgagct T/C gtttattgtcttttaag	76
EPHX2	13	Intron12 + 911	tgaagagacctgacatgtc G/T catccacatactacaggga	77
EPHX2	14	Intron12 + 2425	atcttctcagctgagcaaac G/T gaggctcagagggcttaacc	78
EPHX2	15	Intron12 + 2460	ttaaccccaactggcccaag G/A ccaggtacatgattggatca	79
EPHX2	16	Intron12 - 281	aagtcctttcaagagattat T/C ataagtgatcccttctaat	80
EPHX2	17	Intron12 - 268	agattattataagtagtacc T/G tctcattataggaatallga	81
EPHX2	18	Exon13 + 50	cctgagtcggagctttcaaaa G/T cctcttcagagcaagcgatg	82
EPHX2	19	Intron13 + 1739	tgtctgaacagggttttca G/T atgagcatatttctttgta	83
EPHX2	20	Exon14 + 33	atgcataaagtctgtgaagc G/A ggaagagacatgcttggga	84
EPHX2	21	Intron14 + 314	ggattgagagcttaacctca T/C ggggtgcacactgtgtatgc	85
EPHX2	22	Intron14 + 878	attcccttattccttcacac G/T gctgtcactcattcattca	86
EPHX2	23	Intron14 + 948	gcacaggctgggtatgaagc T/C ggggtgcacactgtcagctac	87
EPHX2	24	Intron15 + 259	agagggttttcaactctttt C/T agtcattgctcctcagagaa	88
EPHX2	25	Intron16 + 459	tctcattgtcaagcagaa G/G atgatttccaatctctggg	89
EPHX2	26	Intron16 + 645	gtaagtgaacacactgctac G/A tgcacagacttctgcagac	90
EPHX2	27	Intron16 + 985	gtcattatcatcatgacac G/A atgaaatgacaaactgca	91
EPHX2	28	3'flanking + 12	aggtgaccttaccacatct T/C gcatggatggcagcattgtt	92
EPHX2	29	3'flanking + 374	tgttcacggagaatgcacgg C/T atgggagatgaacctttcc	93
EPHX2	30	3'flanking + 544	tagccacactgcttttctcc G/A gcttccctagcagagtttgc	94
GAMT	1	intron1 + 429	ctcggaagctgagctcagg G/A agacagctgtccccgggtg	95
GAMT	2	3'flanking + 626	cactgacctcttggcctga G/A agaagggcggctcctgtgct	96
NNMT	1	5'flanking - 228	ataattttctgacagctc A/T agtgcctcctctgtgtaca	97
NNMT	2	Intron1 + 44	cccacataatgtgagtcata T/C agatggagctcagggcacg	98
NNMT	3	intron1 + 149	ggataaaacgaattattgt A/G tagcattccacagtttaca	99
NNMT	4	Intron2 + 158	agataggcccatgtgtgtgc G/A ttttagtaatttgtatg	100
NNMT	5	intron2 + 433	gctgtagccatccaagccta T/G agaacttggctgtgagtgtg	101
NNMT	6	intron2 - 3064	atcatctgactgtaagttc G/T agttctggttaactcaagt	102
NNMT	7	intron2 - 260	atttcattgaggaagtcaca T/G gttgaagcagctgtctagg	103
NNMT	8	3'flanking + 71	ggctcagtggttggggcca A/G tgggtcatctaggacggag	104
NNMT	1	5'flanking - 390	aagaggtgaatggctcgagg G/A gcttgagaagagagatggg	105
PEMT	1	exon2 - 4	agctcagcagacctcctggc C/T gtggggtagctcctttcc	106
PEMT	2	intron4 + 39	actgtccagcagggaglatc G/T cactgctgttgagccccac	107
PEMT	3	intron4 + 1317	acogtccacagctggcccca G/A cctcctgacatgggectctg	108
PEMT	4	intron4 + 1355	ctggagccaggtgtcagccg A/G agtgcctggcctcctgtggcg	109
PEMT	5	intron4 + 5825	gtccaggcactgtggcccta C/T gtggagtgctccagcttcca	110
PEMT	6	intron4 + 6028	ggcagtggtccaaagacag G/C atggactcctcttctcacc	111
PEMT	7	intron4 + 6078	atctgtacctcgggactc C/T aactgcttctgtgacctcacc	112
PEMT	8	intron4 + 6089	cgcggactctacotggcttc A/G tgcacacccccgcagat	113
PEMT	9	intron4 + 6379	tcagggttccccctccat G/A cctcctcaccctgccctctc	114
PEMT	10	intron4 + 7339	tgaaggaatcctgccaaga C/T ggcagatgcacacggggtca	115
PEMT	11	intron4 + 7619	ctctgcacatgtgtccag A/G gaggaaagcatttgacagg	116
PEMT	12	intron4 + 8858	ggcatgtgtgtgtgtgt T/G gtgtgtgtgtgtgtgtgt	117
PEMT	13	intron4 + 9029	tttctggaccagaaagctc G/A tctctgtccagggccttctg	118
PEMT	14	intron4 + 9056	ggcagggcctctgtgacttg C/T gggaaagctgagctgagctg	119
PEMT	15	intron4 + 9512	ctgagctgggcagcagcatt A/G ctctgtgtgtgtgtgtgt	120

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
PEMT	16	intron4 + 9523	agcagcattactctgtg G/C gctggcactggcctgtggg	121
PEMT	17	intron4 + 9622	gacaaagtgtacaacaaggt G/A tctcgaactgggtcagctca	122
PEMT	18	intron4 + 10776	ccattctgtggtctctttt G/A aggtcgaatgaaattccatg	123
PEMT	19	intron4 + 10912	tctgccccactttgtctaga G/C gtgcaacaaggccttcagga	124
PEMT	20	intron4 + 11590	ggacactggcctgatgcaga G/C gtgtgtctctctcctgcag	125
PEMT	21	intron4 + 12090	ggccagggcacccclaccag G/C ctgagtcgccacctgtccagc	126
PEMT	22	intron4 + 12263	taccgccttccagatgga G/A cgggtctctatgggactta	127
PEMT	23	intron4 + 12448	tctgtccctctcctgtctt G/A tagttcttgggctaaaatc	128
PEMT	24	intron4 + 12730	tgggaccagtgcgccacca C/T ggcaccaaggacctgtgttc	129
PEMT	25	intron4 + 13240	gggtccaggcacacagcgg T/C cccagtacacctgtcgttt	130
PEMT	26	intron4 + 13494	tcogtggaaactagagatgg T/C aactccctgcgaagtgggc	131
PEMT	27	intron4 + 13817	aactctccctctcgtctgag A/G cagatcttggagcctcgcc	132
PEMT	28	intron4 + 14773	ccgcccgtgtcttcatgccc C/T ctatgcctctcactgcttg	133
PEMT	29	intron4 + 14951	gtcctgaggcccccctccac G/A gagcctgggtgcccctaca	134
PEMT	30	intron4 + 16896	gcctgactgtcttggagao T/C ggtcttggcggcctgtg	135
PEMT	31	intron4 + 19439	ccaggagcctctgaggcagc G/A ggggtcttccaccacacac	136
PEMT	32	intron4 + 19559	attttgcagcctgtcact C/T cctttcatatgaagcaagg	137
PEMT	33	intron4 + 20051	acagcactgcggggccacc A/G cctctgcagagcattgtat	138
PEMT	34	intron4 + 20816	tggcctctctgctccatc C/T agccacttcagtgcacgtg	139
PEMT	35	intron4 + 21196	ggctggctggcctggat C/G atcgtgacagcgtttagtgg	140
PEMT	36	intron4 + 21628	acagggtggggccaggcto G/T ggaagtggccggcgtgagc	141
PEMT	37	intron4 + 21586	ccgcttcccgctgctctg G/T gtacagaaagtgtccact	142
PEMT	38	intron4 + 22672	agcctccactgctgtgg C/T tgaaggcggggccggctc	143
PEMT	39	intron4 + 22713	ctaacgctgtcttcttgg A/T ctgaaaccacaacacctct	144
PEMT	40	intron4 + 23010	tgcggggcagcggggggga G/A ggcgagtggttccccaggt	145
PEMT	41	intron4 + 23588	gtccaggcgcctgcctccc C/T gcagcccaagtcttggcgga	146
PEMT	42	intron4 + 23627	gcactgcctgagccagga C/T ggtgaggtggagccttcc	147
PEMT	43	intron4 + 23941	tggagggtgggactctaca G/A agpagagtggactcacgggg	148
PEMT	44	intron4 + 24091	gacaccttccactgctgac G/T ctgagacacgcctctgccc	149
PEMT	45	intron4 + 25348	caggccagttggaatcctac G/A taggtgaaagcattctcagc	150
PEMT	46	intron4 + 25603	taagcagttaacactgatgc G/A tgaatgaaattccaacagca	151
PEMT	47	intron4 + 31540	cctccaggtgagcaggaacac T/C gtgagggcatgcaacgtgc	152
PEMT	48	intron4 + 31637	gtgggtgagcagccaggac G/A gtgagggcttcaaggtgtg	153
PEMT	49	intron4 + 31642	ctggagacgcaggacagatga G/A gggcttcaagggtgtttgt	154
PEMT	50	intron4 + 35593	ggaggagctgaaagagctgg G/A gctcgggtcaggtgttca	155
PEMT	51	intron4 + 35647	actttggggcaccaccgac C/A tgcctgtcgtgaggagac	156
PEMT	52	intron4 + 35862	tccagtggtgtgtctgtcc G/T cgtctcagccagcactcag	157
PEMT	53	intron4 + 35882	ccgtctcagccagcactca T/G cggccagggtgtcgtgactc	158
PEMT	54	intron4 + 37141	ccacaggccggatgccttga T/C acttctcagctcaggcgtg	159
PEMT	55	intron4 + 38862	tggagagaccacctcagaca C/G caaggacgggcatgcatgg	160
PEMT	56	intron4 + 38872	acctcagacagcaaggacgg G/T catgcatggttcccggcag	161
PEMT	57	intron4 + 39140	atgtctcaaatctcccctcc C/T gggaaatctaggcacagtc	162
PEMT	58	intron4 + 39635	caggcccaaggcaggtggg G/T cctctcagagagcagggc	163
PEMT	59	intron4 + 39713	actctgagcatgtgtctcc C/T tcttcttccagggcagca	164
PEMT	60	intron4 + 40436	cctgttctgtcttggaccc G/A gaggcagacagaggcct	165
PEMT	61	intron4 + 47485	acaatgactgttgagccct C/T gaggcagctgtgtcacgtg	166
PEMT	62	intron4 + 48131	actggggatcctgaatccc G/A cctcctgatgccagtgagc	167
PEMT	63	intron4 + 48558	cacagtgtgaactgttaggc C/G acggccacatcttgcggag	168
PEMT	64	intron4 + 48702	gagatggggcggttcagga G/A gcaaaagcaggaaggcagaa	169
PEMT	65	intron4 + 50302	gcattgtcatggcagaggc T/G gttcccaactgagtgagcc	170
PEMT	66	intron4 + 54102	ggccgctgtctcctgcagcc A/T tgggtctcctgtggcagttct	171
PEMT	67	intron4 + 54220	cccaggacagatcttctcc G/A ccagacgtcttcttctcct	172
PEMT	68	intron4 + 54371	gcagataatgtcagctggg G/A tgcattgtgttctgtccc	173
PEMT	69	exon5 + 79	tggcctgtactctctaagc G/C tcaccatcctgtcctgaac	174
PEMT	70	intron5 - 6796	ggagggaagtcagcttctac A/C gatgtgtgtccagcttcc	175
PEMT	71	intron5 - 6636	ttttctctctacacctttt T/C gttcagaggcagaggtgtgc	176
PEMT	72	intron5 - 6448	gttgggcaggctctgacag G/A accctcgggaccagctcctg	177
PEMT	73	intron5 - 5218	ggagccctggtgaagaagc C/G ttacgcccgaaggcctggag	178
PEMT	74	intron5 - 4824	ggacaggccgggggtttagc G/A gctcgtgaggggggggg	179
PEMT	75	intron5 - 4249	tcaccagagtgatttctcg C/A ggcagggtcctgggtagcc	180

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
PEMT	76	intron5 - 4230	gaggcagtgccctgggtag C/T cactggcgccggctccatgag	181
PEMT	77	intron5 - 4182	ggagagtaagggtggggg G/A cacttaggcagggaggtcg	182
PEMT	78	intron5 - 3369	ccagggtggccgtgtgct G/O tggcctgtgtgtggccag	183
PEMT	79	intron5 - 2625	cagggaagctggccctgaa C/T gagctggcttttggccac	184
PEMT	80	intron5 - 1200	attattgtgagcatgggaag A/T gcacatttggcacaatgt	185
PEMT	81	intron6 + 606	gcctagctagacgcccacca A/G tgacctgatgtggcagca	186
PEMT	82	intron6 + 1229	tttggccaggaaggggac G/A gcagccaggagcgctggat	187
PEMT	83	intron7 + 716	atggagatgtgtcccccgg C/G gggcagaggaacctgcgtc	188
PEMT	84	intron7 + 1537	ctctggggacgcataagcc G/A cctccagaggacatcagcca	189
PEMT	85	intron7 + 1718	ggcctccaggtgtctgagc T/C ccccgccatgtaggacccca	190
PEMT	86	intron7 + 2695	ggcttgggggacccctggac C/T catttctagaaaacagcctt	191
PEMT	87	intron8 + 140	ccagggtccaggtcagag C/T ggccatggtagcttacaatg	192
PEMT	88	3'flanking + 179	tacttggaggcgtcaggg C/T tcaactgtccatggccatg	193
PEMT	89	3'flanking + 394	gatgacactgtcttccctaa A/G tgaatggcctgtgtcgacc	194
GSTM3	1	5'flanking - 144	ccaacgcggccttagtgcg G/T cctggcagcggcccttggga	195
ALDH5	1	5'flanking - 2808	ctgtgacgttgggactctc C/T ccacttccctaatcccatc	196
ALDH5	2	5'flanking - 2575	gcagtcccgccggatagga A/G ggtccggtcttcccgctgt	197
ALDH5	3	5'flanking - 2537	tttgggtgaacttgaasaa C/T tgcctgtattoaggagata	198
ALDH5	4	5'flanking - 940	cttcaactatctgggaaca C/T tcaactgttttaattttaa	199
ALDH5	5	5'flanking - 785	tgggaagctgaaneggat G/T ctgagacctgtgttgggg	200
ALDH5	6	exon1 + 183	ccgacggtcaacccctaac C/T gggagggtcattggcacgt	201
ALDH5	7	exon1 + 257	ctgaaagccagcccggaag C/T cttccgcttgggtcccat	202
ALDH5	8	exon1 + 320	gcggggccggctgtctgaac C/T cctggcagacctagtggagc	203
ALDH5	9	exon1 + 605	acttgcgcccgccactgcga C/T agccaacactgtgttatga	204
ALDH5	10	3'flanking + 1527	aaagtccaacttgaagccc G/A tagaasaaactctgttcc	205
TGM1	1	Exon2 + 179	tggcaaatgcggcagatga C/T gactggggacctgaaccctc	206
TGM1	2	Intron9 - 811	acttaccactctgtctctc C/T tgcaggcctcttctgtca	207
TGM1	3	Intron9 - 272	ccgcacactgttaccctgcc C/G ccacttccagcagcgagc	208
TGM1	4	Intron10 + 54	tcagtcatgggtctctgtl C/T ccaacttcacgcgtgactga	209
TGM1	5	Intron10 - 51	aggaggccgggggtcaggcc A/G cccctcagaccctctgctca	210
TGM1	6	Intron12 - 47	ggaggtccctgggggaagcc T/G catgtagggaagcaggctc	211
TGM1	7	Intron13 + 72	ggataaggacatcagggg G/A gcgctaagccagcagcaggc	212
TGM1	8	Intron14 + 1671	atctcttaaccacaccccga C/G catgtggggaggttctcca	213
TGM1	9	Intron14 + 1691	ccatgttggggaggttctc G/A tcttaaggatccgcagagc	214
TGM1	10	Intron14 - 1634	tccttgccctccctctcag G/A gagctcagaacacottcaa	215
TGM1	11	Intron14 - 1459	ggaaacccctcagaaccagg T/C tccaagccaatgctttgcc	216
TGM1	12	Intron14 - 801	cagaatccaaagtggatg G/C gaggcaaggagtcocgttag	217
TGM1	13	Exon15 + 233	ctcgagggtgagcttagccc T/C gtccagaggacatggagct	218
TGM1	14	Exon15 + 369	ggagtcagcttccacttga C/A tgggggaacagatctasta	219
GGT1	1	intron1 + 85	ttatccagtgaaggtggctcc G/A tcaactcttttctgttgg	220
GGT1	2	exon3 + 68	gacggccaggtccggatgt G/T gtggagctgtctggggcac	221
NQO1	1	1 intron 1 80	aggaggtttaggggttgg G/A ctgaattttgttcttgact	222
PIG3	1	5'flanking region -47	gggaaggagaaaggaaaga G/A gggaggggtgttctgtta	223
PIG3	2	intron 2 243	taacacccggagcccgagag A/G agtccagcttcttagactc	224
PIG3	3	3'flanking region 282	agcaggcccccagccctgcc G/A ctactccctgggccccacc	225
NQO2	1	5'flanking region -434	tttctgttcaccacggacc C/G tcaattctgaaccggatgc	226
NQO2	2	5'flanking region -406	gtacccgggtaccagccag A/G gatgggggcccggggcgca	227
NQO2	3	5'untranslated region -102	tcctgcggctcctactggg A/O gtgcgclgtcgaaggtga	228
NQO2	4	intron 1 1919	tcactcaaatagagctgagt T/O agtcaactcagcttggacc	229
NQO2	5	intron 1 2004	acaaactcacatgccaccag C/G catatgatgaacatgtaa	230
NQO2	6	intron 1 3391	aaagcagagggtgtgcagg C/T gcccctggccctaggctagg	231
NQO2	7	intron 1 3456	caaggccctcatcctcagg G/A ggccaactcttctgttttag	232
NQO2	8	intron 1 3595	actgccagctttaggttca T/C tcttgtaagtgtctgggtg	233
NQO2	9	intron 1 3598	ctgccagctttaggttcat T/C cttgtaagtgtctgggtg	234
NQO2	10	intron 1 3598	gccagctttaggttcatc T/C tgaagtgtgtctgggtg	235
NQO2	11	intron 1 3651	ccctgcactttgaaggatg A/G atgtgacctctcccacatc	236
NQO2	12	intron 1 6036	tgtgtgcggcttcaactgat C/T cccagccctctgtctgatc	237
NQO2	13	intron 2 14	atggcaggtatgattcact A/G ttgtgagtaagacttttt	238
NQO2	14	intron 2 192	gccacgtgaagtgtataa C/T tatctgaattatctgttt	239
NQO2	15	intron 2 635	ccacctgttagccactagc A/C ccactccctggcctctgccc	240

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
NQO2	16	intron 2 685	agtagcccccctccccacc G/A gctgtgacaaaccasaatgt	241
NQO2	17	exon 3 139	ctgatttgatgcatgaac T/C ttgagccgaggccacagac	242
NQO2	18	intron 3 36	aatgctctatttataaaac T/C atctttatgtttttat	243
NQO2	19	intron 3 728	aacgtggcataaaaccacca T/C ctatgccaanaagcaggig	244
NQO2	20	intron 4 1577	tgccctgcacaccccttcc C/T gacaccagccctttcttac	245
NQO2	21	intron 4 1832	tcggccggccacgtggagcc C/T gctttcctctcgcacccac	246
NQO2	22	intron 4 2583	tgtgttaacgcacagctcct C/T gtcccctccctgcctgccca	247
NQO2	23	exon 5 330	ctgtactgttcagcgtgcc A/G gccatcctgagggcgtgat	248
NQO2	24	exon 5 405	atcccgagattctacgattc C/T gttttgctccaggtatgtc	249
NQO2	25	intron 5 21	gtatgtctcttgataagg A/T tcactatggatagtggagg	250
NQO2	26	intron 5 253	atggcaacaaggagtgagg T/C caggtgtcaggtgacgggg	251
NQO2	27	intron 6 2435	cccccttaaatcatttaac T/C gaatgtatgtaacaggtgt	252
SULT1A1	1	5'flanking region -1597	gcagagtaaggagctact C/G aagaagaggaaactgggggt	253
SULT1A1	2	5'flanking region -1481	gaggggtatattcatgaaga G/T tccaggaaaggttaagatt	254
SULT1A1	3	5'flanking region -1376	cgtttcatatgttactgat C/T atacaatggatcctagggtg	255
SULT1A1	4	5'flanking region -1375	ggtttcatatgttactgatc A/G taacaatggatcctagggtg	256
SULT1A1	5	5'flanking region -1370	catatgttactgatcataca A/G tgaatcctcctggtaaacct	257
SULT1A1	6	exon 1B -65	aacctgtcattccccacaca G/A caaccacatcagccactgc	258
SULT1A1	7	intron 1B 442	gagccacccctgctaggcct G/A tctttttgtgagtcacag	259
SULT1A1	8	exon 1A -197	gctgggggtccacagggaa A/G tgggtgagcaaaaggccgtg	260
SULT1A1	9	exon 1A -159	ctggctggcaggagacagc A/C caggaggtcctagagcttc	261
SULT1A1	10	exon 1A -95	gagaccttcacacccctga T/C atctgggcttgcccgcga	262
SULT1A1	11	intron 1A 60	ctggttttcagcccagccc C/T gccactgactggcttttga	263
SULT1A1	12	intron 1A 69	agccccagcccccactga C/G tggctttgagtgctggcca	264
SULT1A1	13	intron 1A 174	tgtgtgtgtgtaagggaac G/A ggcctggctctggccctga	265
SULT1A1	14	intron 6 11	catgaaggaggtgagaccac C/G tgtgaggttccctccatgt	266
SULT1A1	15	intron 6 17	ggaggtgagacacactgta A/T gcttccctccatgtgacac	267
SULT1A1	16	intron 6 35	gaagcttccctccatgtgac A/T cctggggccggccactcac	268
SULT1A1	17	intron 6 71	ctcacaggagaccacaggg T/C caaccagccccctccttg	269
SULT1A1	18	intron 6 108	tggcagccccccacagcagg C/A ccggattccccatcctgct	270
SULT1A1	19	intron 6 111	gcagccccccacagcagccc G/A gattccccatcctgctct	271
SULT1A1	20	intron 6 270	ctccctgccaaagggtgtgc C/T acccaggccacagtcagtg	272
SULT1A1	21	intron 6 488	ttttacttttctgaatcag C/T aatccgagcctccactggg	273
SULT1A1	22	intron 6 509	aatccgagcctccactgagg A/G gccctctgtctgcagacc	274
SULT1A1	23	exon 7 600	ccctctgtctgcagacc C/G aaaaaggagattcaaaagat	275
SULT1A1	24	exon 7 645	gagtttggggcactcctcct G/A ccagagagagacgtggactt	276
SULT1A1	25	exon 8 902	gctgtgagagggtcctcctg G/A gtcactgcagaggaggtgtg	277
SULT1A2	1	5'flanking region -547	tgtttcttttctgtttatg G/C atccatgctctgtccaccc	278
SULT1A2	2	5'flanking region -425	tgtgtgtgactgggcaag G/A aacctggcaccttcaagac	279
SULT1A2	3	5'flanking region -358	ctttccaggcctgctctatc C/T cagtttctctcttctgct	280
SULT1A2	4	5'flanking region -355	tccaggcctgctctatccca G/T ctttctctcttctgctgg	281
SULT1A2	5	5'untranslated region -28	actcggcgaggagggcac A/G aggcaggttcccaagcgt	282
SULT1A2	6	intron 1A 85	ctgactgctgtgtgagtc G/A ggcaagtcaactcagcctccc	283
SULT1A2	7	exon 2 24	ggctgatccaggacatctc T/C gcccggccactggagtagct	284
SULT1A2	8	intron 2 34	gccacccacccctctccagg T/C ggcagtcaccaacttggcca	285
SULT1A2	9	intron 5 77	cagcaaacctgtgtccgac T/C ccttggccgttctccagtg	286
SULT1A2	10	intron 6 684	actgggttcccgagggtcga G/C gagctggctctatgggtttt	287
SULT1A2	11	3'untranslated region 895	gctctgagctgtgagagggg T/C tcttgggtcactgcagagg	288
SULT1A2	12	3'flanking region 98	cctccccgctccagctctc A/T acttgcctgtttggggagg	289
SULT1A2	13	3'flanking region 817	ccactgactcggggttgcc A/C aggtgcccagggtggcaaa	290
SULT1A2	14	3'flanking region 1006	cctctccctggaggtgct T/C taccgcgtggggggcgcct	291
SULT1A2	15	3'flanking region 1464	tcccgtagccaggaagtt C/T ggtgaccagagcagccccc	292
SULTX3	1	intron 1 332	cctgcttctccttttactg G/T ctgctgtgtgacctggac	293
SULTX3	2	intron 1 1167	taggaatggctaagcgtgtc G/A ttgcttctgtggcactca	294
SULTX3	3	intron 1 2872	catcttcactgatgcagac G/A aagcttctgggctgggctg	295
SULTX3	4	intron 1 6242	cacccttggcttttaccagc A/G tggaaacattttaccta	296
SULTX3	5	intron 1 6601	gcgtggcttctggaggagg C/T gagagagagtgaggggccc	297
SULTX3	6	intron 1 6768	agcttgaaatgagccagact C/T tcttgggacctgtggcccc	298
SULTX3	7	intron 1 6905	agtactttgttttactctc C/T catctcacaactttgccat	299
SULTX3	8	intron 1 7464	gccaggatcccttgaggagc G/A acatgaacacagccaggagc	300

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
SULTX3	9	intron 1 7833	tgcttcgggctgggcttggc G/A ggggcagctgtgtccgggc	301
SULTX3	10	intron 1 8189	caaacctggggcocttaatgc C/T gcacaccagagccctccttc	302
SULTX3	11	intron 1 8316	ctctcacacagggcgggagc G/G tcttccccttgaggcagagc	303
SULTX3	12	intron 1 8617	agacagagggctggggccaag C/T cagggttgcggagcttct	304
SULTX3	13	intron 1 8631	gccagccagggttgcggc G/T ctctcctggactgtcaggcc	305
SULTX3	14	intron 1 9493	ttttcctcttagagcttccc G/A tegtgtctgtgtcagggc	306
SULTX3	15	intron 1 10306	caggcggggagcctgaatgc C/T gcgtgtgtgagggtggccag	307
SULTX3	16	intron 1 11987	tcataaaatgatatcag T/C acacttttggaaatttgag	308
SULTX3	17	intron 1 13085	ctotgtgcccgtgttgaga C/A agcccatgcccagatgctct	309
SULTX3	18	intron 1 13108	gccatgcccagagctcctgg G/A gatttccaccccagaaacagc	310
SULTX3	19	intron 2 700	gaaccatctggagctgttc C/T gtaactgcccggaggagcc	311
SULTX3	20	intron 2 818	agccatagtgatgcccagc G/A atcagccgtggaggggggc	312
SULTX3	21	intron 2 1677	actccacttcccgaaccc C/T accccttcttctctcctctg	313
SULTX3	22	intron 4 4954	gcgtccgagggcgggggg C/T tggaggtgtcaagacgtga	314
SULTX3	23	intron 5 3632	ccagctgactcccacaccag C/T ggtcagagaaactgtcttt	315
SULTX3	24	intron 5 3662	acattgtcttttaagggttc C/T gaagtgtcgaataaagaaa	316
SULTX3	25	intron 6 1874	ctgatctcagagagctgac A/G atggaagaaattctaaacga	317
SULTX3	26	intron 6 2133	agcccggtgcgcagttta T/G cccacagctcggccctcct	318
SULTX3	27	intron 6 2524	ggagggccagggctgcctg T/C gatgccagagcagtgcact	319
SULTX3	28	intron 6 2573	agctcatactgctcctggg A/G tgtttattaacacactgcca	320
SULTX3	29	3'flanking region 12	gttccggcgttgctgcag C/G gtttctgcttgggggtag	321
SULTX3	30	3'flanking region 445	tccaaagcctgtcttctga T/G ttccgtgtggaaggagctcc	322
TPST1	1	5'flanking region -288	accggcccaatgcccagct A/C atttttttgtatttttt	323
TPST1	2	intron 1 3520	agaaagagcagtaattgaa C/G agtgacgcttgacacaaag	324
TPST1	3	intron 1 3610	ggcagaaagagaaatagca A/G ctattaacaacaaataaatt	325
TPST1	4	intron 1 20828	tattgtctgccacctgttca A/G tgtgtcctgcgataagtgc	326
TPST1	5	intron 1 -6761	aatccactacttcttctga T/C aattctagaggggccagaga	327
TPST1	6	intron 1 -544	tagaacaagtgaaatttta C/T gttcttagtggtttatggtt	328
TPST1	7	intron 1 -526	tacgttcttagtggtttatg G/T ttggcagtttcccccaaca	329
TPST1	8	intron 1 -234	tcaagacatttaataatgca C/T atgttccagctaacctttt	330
TPST1	9	intron 1 -48	ttatgtgggttttaagcatg A/G ttctaaasatttaaatga	331
TPST1	10	intron 2 -18944	aaaacattagaactgggaag G/A ttaaaaatcttttagcttt	332
TPST1	11	intron 2 -18687	tatgtgcacctataaacat A/G ttctcttaaaactagtacta	333
TPST1	12	intron 2 -18501	ttggaagtgaaactaattga A/G gtgcctgaaanaacagggta	334
TPST1	13	intron 2 -159	gaatgggatttccctcagt G/G ctgcccaactggctgctctg	335
TPST1	14	intron 2 -19	acctgttgcttaaaactca G/A cctgtttgtttttccaggt	336
TPST1	15	intron 3 158	tgctggggaagaagatcag C/G gtotggagctgtgtattt	337
TPST1	16	intron 3 3779	agcagggcacgtcccccctc G/T ggcacaccatgtgttacc	338
TPST1	17	intron 4 292	ttgtattttcattatgac C/T atgaatatctcagctgaaa	339
TPST1	18	3'untranslated region 1518	gttgctgtacatgttctaa T/G gttttgtagaacscgtgtc	340
TPST1	19	3'flanking region 264	acgggtcttggcctgcatc C/T catttttgatgaagttct	341
TPST2	1	intron 2 578	tcaactatcatctcactgc G/A aggatgccagatacctccc	342
TPST2	2	intron 2 789	cttaagccatcgtgcaggtc A/G ttgctgtcttctgctcaatt	343
TPST2	3	intron 3 2009	cccaggctggagtgatgg T/G gtgatctcggctcactgcaa	344
TPST2	4	intron 3 2017	ggagtgtagtggtgatct C/T ggcactcgaacctccgcc	345
TPST2	5	intron 3 2035	ctcggtcactgcacacctc G/A cctcccgggttcaagcagtt	346
TPST2	6	intron 4 104	aatgttcagttctcaattc C/T tggatcctgattttgtct	347
TPST2	7	intron 4 379	taataaataaacttttgt C/T cctttctgtttataaggt	348
TPST2	8	intron 4 588	tactgcagcctgatactct G/T gcttaagccatcctctcac	349
TPST2	9	intron 4 626	caccccaggtccttgatag C/T taggactgcaggtgcacgcc	350
TPST2	10	intron 4 718	cccaggctgtgtagaactc C/G tggcgttaaggatgcccct	351
TPST2	11	intron 4 873	gttgatggcctttattatc G/A ttccattacagcttctagt	352
TPST2	12	intron 4 949	caaatattgaatgggac C/G caggcctgagggaagacttt	353
TPST2	13	intron 4 1033	taagctcagcatttctgagc G/A tgtgtgtatttaggaata	354
TPST2	14	intron 4 1051	gcgtgtgctgattttaggaa A/G taacagttatcgtattgaa	355
TPST2	15	intron 4 1356	gcttcaacgtacataccagc C/T gacattgacaggtgaatggc	356
TPST2	16	intron 4 1707	gttcccttaaaaggtggctc G/T ctgcccctggcttccccag	357
TPST2	17	intron 5 215	aagaccagcctgacccaaac G/A gtaaaccccgtctctacta	358
TPST2	18	intron 5 341	tgggagggcagggctcagct G/A agctgagatcacgccttgc	359
TPST2	19	intron 6 31	ggacttcaactgggggttccc G/A ctgcttctgggtggccccc	360

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
TPST2	20	intron 6 273	gtttgtcgcactggggac A/G gggcaggagccaccatg	361
TPST2	21	intron 6 693	aaaggggtttttgaactt G/C gtaattcaagatttaagat	362
TPST2	22	intron 6 1635	tcttgggtacagagttggcc T/G tgaacaaacatgagtccttc	363
TPST2	23	3'untranslated region 1147	cttcccaactttcagatctc C/T gcaaatgacttcatggcaa	364
SULT1A3	1	exon 8 843	cgcttcgatcgccactatgc G/A gagaagatggcaggctcag	365
CST	1	intron 1b 6302	agagctccccagagaggact A/G tgaggctgatgatcatga	366
CST	2	intron 2a 1004	gagtgagacccccatctcta C/T aaaaattttttttaaagta	367
CST	3	intron 2a 1395	atgcctaagtttaccagtagc T/C aggcaggaaaggcacaacca	368
CST	4	intron 1d 473	ccagagccctgaggttggtgc T/A ggggccccctcatgagctgcc	369
GST	5	intron 2b 726	ctatctctccagtgccctctc T/C gtcctgtctggaccctgct	370
CST	6	intron 2b 745	ctgtccctgtctgacccctg C/A tggggggccacagagccggc	371
GST	7	exon 3 85	tcactagtcttctgtctgtg G/A tgaactctatgcccgtgcc	372
CST	8	intron 3 308	tgtctgaggtcaggagtgc G/A agaccagcctggccaacatg	373
CST	9	intron 3 853	ttttgtctataaaatggca G/A ttctatgtggcccaagctga	374
CST	10	exon 4 198	gagcgatgatccgggcaa C/T ggctgcgggggagtgcca	375
SULT1C1	1	intron 3 2280	gcaaatitttgatlttta G/T tacegtcagggttttaccat	376
SULT1C1	2	intron 3 3742	gcagatctcactttctggca G/A attccctgaattgtctccc	377
SULT1C1	3	intron 3 4453	ttcatagggtttttccctca C/T ttgttttgtaatttgata	378
SULT1C1	4	intron 3 5234	gaaaagagactagaggcagg A/G gagctttgcagttctttaa	379
SULT1C1	5	intron 3 6175	tggctggcaggaggtgagg G/C agtctctctctctcgtctcc	380
SULT1C1	6	intron 4 205	acatgaggcaggatccaga T/C tgaatgtttggagggaacta	381
SULT1C1	7	intron 4 408	ggctcagcctgtatccca G/C caatttggaggccagggcg	382
SULT1C1	8	intron 4 429	caatttggaggccagggcg G/C gtgatacaaaagtcaagg	383
SULT1C2	1	5'flanking region -110	tctgttaactcacagagaa C/T ggaagggtggaacgggacc	384
SULT1C2	2	exon 1 15	gcactaatggccttaccaga C/G atggagggttttaccattga	385
SULT1C2	3	intron 1 297	gtagcttgtttttttttt A/C ttcccaatctaggccottat	386
SULT1C2	4	intron 1 363	gagtggtgagctgaaagg T/G gatcctgagctgatttggg	387
SULT1C2	5	intron 1 2300	gggtctactatcagcagccac C/T acctcaggaggtgacttc	388
SULT1C2	6	intron 2 455	agagcttggagcaaataga T/G aaaaaaaacatctagaact	389
SULT1C2	7	intron 4 55	caaaatctccaaacacccta G/A aaggaagaatcttttttt	390
SULT1C2	8	intron 4 111	ctgctctttaaagtgaca T/C tctcactctcttcaggact	391
SULT1C2	9	intron 5 1657	ctttgtgttactttgttt T/C acttggtcaaaagtgtgt	392
SULT1C2	10	intron 5 2082	tctctcctagagatggagg C/A gtccacagccacagtgatg	393
SULT1C2	11	intron 6 933	agctactgaacctctccac A/G taactgtatttcaggggcag	394
ST1B2	1	intron 1 80	acttgccataaaatcatta G/T cattctaaataaagttaata	395
ST1B2	2	intron 2 -352	aacatttaaatgacttlla T/C agcaatgcacaggtataata	396
ST1B2	3	intron 2 -85	attacataatgctcaaaat G/A tcttgaaaaactggttgca	397
ST1B2	4	intron 4 460	glactgacattaaaaata T/C ctgatgttataatccata	398
ST1B2	5	intron 4 470	ttaaaaaatctctgatgttt A/G tatatccataaagctaat	399
ST1B2	6	intron 4 518	tttaagattgtctcatatt C/G ttacttcttttggttactaa	400
ST1B2	7	intron 4 616	aattgtttatgaaatagact T/C ttatctggttttagtgccct	401
ST1B2	8	intron 5 58	ctgcctcatgctgtaaaagg G/A ttgatatttgccttcaact	402
ST1B2	9	exon 6 612	taatagaatcaaaaggagg A/C atcaagaagatcattagatt	403
ST1B2	10	intron 6 582	aatacttacttccatttaa G/A tagtctgtttttgtggctt	404
ST1B2	11	intron 6 3130	agatgaaaaatttttcaa A/T ttttaaaagcctgaaaaatt	405
ST1B2	12	3'untranslated region 907	tttaaaagtctcaatcaca C/A atctgaagaataaagagatt	406
ST1B2	13	3'flanking region 50	tcagctccagttttgtcc T/G ttgattctgatttccaaat	407
ST1B2	14	3'flanking region 328	tttgaccaggacactgtgt T/G ccactgtctgtaccagggtt	408
ST1B2	15	3'flanking region 446	gtagtccagattttgaaat C/A tttttctatctcacccta	409
CHST2	1	5'flanking region -260	agccggacagtcgcccggc G/A gtgacccggggccgctccc	410
CHST2	2	5'flanking region -56	gcgctggggaccagccggc C/T gccgcctcggagtcgggc	411
CHST2	3	3'flanking region 218	aggagtgaaacacatctttg T/A attctaaaggcagaaccaa	412
CHST2	4	3'flanking region 383	gcagagaccatgttttgg G/C ctgaggctgttcagaaaaa	413
CHST2	5	3'flanking region 952	tactgaacattctgcagaa T/C gttatactgtggaagaaat	414
SULT2A1	1	intron 2 478	ggctgggtctgtgacacac T/C tctgttactgtgtgtaaat	415
SULT2A1	2	intron 3 382	caaaaccccttaaatctct G/A ttctatctgtctcagaact	416
SULT2A1	3	intron 3 409	tcgtctcagaactgttgc A/G tgactctaggatcgctalat	417
SULT2A1	4	intron 5 249	agctgaaattacaggcaca C/T gccaccacaccagctaatt	418
SULT2A1	5	intron 5 395	aggcatgagccacggcggc G/A gccaatatcagctttaat	419
SULT2A1	6	3'flanking region 33	ttctgtttaaagttacca G/C gtttggcaggccaggtgt	420

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
SULT2A1	7	3'flanking region 46	gttaccagggtggccaggc A/G cgrtggctcatgctgtat	421
SULT2A1	8	3'flanking region 199	ttagccaggcgcattggctc A/G tctctgtatccagcactt	422
SULT2B1	1	intron 2 4162	ttctccctctcctcccat C/T cgcacacaggtgtctcat	423
SULT2B1	2	intron 3 879	gaggccatccagctctggg G/A ctggacctgggggttgg	424
SULT2B1	3	intron 4 3882	ttccacgtccttctctggc C/T ggtgacctccctccgtga	425
SULT2B1	4	intron 5 1780	cctgcagaagggtccctt C/T catgtccagcagtaatggc	426
SULT2B1	5	intron 5 1814	taatggctgcagcatggagc G/A ttgtggggcattgagacag	427
SULT2B1	6	exon 6 789	ccctcttctccagggtgtg C/T ggcgactggaagaccactt	428
CHST4	1	5'flanking region -1092	atgaagccttggtccatctc G/A ctgtgtgtgcccagccctg	429
CHST4	2	5'flanking region -941	ctgccagagagaaacaggaa G/A gagggaagagccacacaatt	430
CHST4	3	intron 1 -150	caggaaatgattggagaag G/T actgtgcccattgtggcac	431
CHST5	1	intron 1 -144	ggcctcttaggtttcagcca A/C gacaggtgactcttagcacc	432
CHST5	2	intron 2 17	caacgttaagagcgtttctca T/A tctcagctccttgtttct	433
CHST5	3	intron 2 139	aatccacagcactttggagg C/A gggatgtgaggatgatca	434
CHST5	4	intron 3 1829	gactgtgtgtctctattca T/C ataggaaacaataattcatg	435
CHST5	5	intron 3 2037	aactgaacacacacacaa C/G tgcagagaagcaaacacaaag	436
CHST5	6	intron 3 2134	aagcagctaaattgtgttc G/A tacaggtgcaattggcagg	437
CHST5	7	intron 3 2528	atgttaagtttgcctgggt G/A cagtatgtcagctcctgct	438
CHST5	8	intron 3 2674	gcacttatctagaaaggcc A/G ttctgaagactcagcagg	439
CHST5	9	intron 3 7039	ctgctcccccgcgcacccc T/C gggaccgcagccacgtctga	440
CHST5	10	intron 3 7211	gtagccccaggacaccccca T/G cttcaacalcccatttggg	441
CHST5	11	intron 3 7294	ggagcttcagtggttgggt T/C acccccgaactcttctccat	442
CHST5	12	intron 4 108	gcagggtcctgcactctgca G/A ggggcaatccaggtggag	443
CHST5	13	intron 4 402	agcactggaaaaagtagct T/C gcaactgtagcggagtgagg	444
CHST5	14	intron 4 547	ctcctgtcccccattggagg C/G gaaggagcagaggtgagtc	445
CHST5	15	intron 4 1142	gccccaggtctatagctcc C/G catggcagtgctgggattt	446
CHST5	16	intron 5 1187	ccctggcagtaattggggc A/G tgggatgggcatgaggccc	447
HNK-1st	1	intron 1 139	gtgtttgggaactgaaga C/T ctccctagttcggggagta	448
HNK-1st	2	intron 1 1020	acctgagcagaaattctct T/C ctctgtgaatgaaattg	449
HNK-1st	3	intron 1 1091	aagaatttgaacatcaca G/A gcaacttgcaatttatctg	450
HNK-1st	4	intron 1 1971	ctataactatttcaacata C/T gaaacagccataattggatt	451
HNK-1st	5	intron 1 2096	atttagaatatttacc A/C agaaatccaatataacctg	452
HNK-1st	6	5'untranslated region -91	ctatccagtgacaagaggaa C/A caagaacctcagttcaggg	453
HNK-1st	7	intron 2 -530	agtggcagaggcagagaagc G/A tcaggtgttattccttct	454
HNK-1st	8	intron 2 -466	gctacatcttctcagccagt C/T agaattttaaacacagccag	455
HNK-1st	9	intron 2 -92	acggaaatatttctgtgat A/T cttaactgactgaattcact	456
HNK-1st	10	intron 3 152	catggcctccgttctctcat G/A ttacagaggtgtgaggag	457
HNK-1st	11	intron 3 312	cacagtgcccttatgcttg C/T agcaggcgcctctcaggct	458
HNK-1st	12	intron 3 1948	tcctttgagtatcaagttt T/C gtgtgaatttttcagtt	459
HNK-1st	13	intron 3 2140	ttacacctggagaggagcac C/T gcagcgttcttaatactgc	460
HNK-1st	14	exon 4 187	agaagccatttctgaggaa C/T tgaaggtgggcacagccagg	461
HNK-1st	15	intron 4 581	cctgctatttccctagctgg G/A atgagggtgcaacttgaa	462
HNK-1st	16	intron 4 615	tcggaaggccctctcacttc G/C taaccccccttctgactca	463
HNK-1st	17	intron 5 7	gattgttclaaatgggtgt G/A tgggtctactgaattgccac	464
HNK-1st	18	intron 5 123	acctgaaggagctggggcc G/T tcagacagggcctgttttg	465
HNK-1st	19	intron 5 721	ataattatgggtctgtctta T/C gaaatttagcttcagacagg	466
HNK-1st	20	intron 5 867	tgctgccacagagtcggg G/A tcaactcctggccactgtttg	467
HNK-1st	21	exon 6 444	ccaggagcattttcttccat T/C gaggagtcgccgaaacgt	468
HNK-1st	22	intron 6 94	ctggttctgtacttggcag A/G ttgatogggggccacagag	469
HNK-1st	23	intron 6 247	catgaagtgacatctttt G/A ttaatagaanttagcaggca	470
HNK-1st	24	exon 7 696	aggaggaccggacagagac C/G cggggatccagtttgaaga	471
HNK-1st	25	exon 7 870	gagaccctggaggagcatgc C/T ccatacatctaaagaggc	472
HNK-1st	26	3'untranslated region 1110	tcaaatattttattagacc T/C ggggctaaccaggtgagat	473
HNK-1st	27	3'untranslated region 1178	ccacacccctcctttgagga C/T gcccggggtctccacagggc	474
HNK-1st	28	3'untranslated region 1393	ggaagcatcacacagctta G/A gagcgttttctctcaggtgt	475
HNK-1st	29	3'untranslated region 1452	tgggttctctgctgtgtc A/G ggggtgcttccacctcaact	476
HNK-1st	30	3'untranslated region 1540	gcaaggggctgctgaatc G/C cagagacttttgagacatca	477
HNK-1st	31	3'untranslated region 1696	gggtgtgtgtgttccagg G/A tccatctttccagaatccat	478
HNK-1st	32	3'untranslated region 1829	agggagagctttttctacct G/A agaaggggagtgctttgag	479
HNK-1st	33	3'untranslated region 2211	tcacagcgtgcggcttctg G/T caacaaggtaggccctggtg	480

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
HNK-1st	34	3'untranslated region 2212	ccagcagtcggtcttcctgg C/T aacaaggtaggccctggtgc	481
HNK-1st	35	3'flanking region 1016	cacacgaagggtgacactca G/T ggcctgcaggcccccaggt	482
HNK-1st	36	3'flanking region 1152	gcctgctttgctcatctgga A/C tctccgaagcagggaacag	483
HNK-1st	37	3'flanking region 1291	gccgagaccctcagcaggat A/G gtgcagttccgggctgggc	484
STE	1	5'flanking region -605	caggtttctaaataataat C/T gaaaggtgagtggtttac	485
STE	2	5'flanking region -536	taaaattttcaggtctgctt A/G agagttaaaggcaagggtt	486
STE	3	5'flanking region -231	cctttctcccaacccctga C/T ggcagacttgggaatttgaa	487
STE	4	5'untranslated region -64	tgcagcttaagctctgctt G/A gtatttgaagatataaac	488
STE	5	intron 1 69	aaatataagatgaatttat G/A tattacaagctcttaaaaa	489
STE	6	intron 1 311	caatgagaaataaagcaag C/G agggtagaggaggtgaat	490
STE	7	intron 1 655	tctaagaagtagggactat G/A agaaccctatgtatctata	491
STE	8	intron 1 671	ctatggaaccctatgtat C/T tatatcaccctatgttct	492
STE	9	intron 1 772	aaaaggcaggttgaagatg C/A aggggggagtagtcagaaa	493
STE	10	intron 1 1715	taaccatttgccttaacctt A/G tcatttttagccagtcatt	494
STE	11	intron 1 1928	aaatgatcatattcaggaa A/G tcaaaatctctgacttaga	495
STE	12	intron 1 1953	aaatctctgacttagatacc C/T ggcataataatcaaatga	496
STE	13	intron 1 2087	aatttgaaagaattgaag T/G tctgtgtttttattttatca	497
STE	14	intron 1 2323	taggtatgtaggagggtccc G/C ttatatacatagttgttaat	498
STE	15	intron 2 165	tctattccatgaccacaatt T/G ttacctgtactgtgaatagt	499
STE	16	intron 2 1707	cctaggaccaacatgagac A/G taatataccatcagtaaat	500
STE	17	intron 3 850	ggtgtccattccctcaagaa T/G ttatacttltgtttacacac	501
STE	18	intron 4 1653	agtaacaggctagtagata T/C ataataactgagcccaacg	502
STE	19	intron 4 1899	tacatgaacttagagaatca A/G gtatgacacacacacca	503
STE	20	intron 4 1930	cacaccaacaataaaattac A/G cagaatgataaaagatttg	504
STE	21	intron 5 666	ttctgatcatgtagtaacaa T/C tataaagaaataataatgt	505
STE	22	intron 5 982	aggcaaaagcagaaccttttg A/C ctacacacaactattatt	506
STE	23	intron 7 369	agattttatctctctctt T/C ttgagttgaagaataagt	507
STE	24	intron 7 447	caaccttcaaggtaagtgg C/A aaaaaatagaattcaata	508
STE	25	intron 7 672	aatctgtcttttgaccat A/T ctgtcagtgagagtcagga	509
STE	26	intron 7 856	gttaccagaggactaaac A/G gtgtcttctgttgcacacgg	510
STE	27	3'flanking region 218	cagccctccaaagtagctagg A/G ctacagacatgtcaaccat	511
ADH1	1	5'flanking region -55	atcatgtgtgaactggaat C/T ggggtttattcaagcaaaa	512
ADH1	2	intron 1 268	acatttgcgttaaacgata A/G ttatttccaagctaatcatg	513
ADH1	3	intron 3 442	aaatggaggctacatggcta C/A ggcagatgagctgacctt	514
ADH1	4	intron 6 56	tacaacttgaggatgcatt T/G aggtcgcagaatatatgttt	515
ADH1	5	intron 8 74	gtctagcagaatggaag G/A tgaagagatgagaatatta	516
ADH2	1	intron 2 340	ctatttttaaaagctgcat T/C cttaacataagacttaatat	517
ADH2	2	intron 3 91	aaggcaatggagagcgaag T/G gcttgcacaaggtcaccg	518
ADH2	3	intron 3 205	atgtattgtaccttcaacc A/G ttatgtaccgagtatctact	519
ADH2	4	intron 7 108	acaattgacaaggcaagatt T/C tgaacaacaatcaaaataa	520
ADH3	1	5'flanking region -254	tgagagaagagaagcaggaa C/G ttgagagaggaggaagagag	521
ADH3	2	intron 2 355	tatgcattctctatattat A/G caagacaaaatttttagat	522
ADH3	3	intron 3 32	acactcagggaacatgcctt G/A gttcaccatcacaagattag	523
ADH3	4	intron 4 6	ctgctgaaaatgagtaag C/T ttctgtatgctttcttgcac	524
ADH3	5	exon 5 453	agcaccttctccagtagacac A/G gtgtgtgagagaatgcagt	525
ADH3	6	exon 6 815	ttcgtttgaagtcacgggc A/G gcttgacacatggtatgat	526
ADH6	1	intron 3 249	tgaactggacttgaagta C/A aaatgagacaaaatttttg	527
ADH6	2	intron 6 1072	taaccctatactgtattgc A/G tcaatttcaacaggcagct	528
ADH6	3	exon 7 885	gtctgtgtgtgtgtgggt G/A ttgcctgccaggtttcaact	529
ADH6	4	intron 7 1292	gttgagaacactgcctagt C/A ccgtctgtgttcttagaatt	530
ADH6	5	intron 7 1616	ctatcacagaataatccga T/C agaacactaagcagattccg	531
ADH7	1	5'flanking region -528	tgtgcagccacagaaagttt T/C acttaactttctacacctaa	532
ADH7	2	intron 1 361	tcagtgcagtgtgctgcaat C/T gctgcagtggttcaatggga	533
ADH7	3	intron 3 183	aacctcaacccttagaagga A/G aaccttccgtgtttataaa	534
ADH7	4	intron 4 76	tgaattgaaatattatcc G/A tttatttggatatacaaca	535
ADH7	5	intron 6 615	tggcctgcgtaagagagact T/A ggaataatggaataagcca	536
ADH7	6	intron 8 532	aagtctaacatctaccaca T/C ttatgtatgccattgtactat	537
ADH7	7	intron 8 651	gtctgtattttttcaagta G/A gcccacaaatttcttattt	538
ADH7	8	intron 8 760	catttttagatgaagaccaa T/G gttgtgaagcaataaata	539
ADH7	9	intron 8 1207	tctccacatttggctagacc T/C acaggatcatcatattatga	540

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO
ADH7	10	intron 8 1691	tcacctatctcattgcccac G/A ctcattgctttaattcagtc	541
ADH7	11	3'untranslated region 1364	atttacatttttaagccta T/C aattgtatcttttaagaaa	542
ADH7	12	3'untranslated region 1498	gatalatgaaatgcacatcc T/C agaglaattacacttaaca	543
ADH7	13	3'untranslated region 1584	aaacactgttatgagttaa C/G ttggattacattttgaatc	544
ADH7	14	3'untranslated region 1818	aataaacaatagagctaga A/G tcatattatcatacttatca	545
ADH7	15	3'flanking region 865	tacatcaaaagaaataatc G/T aagaaggataaacacattt	546
HEP27	1	5'flanking region -191	tcagcacctctgtctagct A/T aaggtttgtaaatgccacaa	547
HEP27	2	5'untranslated region -163	gaacccatcaattccgtaca C/A attttggactttgaagag	548
HEP27	3	intron 1 1941	aaatttacctaaccagcct G/C actctctgccactttctgtt	549
HEP27	4	exon 3 289	ttgtgtccacgtggggag G/A ctggagaccgggagcagctg	550
HEP27	5	intron 4 1070	tgctcagttcacaggatca T/C gactctttttctcgaactg	551
HEP27	6	3'flanking region 362	ggctttgtgtgtcctcatt A/G tctgaactggcctgtctgg	552
L1CAM	1	intron 1 + 767	tttgacttcctacatgggt G/A actgtgtgactcactctgtt	553
L1CAM	2	intron 1 + 862	gcattgggtcatgtatgt G/C tgagtggggtgaatgaag	554
L1CAM	3	intron 1 + 1332	caggatgaaggagcagagc G/T gctgagaggccacacagtg	555
L1CAM	4	intron 4 + 502	tttccotgggttttccctt T/C gcatccatcctccctgagc	556
L1CAM	5	intron 18 + 147	agcgacgttatgaattccc G/A acacttcacatttctataat	557
L1CAM	6	intron 24 + 221	ctccttagcccccagagg G/T cccaacttaagagcatact	558
AANAT	1	5'flanking -542	aggggtcaggatgaggtgt G/T agctggaggcaggaggtag	559
AANAT	2	5'flanking -263	ccccccacataagaggtgg G/G ttgtccaagactccgaggga	560
AANAT	3	intron3 39	cgcccgaccgccaggagggc T/A ctgaagacagaggtcagcca	561
AANAT	4	exon4 150	cagccggcgtgtgcggggc C/T gcgctcatgtgcaggagcg	562
ARD1	1	intron1 + 317	ccgtcggctgtctcggccccc G/G ctccctcgggctggcagg	563
ARD1	2	intron6 + 322	gtctctcgcactctgtctac G/A ccaggagccacacactctct	564
ARD1	3	intron6 + 1095	aaggctccatcctgagacaa A/C aagtcaggtgacactgccc	565
ARD1	4	intron6 + 1179	aggagggaagactgtatccc A/G gggacacccctcctccactcc	566
ARD1	5	intron7 + 159	cctccaggctgctaggcaga C/T ggcctcctctaagcccagc	567
ARD1	6	intron7 + 295	tgaccagccctgccaccga G/T gagccttggcagaaacctg	568
ARD1	7	intron7 + 416	actaccatggagggccccc G/A acagagcgtgcgcccttgac	569
NAT1	1	3'UTR 215	aataataataataataaa A/T aaatgtattttaaggtggc	570
NAT2	1	exon2 867	cglgcccaaacctgtgtatg G/A atcccttactatttagaata	571
NAT2	2	3'flank 521	ccatccatactttgccacaa G/A agaaggacatgagcgttat	572
NAT2	3	3'flank 573	gatttgaalccctgtggaca C/T ggggtgaattacttttaaaa	573
NAT2	4	3'flank 918	attttctgttgtaaatcc A/G gtatcagggtctatgtttaa	574
NAT2	5	3'flank 979	actatttccctctctgact C/T gtatgactataataatctt	575
NAT2	6	3'flank 1958	tacctattgaagtaagccta C/T gtccatccactatttgtt	576
NAT2	7	3'flank 2034	ccactgattccagagctag T/G tcattaagaagacagtgctt	577
NAT2	8	3'flank 2201	cagattactgggggctact G/A ttgtccoccatgccaatg	578
NAT2	9	3'flank 2818	gggtatttgtctctttct C/G cccagtgcatgttggaaacc	579
NAT2	10	3'flank 3237	atctatttccaattaaaa A/Δ caaataaatttccgaact	580
NAT2	11	3'flank 3386	caacaagagatttttttaa G/A ctttttaaacaccagacag	581
NAT2	12	3'flank 3660	cagcactattcgcaatagca A/G agatgggaatcaatctaaa	582
NAT2	13	3'flank 3973	agcagaaaaataataatg C/T gtactaggcttactacctgc	583
NAT2	14	3'flank 4029	caaaacaacccccatgaca T/C gagttatctatatacaaaa	584
NAT2	15	3'flank 4118	ataagattaatctctgata C/A aaatctttgtttacagcttg	585
NAT2	16	3'flank 4146	tggttacagctgttatata C/T tgaattatgtctctccccc	586
NAT2	17	3'flank 4279	ttaatctgataggattgtg G/C ctttataagaaaagaaaag	587
NAT2	18	3'flank 4323	ttgctctctcccgagtcag T/G taccaggaagggccatgtg	588
NAT2	19	3'flank 4446	tcaattgctttatctcgga T/C tctggaatcaggcaatacto	589
NAT2	20	3'flank 4462	gcgattctggaatcaggcaa T/C actccattcataaaacaga	590
GZMA	1	5'-flanking -462	cctcagcttgcaattggcct A/G ctaattcttatataatccaa	591
GZMA	2	5'-flanking -172	agcctgcctgctgcagtg G/C ccactatccaccattctcac	592
GZMA	3	intron1 1949	gacataaggtctctctatc A/T gcatgtatgtttgccttgt	593
GZMA	4	intron2 + 683	gactcgtgaccaggtggaa C/T tagcctcagatggaagggt	594
GZMA	5	intron2 + 1250	gttggtgtagtattactag G/A ttatgaatgatagccttaat	595
GZMA	6	exon4 + 105	tgccaagttgcagggtggg C/G aggaactcacaatagtgcato	596
GZMA	7	intron4 + 696	atagagccttaactgaagaa A/G ggtgtgcagtatgcagctt	597
GZMA	8	intron4 + 1141	ctgttcaggaggtatccgg G/A ttccaacatggttcttatt	598
GZMB	1	5'flanking + 529	gcctcgtctcacaccaaca A/G gcagattccccaccagggc	599
GZMB	2	intron3 + 141	gagggaagattgtgcagccc C/T atcactgtgtcggggccag	600

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
GZMB	3	3'flanking + 448	ttttcagggcctgtccctcc G/A atggggcaggcttctccca	601
ESD	1	5'-flanking -333	gtcttgggacagagggttg G/A gggagttgaattagccct	602
ESD	2	intron 1 603	gtcatttctgtatgggtcat C/T agggaaatgggattgagcgc	603
ESD	3	intron 1 717	tgtgtgttagaagcagcatt C/T taagcactacgtgaattaac	604
ESD	4	intron 1 1864	gccttcacgcaggattgato G/C tagtgggtgtattagggaag	605
ESD	5	intron 1 2389	ttttgggaacacctgtctag G/A tggttaagagccagtggaata	606
ESD	6	intron 2 21	taaactgttttattgttta T/C atgttactctgaaccttgaa	607
ESD	7	intron 2 588	taaaattagtatctctctct G/A taagttcattattttaagata	608
ESD	8	intron 2 1498	tagaaaaatgtgtatcacac C/T gtaagtttcagttaatttta	609
ESD	9	intron 3 92	ctttatctagatattatagt C/A cctcatttttacttttaact	610
ESD	10	intron 3 422	gtaaaagattaaacacaca C/T gcaacatacatatstacotat	611
ESD	11	intron 3 581	agaaaacctgagaatgaca C/T aatttatttaagccatagt	612
ESD	12	intron 3 2270	gccagtaattacatgtagccc G/A ttacatcaaatagctaact	613
ESD	13	intron 3 2951	taatgaagtaaatgtttca A/G cttccctaacaaaagtigaa	614
ESD	14	intron 3 3001	aaatgtcagaaatttttgt G/A ccgtcagtcacatacaagaa	615
ESD	15	intron 3 3096	agggagcatagcaaaaactt G/C ccagtgtgggctttgtgg	616
ESD	16	intron 4 1611	tctaagttccccagtttta A/G tgggtcacatcttcagtcc	617
ESD	17	intron 5 390	tcttttttcatctctgttaa C/T atcaaccatacagtttaaca	618
ESD	18	intron 7 107	ttagtattggactaaactt T/C tctagtgttgagaactttgg	619
ESD	19	intron 8 1090	aaattctactaatlaaagg G/T ttcatccttagtaactaga	620
ESD	20	intron 8 1651	tataaagttgtggttaata A/G tatatatgaataagaatatt	621
ESD	21	intron 8 2047	agaaggaataagccatttt G/C ttaagaatccctgagatag	622
ESD	22	intron 9 -3490	ataaggaagagggtctatct A/G cctccttaagtctcaggacc	623
ESD	23	intron 9 -2596	actaaggataaaatatggc A/G tactcagtcacattggaact	624
ESD	24	intron 9 -666	aggccttaatacatatttc T/C cctcacataaagatacaaca	625
ESD	25	intron 9 -660	taatgacatatttcccctca A/G ataaagatacaacatgctt	626
ESD	26	intron 10 799	tatgttaactgaagaaaatg A/G cattaagttctaaagttat	627
DDOST	1	intron2 629	attctgttaagaagtcttta T/C attaagaatattgtctcct	628
DDOST	2	intron2 3126	gggaataagggagctttcgc G/A tatgcctgaagtcagtcag	629
DDOST	3	intron2 3920	attactcatitaaatgaata A/G tggattactgagcactgtct	630
DDOST	4	intron3 189	actgctgtccaggggtccat C/T tgggctgagcccagctgga	631
DDOST	5	intron6 185	ctgtcctctgttgcggagg C/T gtggcagcttttcccttact	632
DDOST	6	exon8 37	aaactatgaactagctgtggc C/T ctctcccgctgggtgttcaa	633
DDOST	7	intron9 37	tcctgcccaagaatgtctgc A/Δ aaaaacggccccggccctca	634
MGST1	1	5'flanking - 5	tctggacccctgaacaggagg G/C gacatcgtgacaagcgaat	635
MGST1	2	intron1A+330	atcagcggcgatgtgttact C/G tggcgggttaactcaggtag	636
MGST1	3	intron1C+1428	gtaaagggaaggcgtttcc T/A caactgagaagtgaagattc	637
MGST1	4	repeat	attatttgcctaccctcagg G/A tttttcgggtcaagcgagat	638
MGST1	5	intron1C+2914	ctcatcaggtgtgtgtcaga G/T ggcttgggtgtgcccagttc	639
MGST1	6	intron1C + 4274	attgtaataagattaacaaag G/T tgatgaagtagtgtacata	640
MGST1	7	intron1C+4276	tgtaatagattaaacaaagt T/G atgaagtagtgtacataat	641
MGST1	8	intron1C+4306	gtgtacataatgtacatagt A/G tagttgaacacatacgaagc	642
MGST1	9	intron1C+4406	gatggctatatgaccaataa T/A gatcacataaatgtataga	643
MGST1	10	intron1C+4464	agaagagattgcagctgatag A/G tgcaggcttaataaggacac	644
MGST1	11	intron1C+4683	aatggcagaggactggaat G/T tacattttaagctttacccct	645
MGST1	12	intron1C+4767	gccttctcttccagcacatt C/T ccaattatacttcccaattcc	646
MGST1	13	repeat	atttcaattttttttttt G/A gggggagacagagttctcact	647
MGST1	14	repeat	aatlacctcccaaggccctc A/T tatcccgatactatcacat	648
MGST1	15	intron2+2379	ttctcaaatctattatata C/G tattttcaacccaaagttt	649
MGST1	16	intron2+2767	tttaactatagatgccttct T/G ctctcttgtgtttgattta	650
MGST1	17	repeat	tccctgcagcctcaecctct C/T gggctcaggtgatcctcca	651
MGST1	18	repeat	aaaaaaatttgtatagatgg T/G tactcctctatgttcccagg	652
MGST1	19	repeat	ctccctatgttcccaggct A/G atcttgaattcttgggtca	653
MGST1	20	intron3+1495	gtcagacaatggcctcagc G/A tctctctttgcagaatatg	654
MGST1	21	intron3+2528	ttttgggacacttttccaga G/C agagcgtttccagcatctc	655
MGST1	22	intron3+2567	tccctttccatttttaagtt A/Δ gacttttttttttcaacct	656
MGST1	23	intron3+2731	atacacatatggacaatta A/C ctaaaacttaaggtaatat	657
MGST1	24	intron3+3288	gggtttatagtgttcccccc C/Δ tcccgcggcccaaaagacc	658
MGST1	25	intron3+4288	ccattctattgtccaaatgc G/A taaccagggcgtgaagttgg	659
MGST1	26	intron3+4378	aaatgtctgtccttttgcca T/C gtgtgaaggagaacactaa	660

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
MGST1	27	intron3+4429	attggaggtgacgatctc T/C gtgatctgtggggagaaatc	661
MGST1	28	intron3+4817	attgctatagaagagagtaa G/T gtaagcagaaatagttttc	662
MGST1	29	intron3+6077	tttgaaattagtgcttttaa T/C agttatctttttccacagag	663
MGST1	30	exon4+304(3'UTR)	aagaattctgtacttccaat T/G tataatgaatactttcttag	664
MGST1	31	3'flanking+1581	ttgtgtgcatgaacatgca C/T ggtgcaagcgcaacacacac	665
MGST1	32	3'flanking+1729	tatgtggagcaatttgaaaa A/T agtatattctaagccattaa	666
MGST1	33	3'flanking+3407	ggatcactgtaaaagatccc G/A gagtactccatgtcccagt	667
MGST1	34	intron1B+36	ggagaaggagccgcagca G/A aggtggcagccagggagg	668
MGST1	35	3'flanking+25	gggtaaacccattttgaata T/C tagcattgccaatattcgt	669
MGST1	36	exon4+266(3'UTR)	aaagaaatcatacaactca G/A catccagtgtgcttttaag	670
SULT1A2	1	intron 4 1728	tcagcttcctcctttgccaa A/Δ ccaagagatgagctggcctg	671
SULTX3	1	intron 1 6415	tgacctctccctgttagtgt G/Δ ggggcagctctttccagtgt	672
SULTX3	2	intron 5 2457	ggccttaaaaggaagttcat C/Δ ctctctgcttccagcctc	673
PIG3	1	5'untranslated region-93	tcgcgagggatcacagcgccc (CCTGY)n cagacaatatgttagccgtg	674
ADH2	4	intron 7 + 108	ccattgcaaaaggaagatt T/C tgaacacaaatcaaaataa	675
ADH2	5	intron 3 +(1721-1723)	actgcatagaatttaagaa GAA/ Δ ctgtttattctctccag	676
ADH2	6	3' untranslated +(2305-2306)	gttaatgctttccactctc AG/Δ gggaggaattgtcatttga	677
ADH5	1	5' flanking - 115	taactgctgtaaaagtacac G/A gggagccctttccgacaa	678
ADH5	2	5' flanking - 114	aactgctgtaaaagtacac G/A ggaagccctttccgacaa	679
ADH7	16	intron 8 + 727	ttcagctccctgtaagccag G/A tatatttttaccatttta	680
GSTM1	1	5' flanking - 694	tacgaattggctaaattaca C/T agtacttagccagatgaccg	681
GSTM1	2	5' flanking - 661	gatgaccgaaggactcagta C/T ccgagggcccttaacagaa	682
GSTM1	3	5' flanking - 658	gaccgaaggactcagtaacc G/A agggcccttaacagaaaca	683
GSTM1	4	5' flanking - 656	ccgaaggactcagtaaccga G/A gggcccttaacagaaacaca	684
GSTM1	5	5' flanking - 537	tagggggagactaaagccct G/C ggaatagctttcgaatcaga	685
GSTM1	6	5' flanking - 525	taagccctggagtagcttt C/G ggaatcagaggaagtcctgt	686
GSTM1	7	5' flanking - 465	aattaaattccaggttggg G/A ccaccacttttagctgac	687
GSTM1	8	5' flanking - 383	gcgagagaagagctgagga C/T acccgggcagggagagaa	688
GSTM1	9	5' flanking - 382	ccgagagaagagctgagga A/T ccgagggcagggagagaa	688
GSTM1	10	5' flanking - 378	gggaagactgaggaacccg C/T gggcagggagaggaagggag	690
GSTM1	11	5' flanking - 343	agggagaagagctttgctcc G/A taggagctgtggtgtct	691
GSTM1	12	intron 2 + 118	tactgagctgcagctctc T/C ctccctgagcccccgtgag	692
GSTM1	13	intron 3 + 233	agtgaagtgcgcgtctctc T/C ctgctgtgttatgggaag	693
GSTM1	14	intron 4 + 26	tttgggtgctcgaattgt G/A ggggaaggtggtcctctcc	694
GSTM1	15	intron 5 + 140	actatcagcaattatttcca C/T gactcaaatgcatgtcaac	695
GSTM1	16	intron 5 + 577	ctgccacccattagaagga A/G ctcttctcttccctgagct	696
GSTM1	17	intron 5 + 645	gctgctggaatcagagggc T/A gccaggtgcttggagctcc	697
GSTM1	18	exon 7 + 519	caccgtatatttgagcccaa G/C tgcctgagccgttcccaaa	698
GSTM1	19	exon 7 + 528	tttgagcccaagtgcttga C/T gcttcccaaatctgaagga	699
GSTM1	20	intron 7 + 2421	cagcaccgtgagaattctc A/G taagtgttagctgttactgt	700
GSTM1	21	3' flanking + 42	atttgcctctggccatctac C/T cagactgtctgtctgt	701
GSTM2	1	intron 1 + 7	ggaacatccgggggtgagc C/G aggtccgctggggcgtggg	702
GSTM2	2	intron 1 + 45	gggacgggggtgcgtgggg C/T ggggaagtgtggagcagctg	703
GSTM2	3	intron 3 + 70	gactgcatctcctctcccca G/C cttagaggtgttaagatcag	704
GSTM2	4	intron 3 + 224	agcaggccctgtctctctc T/C tgccttgcatatgggaagg	705
GSTM2	5	intron 5 + 100	ttgattcctctgtgaggtt C/A ttgtcttctgactctaa	706
GSTM2	6	intron 5 + 341	tcctctgtgaggttcatgg T/C ctggtggttccagggtga	707
GSTM2	7	intron 5 + 696	occttagctagacacagag C/T gctgatttgcatttcaaa	708
GSTM2	8	intron 5 + 723	ttgtgcatttcaatcttt A/G gctaggcagaaagtctcc	709
GSTM2	9	3' untranslated + 1006	ctcagcccccagctgtcccc G/A tgttgcataagggagcagca	710
GSTM2	10	3' flanking + 139	ttctgctggcctagtaagg C/T gcttgagaatttctgtccc	711
GSTM3	2	5' flanking - 144	ccaacgcccggattagtcg C/T cctgcagcggccctgtgga	712
GSTM3	3	intron 7 + 165	agcctaactctatcccttg A/G aggcactgtctacaaaaaa	713
GSTM3	4	intron 7 + 257	ctgttgactgggtgggtc T/G ttataagattgtgtatttt	714
GSTM3	5	exon 8 + 91	cccagtggggcaaacagcct A/G tatgtgagcaggagcaga	715
GSTM4	1	intron 4 + 67	ttgctgacttgggtgcta T/C gctcaggtgagctgtgtt	716
GSTM4	2	intron 7 + 77	gtgtgtttccagtcctgga T/G ctgcataagaataacttgc	717
GSTM4	3	intron 7 + 80	gotttcccagtcctgact G/A cataagaataaacttcatt	718
GSTZ1	1	5' flanking - 546	agcaggcccccagccgac C/A gctcgaagccctgagcc	719
GSTZ1	2	5' flanking - 321	ttctgaccagccgcccgc T/C aaggagtcacaagagggcag	720

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
GSTZ1	3	intron 1 + 2890	aaatactgcatcaaaacca G/A gccacgtctgttggggga	721
GSTZ1	4	intron 1 + 2896	otgcotcaaaaccaggccac G/A ctctgttgggggacccaa	722
GSTZ1	5	intron 2 + 255	ttcccaacactgctctcca A/G agcccttggcaaccatgtt	723
GSTZ1	6	intron 2 + 1560	caaccctgttaaggccctg G/C gggggcaggttaaacaaa	724
GSTZ1	7	exon 3 + 94	ccttgaaaggcatcgactac G/A agacggggcccatcaatctc	725
GSTZ1	8	intron 4 + 297	agaaggaggatttgcctggc C/T ctgtccctctgtccagg	726
GSTZ1	9	intron 6 + 94	tatctgaaccagcctccag G/A ctgttggggcctgacagt	727
GSTP1	1	intron 1 + 269	ctccccggggctccagaaa C/G ttcttctgttctgtcag	728
GSTP1	2	intron 2 + 134	ccccggggcctcttctgtt G/T cccgcctctccgccatgcc	729
GSTP1	3	intron 5 + 438	gtgtgtgcgctgcgtgtgc G/A tgtgtgtcgtgtgtgtgt	730
GSTP1	4	intron 6 + 162	cccgtgctggtgctccctag C/T cccctgcccctgcagctctc	731
GSTT1	1	5' flanking - 103	taaagagtgtcccaggcgtc C/T gtccggcccaatggggcaca	732
MGST1L1	1	5' flanking - 105	tgctccgctgcctgtgggc G/A gggcgtggcggctgtcgt	733
MGST1L1	2	intron 1 + 277	agtgctgtgagagagcag G/A ttctgggggggagtgtgg	734
MGST1L1	3	intron 2 + 8030	gggttatccagagccccc C/G gcccccaccacacatatga	735
MGST1L1	4	intron 2 + 8499	gtatggcaggagtggtggcc C/T ggcagccatagaggtatgg	736
MGST1L1	5	3' untranslated + 468	cgccacctgtgaccagcagc T/G gatgcctccttggccaccag	737
MGST2	1	5' flanking - 46	ggcagcattcaasgtccag A/T agccatttatcttccgt	738
MGST2	2	intron 1 + 176	ggcaccctgcgcctgtct A/C cctctctccagggggcaag	739
MGST2	3	intron 1 + 204	ttccaggggcagcagagac T/C gagacattccagagattag	740
MGST2	4	intron 1 + 373	ttacaagtgtccaaaggaa A/T cgtgcctgtcttcaaccctg	741
MGST2	5	intron 2 - 3245	cctcgtgatttggccacctc G/A gcctcccaagtgctggat	742
MGST2	6	intron 2 - 1998	agccgagggtggcggatca T/C gaggtcaggagatcgagacc	743
MGST2	7	intron 2 - 1640	tgatttctcctgcatagcc A/G taataaaagtatgaatttt	744
MGST2	8	intron 3 + 41	actgtgtctaatgtgact A/G tgaigtcttaaacgttaagg	745
MGST2	9	intron 3 + 453	atcagagtgtctatgttcag A/G tatatgaacttggcttcat	746
MGST3	1	5' flanking - 520	acaaaaaggccctaaccagc A/C taatccattcacttccgga	747
MGST3	2	5' flanking - 356	cgctcaaaacccgtacggcg G/A ctctgtctggggcacaattat	748
MGST3	3	5' flanking - 234	clggggagtagatattgt T/A ttgagaatgagaggagtaa	749
MGST3	4	intron 1 + 74	agcctttgcaggcactcc C/T atatttcagcctatcgagc	750
MGST3	5	intron 1 + 682	agaaaatgcccttctttt G/C tgggtggcggcggggcc	751
MGST3	6	intron 1 + 832	cggtttacaagctacata T/C agcgtcggggcaggtaagt	752
MGST3	7	intron 1 + 1919	aataaaattcctgagtttct G/C tcaactgccttaccagacc	753
MGST3	8	intron 1 + 1991	tgttaattggcacaaggaaa A/G ttgtactctcttcaatgc	754
MGST3	9	intron 1 + 4458	tcttcacatcctcctaacata T/C agttagcttccacttccaa	755
MGST3	10	intron 1 + 4676	tgaatgtcaatgcaattgt C/G gggggatgttactttcat	756
MGST3	11	intron 3 + 278	cgcctgaccctctaaacc G/G atgttgaactctccagcct	757
MGST3	12	intron 4 + 423	cttgcccttttgggtggg T/G gtgggtggtgcacagagag	758
MGST3	13	intron 4 + 506	gtcagagagagaaacaaag T/C ggggaaggtggaaagggat	759
MGST3	14	intron 4 - 162	tcacagatattttattttcc C/T gactgaacttaacttaattc	760
MGST3	15	intron 4 - 130	acttaattctacctaatttg G/G gtggggagtagtggccaaa	761
MGST3	16	intron 4 - 105	gggtggttggccaaatcat C/G aaattgttaacttttgot	762
MGST3	17	intron 4 - 65	aaatattgtgtaatcaacc C/T taggtgttaaaaaggttg	763
MGST3	18	intron 5 + 105	atcccgacacttggggggc G/C aaggcaggcagattgctga	764
MGST3	19	intron 5 + 197	aaaaaatcacaaaattagcc G/A ggtgtggtgtgcacacctg	765
MGST3	20	intron 5 + 222	tgtgtgtgcacacctgagt C/T ccagctacttgggggctga	766
MGST3	21	intron 5 + 374	tttatgtactatatttt T/C ttcttgggaatttgagaaaa	767
MGST3	22	3' untranslated + 517	atgaattacctttatttcca G/T ttacatttttttctaata	768
MGST3	23	3' flanking + 168	agtctgattgtgtgatga G/T gtatgtcatgccacagtga	769
GSTA1	1	5' flanking - 266	ttgcaaaagagcaaatct C/A ggtgaatgtattgtgtaa	770
GSTA1	2	intron 2 + 1220	gagacacaggcttctctag A/G tatgacacaccataactag	771
GSTA1	3	intron 4 + 1813	aaaggcaccactgggggtg A/C attatttggcatcacctga	772
GSTA1	4	intron 5 + 732	gaagagtgtgtcatgaagg T/C ggaagtactcccaaggag	773
GSTA1	5	intron 6 + 333	ttatcccatatgtgccaca A/G tgagcgggtctgagcagagc	774
GSTA1	6	3' flanking + 412	ctttcttatgctttgcaaa A/C caatgattctgtctgtgtg	775
GSTA4	1	intron 1 + 280	gcattgttggaggtgggct C/T ggtcgtccccgggctggc	776
GSTA4	2	intron 3 + 176	ggaaatcacttctattcaa T/G agttccataaagctggcg	777
GSTA4	3	intron 4 + 94	acaccacatttactttaigt C/G ttacatagttagtagatca	778
GSTA4	4	intron 5 + 1062	cacacttgtgcacatgcaga C/T acccatgggcatcaagagt	779
GSTA4	5	exon 6 + 487	cagatgtgattttactccaa A/G ccattttagctctagaagag	780

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
GSTA4	6	intron 6 + 595	tgagctctgagagcaaatga G/A agatgttagcaccctaaaca	781
GSTA4	7	intron 6 + 630	taaacatcccccaaggat T/A cctaccattctccttctgag	782
GSTA4	8	intron 6 + 3943	tcttcgtatctataatcc T/C tttttagccttaaaagt	783
GSTA4	9	3' untranslated + 1099	taatacaaacgaatgtctc G/A taastgactctcctctgagc	784
GSTA4	10	intron 5 + (370-371)	gtgtcgaacagctgtctca (TA) gctgacatcctccctgataa	785
GSTA4	10	intron 5 + (370-371)	gtgtcgaacagctgtctca gctgacatcctccctgataa	786
NDUFA1	1	5' flanking - 1437	agggtcaaaaatcctgatta T/A acctacctlgaagcttttaa	787
NDUFA1	2	intron 2 + 3071	aataaaagtacatggcatai C/A ttgtatgggaacagacttgt	788
NDUFA1	3	3' flanking + 1218	aactccatgtgtataaagca A/G caccacagatgacacttcca	789
NDUFA1	4	3' flanking + 1411	ggattgtgccatcccttgat C/T/G ggcaatgaccttttactttt	790
NDUFA1	5	3' flanking + 1411	ggattgtgccatcccttgat C/T/G ggcaatgaccttttactttt	791
NDUFA2	1	intron 2 + 1087	aacatacaaaaattagccgg A/G tatgtgtggcggcacctgta	792
NDUFA2	2	intron 2 + 1089	catatacaaaaattagccggat A/G tgggtggcggcacctgta	793
NDUFA2	3	intron 2 + 1356	tlccctgaacaccccttg T/C ggccatccagaatcagccaa	794
NDUFA2	4	3' flanking + 467	cacagcctcatgggtcagcc C/T actccagagggtgacttccc	795
NDUFA2	5	3' flanking + 744	ggagcagggggccctggcca C/T agccgtgagcagtaagcagg	796
NDUFA2	6	3' flanking + (844-845)	tatagtctacaaagaatgaa (ACAC) aaagatcataacaatagcta	797
NDUFA2	6	3' flanking + (844-845)	tatagtctacaaagaatgaa aaagatcataacaatagcta	798
NDUFA3	1	intron 2 + 2656	tccttgctccctccctgc G/A caatttatcttcccttgcc	799
NDUFA3	2	exon 4 + 241	aggcccccagcctggagtg G/G tgaagaactgtgagcacct	800
NDUFA3	3	3' flanking + 1019	tccttaccctgactggcacc A/G gctctggagccccagtcct	801
NDUFA5	1	intron 3 + 2155	agactctagcatgttacctg G/C aacataaggttccttagaaa	802
NDUFA5	2	intron 3 + 2493	ggcatattgttagttttctc G/T gtctcaatttcacatcat	803
NDUFA5	3	intron 3 + 2712	acaaattttgaactgttcc C/T taacacaggctttttctgaa	804
NDUFA5	4	3' flanking + 1296	aggatctaaaaggatfgc A/C atttgtcattgtgttttc	805
NDUFA5	5	intron 3 + (30-31)	aagtacgtttttgtgttg (GATTTGTGGTATCCAG) tgtaa cattaaacaaaaa	806
NDUFA5	5	intron 3 + (30-31)	aagtacgtttttgtgttg tgtaa cattaaacaaaaa	807
NDUFA5	6	intron 3 + (427-428)	attaagtagcagttataaa AG/Δ tctagactgctgattcatat	808
NDUFA5	7	intron 3 + (4733-4734)	tataggaaattttaaaata TA/Δ ggatattgaacattcagtt	809
NDUFA6	1	5' flanking - 1148	tttataatttatatgtta C/T gtgctttctttgtatagct	810
NDUFA6	2	5' flanking - 363	actaccagagagcggcg G/A cagccgtagcaggacgct	811
NDUFA6	3	exon 1 + 26	ggggagcggctccgccaag C/T tacttctaccgccagcacct	812
NDUFA6	4	intron 1 + 1318	attcagcagtttgaascat A/G atgtttgcctggcagaatc	813
NDUFA6	5	intron 2 + 562	agttaaagaatctgaaaagt G/C tcagaatgattaccctga	814
NDUFA6	6	5' flanking - (861-862)	ctgtaaaatgggatgtcga (T) ggtacctactgacctatga	815
NDUFA6	6	5' flanking - (861-862)	ctgtaaaatgggatgtcga ggtacctactgacctatga	816
NDUFA7	1	5' flanking - 731	accaaccaaaaggtctatcaa A/G ggggtgtcctctttgaccc	817
NDUFA7	2	5' flanking - 434	aaaggggaaccatcagaaccc C/T gtgatgaaatgagaatcggc	818
NDUFA7	3	5' flanking - 395	gctccggattccggctggc A/G ggggttagggcagggtagag	819
NDUFA7	4	5' flanking - 100	agaggagtcacgtgcttcgg G/A gagagcctttataggacgtt	820
NDUFA7	5	intron 1 + 92	tcacctccctcctaagccgg G/A acccttcgtctccccgaat	821
NDUFA7	6	intron 1 + 133	ctccctgggaacccccagct A/C gtcaccccttcagcccgga	822
NDUFA7	7	intron 1 + 136	cctgggaacccccagctagt C/G accccttcagcccgga	823
NDUFA7	8	intron 2 + 89	tcctttagacccctgaaacg G/C agggctgacatcctgcaacc	824
NDUFA7	9	exon 3 + 196	gcccggggaatctgtcccc C/G? ctccatcatcatgtgtcg	825
NDUFA7	10	intron 3 + 4203	gcctccacccctggggcgcc T/G cctccatcaccocccctcc	826
NDUFA7	11	intron 3 + 4604	gggcctgtgtacgttggag A/G ccaaaagtgggaaggaggga	827
NDUFA7	12	5' flanking - (1360-1353)	agggtccagggtccctgct (CAGAGGCT) aacactggccg aagagaaag	828
NDUFA7	12	5' flanking - (1360-1353)	agggtccagggtccctgct aacacigggcgaagagaaag	829
NDUFA7	13	5' flanking - (1240-1239)	tgatagagccctgatccacc CA/Δ ctctctgaaacttttgtct	830
NDUFA7	14	intron 2 + (4142-4143)	catttttgactgaggtgac AG/Δ gggcccaacagcgggccaatg	831
NDUFA8	1	intron 1 - 75	tttgtttctctattctgac C/T cgcattgaggttaagctgaga	832
NDUFA8	2	intron 2 + 790	caaacctagacaaagtgtgc C/T ctttatccagaagtgcag	833
NDUFA8	3	intron 2 + 900	ttcaggagataaaaagctct G/A attgctcaggccctgagatgg	834
NDUFA8	4	intron 2 + 3837	gaagtgtcttgaagtgag A/G taagaatgtgactacata	835
NDUFA8	5	intron 2 + 3942	tcattgttttcaagagat G/T cccctaaccagctttctt	836
NDUFA8	6	intron 3 - 66	gaggagacaccaggagcgcc A/G ttgatgttacagattcctc	837

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
NDUFA8	7	3' untranslated + 520	tttattctggaccaagtaa A/G gatgggtccgtgcccacac	838
NDUFA8	8	3' flanking + 367	gtcatcaaggggcgccctcc A/G ggtatagaagtgcagaactt	839
NDUFA8	9	3' flanking + 777	attcttttttactactagg C/T tgttctccacatctgact	840
NDUFA8	10	3' flanking + 1053	aaagaaaagccactgttga T/A ctgcatggccgcttctga	841
NDUFA8	11	3' flanking + 1190	gattctctaatgaaaaatga G/T acttttttttgcattttt	842
NDUFA8	12	intron 2 + (449-453)	ggtcattgtgcagtactctaa (GTAA) aaaaaactaagctgtgaat	843
NDUFA8	12	intron 2 + (449-453)	ggtcattgtgcagtactctaa aaaaaactaagctgtgaat	844
NDUFA8	13	intron 2 + (707-708)	ctcattttgaaagactctc (A) acctgtctgtaccaaaatg	845
NDUFA8	13	intron 2 + (707-708)	ctcattttgaaagactctc acctgtctgtaccaaaatg	846
NDUFAB1	1	intron 1 + 8451	cagcacccctgtagggccctc G/A ggtgtgtgagctgccatga	847
NDUFAB1	2	intron 1 + 8495	gacacaggcattctgcagac G/A ctgacaaattttatggcag	848
NDUFA9	1	5' flanking - 807	gatggctctttgtagaacaa T/G gcagattctcaaaagtgacc	849
NDUFA9	2	5' flanking - 769	accacagtttaagaaaaaat T/C acaagccattgccttagaga	850
NDUFA9	3	5' flanking - 353	cacacccclattttgtttct C/G ttctccacttttccctcgt	851
NDUFA9	4	5' flanking - 322	ttccccctgtttgttcccc C/T cttttctctctctggccc	852
NDUFA9	5	intron 1 + 447	ttcatatgagcacaaatga A/G atgataatattacaatacca	853
NDUFA9	6	intron 1 + 1039	ggcttgatgttcagcctgag G/A caagaattaggaggttttag	854
NDUFA9	7	intron 1 + 4010	aattgtatccaaagagattc T/G cattctgtcccatgaagaa	855
NDUFA9	8	intron 3 + 49	gcaaatataattctaaag G/A tcaatttttagggataggg	856
NDUFA9	9	intron 3 + 107	aatttttcccgagtgagac C/T aagggatctctgtttccca	857
NDUFA9	10	intron 3 + 1183	ctctctgttaattatcatc A/G gattattgtatcccttta	858
NDUFA9	11	intron 3 + 1395	cttctagttctttttccct C/T aagttttgtatccattgt	859
NDUFA9	12	intron 3 + 2363	agaaaatgactgaatggc C/T ccaactaacactgltcttta	860
NDUFA9	13	intron 3 + 2608	gtctttgttttccctgagta A/C agtctactgttaccgtttg	861
NDUFA9	14	intron 4 + 561	attttataaattctttgat A/C ctgggggtcttattcaact	862
NDUFA9	15	intron 4 + 860	atttctgtagtgaatgacg C/T agagctgtcaactttttta	863
NDUFA9	16	intron 4 + 879	gcagagctgtcaacttttt A/T aaaaaataatttagcttaa	864
NDUFA9	17	intron 4 + 893	tttttaaaaaataatttt A/G gcttaaaaaataaaaaatt	865
NDUFA9	18	intron 4 + 1090	atcattgtcttttaaaagt T/C aagtagtgaatttcagta	866
NDUFA9	19	intron 4 + 1188	aaccaatcctttttttttt A/T tcttccagaacattgtatt	867
NDUFA9	20	intron 5 + 161	gggtgtgtgaggtttga C/T gttttgattgtgcttct	868
NDUFA9	21	intron 5 + 373	cttttccacccttgcaact C/T agtgtttttgtccactctt	869
NDUFA9	22	intron 5 + 457	gocaggagagtgactatc A/C cacagtgttatgtctcttt	870
NDUFA9	23	intron 5 + 3113	galttttctcttctcaat G/A taagcttctcttaaaataa	871
NDUFA9	24	intron 5 + 3339	tctaaactcacaacaggttt G/A ttgttttattgtttggtg	872
NDUFA9	25	intron 6 + 414	tatagttttgcttttccag G/C atattacatatatgttga	873
NDUFA9	26	intron 6 + 518	cttttctttttttatagc T/G tgaagctcatttctttta	874
NDUFA9	27	intron 7 + 974	ggattatgcgtacttgaaa A/G tacttgatagcgggtatta	875
NDUFA9	28	intron 8 + 368	acattatattttgatggatg T/G cacaatgctccagaggctg	876
NDUFA9	29	intron 8 + 954	gcattgcaatcagttatag T/C ctatagaagaattacaattc	877
NDUFA9	30	intron 8 + 1253	ttctcttgaaattgtatga G/T gtatctacacatttctatc	878
NDUFA9	31	intron 8 + 11608	gaaagatggtgtatgaat G/A accaaaaattcgtgaagaaa	879
NDUFA9	32	intron 8 + 11930	ctacaaatatattcaaat C/T gtaatcatggaatgacaa	880
NDUFA9	33	intron 9 + 1998	tgtttttcaagcctttaaac G/A gctgtggaacctgtgtca	881
NDUFA9	34	intron 9 + 2238	ccagctacttggaagctga A/G gtggagagtcacttgagcc	882
NDUFA9	35	intron 9 + 2885	acagcgtctgtcttctgc A/G gtttctataggcttagctac	883
NDUFA9	36	intron 10 + 801	tacactaaagtgtctctac G/A ttatacttgagaaagtgt	884
NDUFA9	37	intron 10 + 910	tgcagactttcagtggtga G/C gatggggallgctgtgct	885
NDUFA9	38	intron 10 + 1180	aaactgagtcagacgccc G/A tctcagaaaacagggcgt	886
NDUFA9	39	3' flanking + 554	gtgcagcacttaggaatta T/G gaacttctaaggaattctt	887
NDUFA9	40	5' flanking - (1129-1128)	taaacagtagggcgaagata (TC) gattggaacagccaagatt	888
NDUFA9	40	5' flanking - (1129-1128)	taaacagtagggcgaagata gattggaacagccaagatt	889
NDUFA9	41	5' flanking - 341	tggtttctcttccacttt T/A cccctgttttgcctcccc	890
NDUFS1	1	5' flanking - 3	tcttaggggtgtctgtgt G/G cagacagtttagcagaacag	891
NDUFS1	2	intron 1 + 445	gtgttagcaatgggtcaago T/C tctgtttgtgtcttgttt	892
NDUFS1	3	intron 1 + 470	tttgttctctgtttgtt G/T gtccattgaccaggtggac	893
NDUFS1	4	intron 1 + 502	acgttggacagcctttttt A/G ttctttaactaacgggaaa	894
NDUFS1	5	intron 1 + 557	ttttgaaaagttagccagg A/G ttgcatgacaaatacaaaa	895
NDUFS1	6	intron 1 + 5218	tatctcagaatctcagga A/G catltaglacagctatgc	896
NDUFS1	7	intron 3 + 1371	agccctcaaatagatag T/G caatgggaatgaacacaga	897

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
NDUFS1	8	intron 5 + 414	ttttgaaacgaggtctcact A/G tttgtccaggctggcctg	898
NDUFS1	9	intron 10 + 812	ggtgctggtggcgcgctc G/A atctcggtcactgcagcct	899
NDUFS1	10	intron 11 + 233	ggaggccaaaggcagccagat C/T gcctaagtcaggagttga	900
NDUFS1	11	intron 11 + 283	ggccaaactggcgcaaacccc G/A tctctactaaaaatacaaaa	901
NDUFS1	12	intron 11 + 585	ctgtatgtcttaattttaa G/T taatttgcaatttatatat	902
NDUFS1	13	exon 12 + 1251	gcaccactgtttaatgctag A/G attcgaagagggttgaet	903
NDUFS1	14	intron 13 + 5159	attacttttagaaaaacgtg T/G ttactgtatcicaggcata	904
NDUFS1	15	intron 14 + 250	aaaaaltgttatattagta G/T acctgtgttcasaaatgca	905
NDUFS1	16	intron 14 + 550	gataaagtctcactatgtg C/T ccaggttgatctcaactcc	906
NDUFS1	17	intron 14 + 2429	ctgaataacaaaaatagc C/T ggggtgggtggcatgtgcct	907
NDUFS1	18	intron 14 + 2530	ttacagttagccagatcac G/T ccactgcctccagcctggg	908
NDUFS1	19	intron 14 + 2659	acacatttaatttttcat T/C gaaaaactgcagttatgt	909
NDUFS1	20	intron 16 + 150	agaaacatgtattcagaaa C/T aggaattcaagttacagt	910
NDUFS1	21	intron 18 + 279	cactgttagcaattatgg T/C gaattttccaaagtgcaaa	911
NDUFS1	22	3' flanking + 182	tctaggataattataatga T/A aataatcatagtaacaatgg	912
NDUFS1	23	intron 11 + 3226	aaatgtatgtctgtcttt T/Δ aacatttggtaatagtaaat	913
NDUFS3	1	5' flanking - 194	tctgcacaaaggagctagga C/T cagctcacctcagctttc	914
NDUFS3	2	intron 1 + 46	cgggttcaggcgagcgagc G/T gccagtcagagagctcct	915
NDUFS3	3	intron 6 - 439	aaagctgttcaaatgtact G/A ctttagatctggactgtga	916
NDUFS3	4	intron 6 - 280	ggtgggtgagcagctagtt G/A gacgtcctgatgtggagt	917
NDUFS4	1	5' flanking - 439	aactgaatcacgccgtgac T/A gagggcttgcgaagtgaatc	918
NDUFS4	2	intron 1 + 1829	gaaaaaaatcttaatacca G/T ggaagcgttttttaataac	919
NDUFS4	3	intron 1 + 2057	ettaetgggaatatctac C/G taaaattcaattttattgta	920
NDUFS4	4	intron 1 - 521	ttcattttaactaattttat T/G tctccctttttgaaatgg	921
NDUFS4	5	intron 3 - 1259	ataaattatgtattatta G/A tctaatatagccagccata	922
NDUFS4	6	intron 3 - 1174	aatatataaattatagga T/C ctccaggtgacaaacctgt	923
NDUFS4	7	intron 4 + 10682	cacaatataggcacaacit A/C ctacccaaagcaatcaaat	924
NDUFS4	8	intron 4 + 12299	tttactatagatatagg A/T atagactatagagttatct	925
NDUFS4	9	intron 4 + 12560	accaaatagggtattatga G/A gctcatcttttatataag	926
NDUFS4	10	intron 4 + 18801	ggaaagccttgccttgcag T/C gtatccgaacacctgttat	927
NDUFS4	11	intron 4 + 19888	tcgcacagctgagagagca A/G ggggctgttttcaatccc	928
NDUFS4	12	intron 4 + 20178	agaaagctgagttataatc G/A tctaacttaaccattttaa	929
NDUFS4	13	intron 4 + 23016	ctctctgtgaaagtaaggt T/A atgttgaaacagttatata	930
NDUFS4	14	intron 4 + 23124	acittctttggagatgggt T/A ccagcagttgggaatgaat	931
NDUFS4	15	intron 1 + 766	tgtgatgatttttttttt T/Δ ggtgttatcaacttccatt	932
NDUFS4	16	intron 1 + 1261	ttctttctcttttttttt T/Δ ggtatcaattctcaactga	933
NDUFS5	1	intron 1 + 388	ccaaacatagccagcccttc C/T ggtgttaactccggctgtt	934
NDUFS5	2	intron 1 - 13082	agtgaagccagattgcacca G/A tgcattccagcctggcgaac	935
NDUFS5	3	intron 1 - 12905	gttttcaacaaaggactaca G/T agtagtaggaattttctt	936
NDUFS5	4	intron 1 - 12564	attttcatcacacctcaact T/G aaggtataacagccttaaga	937
NDUFS5	5	intron 1 - 12561	ttcatcacacctcaactta G/A gtataacagccttaagaatg	938
NDUFS5	6	intron 1 - 10561	aacaatgtgttatgtggg C/G ggtgtgtgagcaggtgtcat	939
NDUFS5	7	intron 1 - 9065	ccgtgtgtctcgtctcag G/A gtacaccttttccctttaga	940
NDUFS5	8	intron 1 - 8871	tcacacagctgtctgtagata T/G aggaacgcagaccttgcctt	941
NDUFS5	9	intron 1 - 7312	aaatccttggcttctagaat G/T ggtcactgatgtatataat	942
NDUFS5	10	intron 1 - 6827	aaactctgctctcccgatc A/G cggcattctctcctcagc	943
NDUFS5	11	intron 1 - 6725	agtagagcggggtttcacc G/A tgttagccagcatgtctcag	944
NDUFS5	12	intron 1 - 6631	aggcgtgagccactgcgcac G/A gcctagaccttcttctata	945
NDUFS5	13	intron 1 - 6531	cccaacagctcccaatgta A/G acagatctattatattctg	946
NDUFS5	14	intron 1 - 6346	gcaacagactctgacctata T/C cccatagggtacagctgag	947
NDUFS5	15	intron 1 - 6327	atcccatagggtacagctga G/C gactttaatcagaaaggag	948
NDUFS5	16	intron 1 - 6122	tagccttgcctttactctac T/C gttcctcccaatcacacc	949
NDUFS5	17	intron 1 - 2512	acaaactcttaatgcgaatt T/C tgcagatcaaatggcctta	950
NDUFS5	18	intron 1 - 1945	tttaatctcctttaaatlle G/A caatttcaaacctagggtta	951
NDUFS5	19	intron 2 + 75	ttttttttttttttggag G/A aagtctcaactttgtccct	952
NDUFS5	20	intron 2 + 148	ctgtagcctctgcctccag G/A ttacggcattcgtctacct	953
NDUFS5	21	3' flanking + 150	cagattcaagttgttctct G/G cctcagcctcccaagtagct	954
NDUFS5	22	intron 1 - (10682-10681)	attataaacactaaacaaac AT/Δ gtgtgtctcttttaggggg	955
NDUFS5	23	intron 1 - 10272	aggaacaagtgaactacctg A/Δ aaaaagaagatgaacaa	956
NDUFS5	24	intron 1 - 2069	accagacagagttccctta C/Δ tigttttctgtggcaaga	957

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
NDUFS6	1	intron 1 + 26	ggccgctgggtacagatgc A/C ccttctccagccgcacctc	958
NDUFS6	2	intron 2 + 1076	ggatcatggtggtggaggg G/A gcttgtctgtggtgttg	959
NDUFS6	3	intron 2 + 1260	cagttgtcagtaagtggtg T/C atagggtaaagtctctttct	960
NDUFS6	4	intron 2 + 1413	caaaaggagcicatggcattg C/T gaatggacatttctccgt	961
NDUFS6	5	intron 2 + 1568	tggagaaggagggtttctc T/C tagtggatcggtatggt	962
NDUFS6	6	intron 2 + 1692	gaccgtggtgacggagttt C/T ctggcatcgatgggtgtt	963
NDUFS6	7	intron 2 + 6488	tagcttaataattattggc A/G ttcatgttcgaatgacctga	964
NDUFS6	8	intron 2 + 6563	tttaacttttattttaa G/A tccatgaatgggtcgtat	965
NDUFS6	9	intron 2 + 6740	aaagatttaaacctacatat C/T ttatgcccaatcattgat	966
NDUFS6	10	intron 2 + 6832	gcgagggactcatttacag A/T ggttgacacttcactgtgt	967
NDUFS6	11	intron 2 + 7054	ttcactgcggagcttggcc G/A tggaaacccggagccgggt	968
NDUFS6	12	intron 2 + 7186	ggtcagggtcacoccttggc T/C ggcacacataatgacggga	969
NDUFS6	13	intron 2 + 7225	gaggcatcccggtcagtc G/A ccagtgtcaggcgctcagca	970
NDUFS6	14	intron 2 + 7810	cttcacacttggggcggga C/T gctgtagaaggagcacaag	971
NDUFS6	15	intron 2 + 11080	gtacatgttcagtgotttct C/T ctttggatttcagttaaac	972
NDUFS6	16	intron 2 + 11657	gggacagaacgatgtgttg G/A gagaagagggtggcagag	973
NDUFS6	17	intron 3 + 208	cgaaaacccctttcaactg T/C gaagtgtggggcctgttt	974
NDUFS6	18	intron 3 + 1031	ctagatgggactgggcacc C/T ggcattgcccctcctgggt	975
NDUFS6	19	3' flanking + 270	gcttcagagagccaaggttg G/C tcttgaggtgcatagtgag	976
NDUFS8	1	5' untranslated ~ 45	agtgtagcctccgcctccg A/C ttgactggcctgttggcaa	977
NDUFS8	2	intron 1 + 163	aggcgacggggagccggc T/C ctccagggccctgcggccg	978
NDUFS8	3	intron 3 + 123	ttctgagcctgtttccact T/C ttaaatgattatggtgat	979
NDUFS8	4	intron 6 - 505	aggcaaggcagggccggcac G/A gtgctaacgttgttaacc	980
NDUFS8	5	3' flanking + 491	ggccctgagctggcctgctt C/A cagccacactccttctctg	981
NDUFS8	6	3' flanking + 693	ttcatttcatttgcagtgag G/A aaaccagctccgaggggga	982
NDUFS8	7	3' flanking + 1267	tttcccgagctaacccggc G/A tcaggcgtggcattggagcc	983
NDUFS8	8	3' flanking + 1362	cgctgggttcttcccttac C/T gtggtctccaggcacttac	984
NDUFS8	9	3' flanking + 1449	tgctagaacaggcctatggc G/A cccacccacagtcgcccaa	985
NDUFS8	10	3' flanking + 1572	cagcccccagagccctgtgt C/A gctgtgtgggcttaggat	986
NDUFS8	11	3' flanking +(783-784)	cagagaccttgacccccccc (C) atctaccatcatttccaaa	987
NDUFS8	11	3' flanking +(783-784)	cagagaccttgacccccccc atctaccatcatttccaaa	988
NDUFB3	1	5' flanking - 1439	ttaaaagtgaattttttct G/A cggggcagcgtgctcagc	989
NDUFB3	2	5' flanking - 1436	aaagttagctttttctg G/A ggcacgttggctcagcctg	990
NDUFB5	1	5' flanking - 213	ggcagatgaactctctccac A/C aagaaggccaaacggccg	991
NDUFB5	2	intron 1 + 6288	gggagtttattacctagg T/C cagttaagttaaggagcct	992
NDUFB5	3	intron 1 - 1581	cttcggggccactgtatct A/G ttcttccctgttlacct	993
NDUFB5	4	intron 1 - 1487	ccctcttagaccgtatatag T/G tctagcatagatctgcaca	994
NDUFB5	5	intron 2 + 556	ttgtctggccatctgccac G/A gtatataagctctgaatca	995
NDUFB5	6	intron 3 + 467	ggcgcacatgcactccagcc C/T gggcaacagatggactct	996
NDUFB5	7	intron 3 + 497	agtggagctctgtccccc C/G caaaaaaaactataatcct	997
NDUFB5	8	exon 5 + 397	atpatagctcctgaagaata T/C atgaagaacaaatggccgtc	998
NDUFB5	9	intron 1 +(231-215)	attagcatttctaaaagtt GTT/Δ attcaccatcccaattaag	999
NDUFB7	1	intron 1 + 68	cctgaacacctggaccccca G/A ggttgacccccaggcctgg	1000
NDUFB7	2	intron 2 + 266	ggcctctctaggggcctgtt T/C gatgggacagggcaggtg	1001
ABCA1	1	5' flanking - 278	ggcccccggcggggaagg G/C acgacagccgggacccata	1002
ABCA1	2	5' flanking - 99	acataaacagagggcgggaa G/C gggcggggggggggagag	1003
ABCA1	3	intron 1 + 159	gcggttttaaatggggagac G/T atgtcctatgacgagcttg	1004
ABCA1	4	intron 1 + 506	gaattggctatatgtcccc G/C ggaactggagcggcacagtc	1005
ABCA1	5	intron 1 + 5897	gtacaaaaccctttagcttt T/G gcaaacctcctttaagccg	1006
ABCA1	6	intron 1 + 5929	ttagaacccgatttaaatgc C/T tccctctcatgagctctt	1007
ABCA1	7	intron 1 + 5962	aagctcttctgtgacactc T/C ttcccatcactaaagtga	1008
ABCA1	8	intron 1 + 5985	cccatcctagtgagagt A/C agatccctctcttctactt	1009
ABCA1	9	intron 1 + 11416	ttacagtgccctttatagg G/A agaaagaagaattgtct	1010
ABCA1	10	intron 1 + 11935	ttctgtggagcaaatagag G/A gctgtctgacacttggttc	1011
ABCA1	11	intron 1 + 12281	gaotgtttgatttggaaa T/A cttaataacagtagttttt	1012
ABCA1	12	intron 1 + 12924	gtgtgacactcttactc T/C aggtgaacctcggggaag	1013
ABCA1	13	intron 1 + 13002	gagcctcaatcacagattct C/G tctagctcacatgaagtta	1014
ABCA1	14	intron 1 + 17715	ggagcctgactttgtgaag C/T ctctcctttccaccagag	1015
ABCA1	15	intron 1 + 17848	gagggctgactgtacccct T/C gataggagcccgacataa	1016
ABCA1	16	intron 1 + 21384	gtgggtggaggaattggag G/C aggaagcttgccaaagtgt	1017

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ABCA1	17	intron 1 + 22145	gtgcttciaaatacaacgaa C/G tgattcctggagagcagctt	1018
ABCA1	18	intron 1 + 23063	ggagggacacctgtgacccca G/A cggagtagggggcggtgtg	1019
ABCA1	19	intron 1 + 23131	agtgtcatatgtgtgacc G/A tggagcttgttgcgglt	1020
ABCA1	20	intron 2 + 156	ggacacaggactgtgtgtc T/C ggtatggcatgtgcttat	1021
ABCA1	21	intron 2 + 384	gctgtgggtgaagtgaatta A/G tggccccactcttagagatc	1022
ABCA1	22	intron 2 + 1081	agtgcagccaaaattgcasa G/A tcataccattcaaatata	1023
ABCA1	23	intron 2 + 2801	aagaaaagtattttttca A/G gtgtcgtatgcttagattgt	1024
ABCA1	24	intron 2 + 2830	tgcttagattgttagattg C/G aaagatctggttcacatctt	1025
ABCA1	25	intron 2 + 2856	ttgtgcttgatctgtaca A/G ctgcagagaactgggctcag	1026
ABCA1	26	intron 2 + 3187	tgatgctgttgcctgcagc A/G tacggacgttcattgcagc	1027
ABCA1	27	intron 2 + 3190	tagctgttgcttcagcaca C/T ggaagttcattgcagctc	1028
ABCA1	28	intron 2 + 3194	tggtgctgcagcatagga C/T gtctattgcagcttctgt	1029
ABCA1	29	intron 2 + 3204	ggcatagggagcttcattgc G/A cagttctgtctctgagat	1030
ABCA1	30	intron 2 + 3401	acataaagcctgtgtgtgc T/C gccaggaagactagaacgc	1031
ABCA1	31	intron 2 + 13927	gtcccccacatctggcact A/G tgctaaagctgggaatcag	1032
ABCA1	32	intron 3 + 4163	ccagcccacttcattatcc G/A tagttacctcttagatgt	1033
ABCA1	33	intron 3 + 4262	tgtaaaaggaggaactaagga T/C gccagggactttctgcttag	1034
ABCA1	34	intron 3 + 4306	ccctctctcactctccaa C/T gctgtatctatgaacccat	1035
ABCA1	35	intron 5 + 240	gacagagaagaaagtcocag G/A gaagaatactacagacttg	1036
ABCA1	36	intron 5 + 490	gatgggcattgaactgttt G/A tctttaaaagtgaaatctt	1037
ABCA1	37	intron 5 + 563	tatctggggagtggttcattt T/G ctgactgagcattggctgc	1038
ABCA1	38	intron 5 + 1051	ggctacaaaactgtctttc C/T tgggcagtaaaagaggcaa	1039
ABCA1	39	intron 5 + 3051	tagagaaacagictaatctt G/A ttcttcctgaatagtcga	1040
ABCA1	40	intron 5 + 3127	aagtcctatgatttttaggc A/G aaatggcctctcttctctt	1041
ABCA1	41	intron 5 + 5924	ctttctttcacaatgtgcc C/T ccagagctttctggaagg	1042
ABCA1	42	intron 5 + 6831	ccagtcctcagccttgcca T/C tgctatgctgtctgaaa	1043
ABCA1	43	intron 5 + 12678	gtccacgcctcgtctccccc G/C accctctggccatctctct	1044
ABCA1	44	intron 5 + 14214	cagcttggtccagagggcct G/A gacctgggtccaggggtcc	1045
ABCA1	45	intron 5 + 14257	gctgttcccccgtgtgtgc C/T cagagggcctggtgtgtgc	1046
ABCA1	46	intron 5 + 18078	cctacacacacatgcacgtg C/T acagccaaaggtgtgtgact	1047
ABCA1	47	intron 5 + 18795	ctggctctctctggacgtg G/A ccagctaaaggaatctcc	1048
ABCA1	48	intron 5 + 18948	gcattgggtgactaagaac G/A catcttccctctctctatgg	1049
ABCA1	49	intron 5 + 19053	ctcccccacattaaaagt T/C aagggtgctttatcaaatg	1050
ABCA1	50	intron 5 + 19148	ggcccaagaacatgcattht C/A gcaigtccctaaalgaagc	1051
ABCA1	51	intron 5 + 19229	atgtccacagtgtagatga C/T atgtgtgggaagcatcagg	1052
ABCA1	52	intron 5 + 19405	cttgtcaattattctgtc T/C atataactcaattactga	1053
ABCA1	53	intron 5 + 19534	catgtgaccccttagctgc G/A cggatgaactcgtctccca	1054
ABCA1	54	exon 6 + 474	gaacacctctctggttctt G/A tatcacaacctctctctccc	1055
ABCA1	55	intron 6 + 210	gcaacctggcgtcatggccc A/C gctgttaaaataaattga	1056
ABCA1	56	intron 6 + 334	acagttctgaggcaataacc G/A tggtaagggttatgatct	1057
ABCA1	57	intron 6 + 2288	cttcttcaaaagcttggtt C/T cactggaccacgtatgaagt	1058
ABCA1	58	intron 6 + 2322	atgaagtgaatagtittgg T/C ccagaaaggcaattatgtaa	1059
ABCA1	59	intron 6 + 2820	gtgtttgatacattctgag T/G ttcagtaagagacctgatg	1060
ABCA1	60	exon 7 + 656	tgagctttgtgcttcccaa G/A ggagaaactggctgcagcag	1061
ABCA1	61	intron 7 + 416	catcataaagatgacattgt G/A ggtgtcacagttgaaggg	1062
ABCA1	62	intron 7 + 471	agaccacactatttagctta C/T ttagtataacattgcaag	1063
ABCA1	63	intron 7 + 504	ttgcaaaagaaaattccgac G/A aagtttttcagcctaggaa	1064
ABCA1	64	intron 7 + 679	gtctgttggaattctctc G/C ctaccccaaacatcatctt	1065
ABCA1	65	intron 7 + 1740	acaaatgctcacccttccg C/T tggatgattgaattttgg	1066
ABCA1	66	intron 7 + 2122	tgattaaaggtggctactacc A/G ggtgctttctgcatactcg	1067
ABCA1	67	intron 7 + 7753	taggaattccagctgtgaa T/C ttcttactgaagctctttgg	1068
ABCA1	68	intron 7 + 8973	atggaaattgtttattgtt A/T ctacagattgccaattat	1069
ABCA1	69	intron 7 + 8976	gaatttgtttattgtgact A/G cagattgccaattattatg	1070
ABCA1	70	intron 7 + 11327	ctaacaactctatttcatt G/G agtcttatataaagaatgg	1071
ABCA1	71	intron 7 + 11738	ctgacgtttaaggagaccg C/T gtatgtcctttgaggactg	1072
ABCA1	72	intron 7 + 12295	agtctgttaattattgtct T/A tttttcttagcttatgct	1073
ABCA1	73	intron 8 + 387	tagcaaggccaaactttta C/G caacacacatgcttgcatac	1074
ABCA1	74	intron 8 + 697	ggaaactgtctgtgtccccc A/T gcataggaagctgagccagg	1075
ABCA1	75	intron 8 + 1312	attgtctgcagatcccttc G/A cagccctctgtccctgttc	1076
ABCA1	76	intron 8 + 3036	ctttatgtgggaagaattt T/G ttttttattggggagtg	1077

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ABCA1	77	intron 8 + 3176	aatggcctggtctctgt C/A cctttctgtctgtatgcoctc	1078
ABCA1	78	intron 8 + 3364	ggcagaaggcaagcttagg A/T ccttagaggtgctggaccac	1079
ABCA1	79	intron 8 + 3373	caaaagttaggacotagaga G/A tgcaggaccacgccactcac	1080
ABCA1	80	intron 8 + 3561	caggatllattaatgattt C/A ttgtgaatgtttgaaata	1081
ABCA1	81	intron 8 + 3654	agtgcgggaatcattttgca T/C gtaagacagacgctgcctg	1082
ABCA1	82	intron 8 + 4715	ggcagaggggtctcagaato C/T gcatttccaacaaigtctcc	1083
ABCA1	83	exon 9 + 936	cttattgtctcgggcatcc C/T gggggggggggctgaagat	1084
ABCA1	84	intron 9 + 2309	ccctcaagagtcaglltaa A/G tgttggtcatgttagttgc	1085
ABCA1	85	intron 9 + 2392	atggagggtgtgtcttca T/C gaaaacattttccagatca	1086
ABCA1	86	intron 10 + 228	tgaggatgggagagactggc A/G cagggtctgtgtatgggt	1087
ABCA1	87	intron 10 + 319	ttctgcgtccctggtctccc C/T acctgaactccagtgaaaca	1088
ABCA1	88	intron 11 + 377	gaagaagtgtagagcaaa A/G gcattgtgttagatgtagac	1089
ABCA1	89	intron 11 + 521	agtgtcttagagacaattgg G/A ttcaaatgtggagcaggctg	1090
ABCA1	90	intron 11 + 2850	ctctataaatcattatgct G/C ccattgaaataataatata	1091
ABCA1	91	intron 11 + 2976	ctccaattcgttagaccag A/G gcttcatctctctgtcgaa	1092
ABCA1	92	intron 11 + 3056	gtttgcagctgtgttttc C/T ggcagcacatctgtcaggc	1093
ABCA1	93	intron 12 + 340	ggcattattgtgaaactta T/C ctaaaatcgaattcgggtcc	1094
ABCA1	94	intron 12 + 381	aattaaattttgaaattt A/G tattaaattattattatga	1095
ABCA1	95	intron 14 + 1728	caggctcagaggccttggcc C/T atccacctggctcactgtg	1096
ABCA1	96	exon 15 + 2040	atggccttgagacaacagat C/A ctctgttttagctgtttcat	1097
ABCA1	97	intron 15 + 1382	cttttagcagaaaagttac G/A tggatattatctccacag	1098
ABCA1	98	intron 15 + 1453	tatataaggagaaacagtt G/A aaattacctattgagaaac	1099
ABCA1	99	intron 15 + 1567	ttctgcgtggtttggtaa G/A tcaattatcttcttagat	1100
ABCA1	100	intron 15 + 1617	cagttgcctcatcagaaga T/A gaacagcattacgcctcgc	1101
ABCA1	101	intron 16 + 95	gtttgagacagagagatgt T/A gtottttccatggacatz	1102
ABCA1	102	intron 16 + 452	tgtgttttctgtgagta G/A tttttgaaactaagcacac	1103
ABCA1	103	intron 16 + 657	ctgttgctcagctgtggct T/C cataggcatcagcagcccca	1104
ABCA1	104	exon 17 + 2473	gcttcaatctcaccacttgc G/A tctccatgatctgtttgac	1105
ABCA1	105	exon 18 + 2649	ggttccaccagagagaat A/G tcagaaagtatgtctgtg	1106
ABCA1	106	intron 18 + 1730	tgaagttcaagcagctgc C/G ctgtgtccttcaactccact	1107
ABCA1	107	intron 19 + 426	aggaccctacagtgagtagt A/G tcaggagggtcaggggctg	1108
ABCA1	108	intron 19 + 468	aaagcaccagcgttagccto A/G gttgcttcagcagcattcc	1109
ABCA1	109	intron 20 + 876	cccttccatctaaagtga C/T acatggggctcatgtcagg	1110
ABCA1	110	intron 22 + 118	catgggatactctctgtta T/G cacagaagagataaaggca	1111
ABCA1	111	intron 22 + 560	aaagctttgccattctagg G/A tcatagccatcagggtgaa	1112
ABCA1	112	intron 23 + 102	accccttttgccatgttga A/G ccacatctccctgctctgt	1113
ABCA1	113	intron 23 + 287	gtcaagaaagagacttgt C/T aagaggaagagccttggct	1114
ABCA1	114	intron 23 + 1063	accttcaacctcaggagac G/A aggtgttccacagccacac	1115
ABCA1	115	intron 25 + 321	ctctttacttaagtagctg T/G gaggacagcagcagcagga	1116
ABCA1	116	intron 25 + 376	gttagaaattcagcaacttg G/C gccagctcagacctaactga	1117
ABCA1	117	intron 25 + 478	catacataggaatgacaaa C/T gtttatggatggatagcta	1118
ABCA1	118	intron 25 + 579	tcatttaattctcaaaaaa G/T atgaaaaaatgaacactcag	1119
ABCA1	119	intron 27 + 153	aatgttaaaagccacttgtt C/T ttgcagcatctgtcatgtg	1120
ABCA1	120	intron 28 + 1058	actatcatggagataatga C/T tatgtgttccatgatltga	1121
ABCA1	121	intron 28 + 1317	caggaccagtggtctggt C/T acctgaatgtgagcactat	1122
ABCA1	122	intron 30 + 372	tatatgttttttaggtttg T/C ttatcagcttctctgtttt	1123
ABCA1	123	intron 30 + 506	ccctttaaaagtgagcagt A/G gataaataaattcagtgaag	1124
ABCA1	124	intron 30 + 1033	ctgtgtttcatgtgctttt G/C attttccacatgaaggtgt	1125
ABCA1	125	exon 31 + 4281	lcttccctttgagagacac G/A ccctgccaggcaggaggga	1126
ABCA1	126	intron 33 + 626	ggctcctgttaactgatttc C/T gtcttttctctgtcctttt	1127
ABCA1	127	intron 33 + 719	taatagccctcatgtagaa G/A ggagccggagcctgtgata	1128
ABCA1	128	intron 33 + 726	cctcatgtagaaggagcc G/A gggcctgtgtataaggccag	1129
ABCA1	129	intron 33 + 869	cttttccatgtctcagct A/G tctaacgtgtgtgtatca	1130
ABCA1	130	intron 33 + 1097	ctgtgcacccactgtctgg G/C ttttaatgtcaggctgtct	1131
ABCA1	131	exon 35 + 4760	tatgacaggactggacacca G/A aaataatgtcaaggtaaac	1132
ABCA1	132	intron 35 + 234	aacctatctaaacctggtt T/C cctcctctgtgaatggaga	1133
ABCA1	133	intron 37 + 411	aactctgtacattttatcag C/T agcttatcatccattgcaa	1134
ABCA1	134	intron 37 + 1224	caggcataggtgattcagag A/G tgaagggtcaagtcctgaa	1135
ABCA1	135	intron 37 + 1720	aaattaaattactcagct G/T ggaatccatcgttcagtaag	1136
ABCA1	136	intron 40 + 251	tgaagglaaggaasetgtg T/G tatttctgttgatccactgg	1137

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ABCA1	137	intron 40 + 252	gaaggttaaggaaatagtt T/C atttgcttgatccactggc	1138
ABCA1	138	intron 40 + 319	agcactgaaagtcacacc A/G taacttgagaattaggtga	1139
ABCA1	139	intron 40 + 957	cttgtaactcttttttctt G/C tcatgggtgatagccattg	1140
ABCA1	140	intron 41 + 146	tgaatgggcaicccgcagc C/T cctccctgcccactcctga	1141
ABCA1	141	intron 42 + 239	cattggtttatatgcttac A/G ttatgtgttagttattaaa	1142
ABCA1	142	intron 42 + 321	aataaatggttgatttgag T/A ttgagttcatagtcacaaa	1143
ABCA1	143	intron 42 + 322	ataaatggttgatttgag T/C tgaatttcacatgccaacaa	1144
ABCA1	144	intron 42 + 533	agtgaaaaattatgtatg G/A ataagatgatacaggttct	1145
ABCA1	145	intron 42 + 546	tgtatgtatgaatgaatg A/G cgttctacaaaagccaggtt	1146
ABCA1	146	intron 43 + 739	tacagccacacttaaatgg T/A cccattatgaatcatatt	1147
ABCA1	147	intron 44 + 18	taggtggaagaaagtgcc T/C tgaattttgctgcaagact	1148
ABCA1	148	intron 44 + 264	acaeataatttgctgttt T/C ttaagatataatttagta	1149
ABCA1	149	intron 44 + 279	tgttttttaagatataatt T/C agtgaatttttgtaattga	1150
ABCA1	150	intron 44 + 508	tttcatatgctacataaat C/T cccctatgtacatgaccta	1151
ABCA1	151	intron 44 + 1477	gatctccctcctgtctctt A/T cattttgcagtagcaatgt	1152
ABCA1	152	intron 44 + 1665	tgggttaagaactgatttg G/A ttggtatagctgtgagggcc	1153
ABCA1	153	intron 44 + 1956	gtgtgctcacactcaaat T/G tctgggcttctcatttgg	1154
ABCA1	154	intron 45 + 68	aatatataccttatgtgttt T/C cccacagcattgactcagg	1155
ABCA1	155	intron 46 + 808	ttatactgacttcaatagag G/C ttccagacaaaagtgttt	1156
ABCA1	156	intron 47 + 336	ttcacaaattgaacacacac T/C acactgaacagcatcctcc	1157
ABCA1	157	intron 49 + 55	aggtgtggatcctcctccc G/C acactcccgcccataggtcc	1158
ABCA1	158	3' UTR(exon 50)+7949	aacaaaaatgggtgtctc C/T aggcacgggaactgtgtc	1159
ABCA1	159	3' UTR(exon 50)+8226	aggagccacactgtaacata C/T tgggcagccttttttttt	1160
ABCA1	160	3' UTR(exon 50)+8682	aactttctcactttttcca G/A aatttgatattaaactga	1161
ABCA1	161	3' UTR(exon 50)+8697	ttccagaatttgaatttaa C/T gctaaaggtgtaagactta	1162
ABCA1	162	3' UTR(exon 50)+9097	aactattttgaagaaacac A/G acattttaacacagttgaa	1163
ABCA1	163	5' flanking - (1033-1032)	tgaactaaattattagacat (AT) ggtgtgagcctgcattcc	1164
ABCA1	163	5' flanking - (1033-1032)	tgaactaaattattagacat ggtgtgagcctgcattcc	1165
ABCA1	164	intron 5 + 6368	ttctgatgggtgtgtgtc G/Δ tgaagatcatgactgggtg	1166
ABCA1	165	intron 5 + 9709	cattttctgtgacacccc T/Δ caccattcaggcagctgct	1167
ABCA1	166	intron 5 + 13816	tcctactctcctcttttt T/Δ catttgctctctacacccac	1168
ABCA1	167	intron 10 + (270-271)	cttttcaggaggagccaaa (G) cgtcattgtctgtgtctt	1169
ABCA1	167	intron 10 + (270-271)	cttttcaggaggagccaaa cgtcattgtctgtgtctt	1170
ABCA1	168	intron 20 + (611-612)	tttagccatcctctccccc (C) gccaccctccttattgagc	1171
ABCA1	168	intron 20 + (611-612)	tttagccatcctctccccc gccaccctccttattgagc	1172
ABCA1	169	intron 32 + (391-392)	gagtgccttgggtactctct (T) gatgggggactccatgata	1173
ABCA1	169	intron 32 + (391-392)	gagtgccttgggtactctct gatgggggactccatgata	1174
ABCA1	170	intron 37 + 847	gctgtatattggaatgccc C/Δ gttttcaaaagcaagccaa	1175
COMT	1	5' flanking - 1287	cgtatgatattcccaattct G/A agtccagatccctgaaat	1176
COMT	2	5' flanking - 1217	tgtgattatgggaagggaa G/A cttttctgtctgtgtccccc	1177
COMT	3	5' flanking - 503	caggggctccaggaggagga G/A tgtgtatcctcccatgtctc	1178
COMT	4	5' flanking - 425	gagaagtgggaagtctgccc C/T agtggggccggtgctgtgtg	1179
COMT	5	5' flanking - 277	cccagcccccagtttcccac C/T tgggaaggggctacttgtg	1180
COMT	6	intron 1 + 12058	ctggcccatgggaaggggg G/A agggggcccccagcggggcca	1181
COMT	7	intron 1 + 12070	agggggggggggggggggc A/G cggggccacagtaaggagt	1182
COMT	8	intron 1 + 18831	tgtgtatgttcttgtaaac C/T agcccttggcttaccatc	1183
COMT	9	intron 2 + 832	cctctctcttggccacccgt G/C actacccccaactccggccc	1184
COMT	10	intron 3 + 90	ggagaagctgtatcacccc A/G ttccagggggctgggaacc	1185
COMT	11	intron 3 + 425	ccccaaggtggcggttcgg T/G gattcagagagggcagctct	1186
COMT	12	intron 3 + 671	ggctcctgctctttggaga G/A gggggggccgtgctgggg	1187
COMT	13	intron 3 + 676	ctgctctttggggaggtgg G/T gggccgtgctggggatcca	1188
COMT	14	intron 5 + 75	tcagccctcagcctctccaa G/C agccaggcattccagttag	1189
COMT	15	intron 5 + 310	accagacaccagggcagaaa C/T ggcacaggacacaggagt	1190
COMT	16	intron 5 + 346	agatgggggggggaagggcc G/A ctctggggccagcctgctct	1191
COMT	17	intron 5 + 3023	aaggcagcccccctgctcaa G/A gcttagggcattgtctcct	1192
HNMT	1	5' flanking - 211	cagagggcagatgacagtctt C/T cgttaagatttcaactgtg	1193
HNMT	2	intron 1 + 5409	aetatacctgataattgg A/G acatttcattgttggcctagt	1194
HNMT	3	intron 2 + 2561	cacttgccttggacaagaa A/G agaaggcctacaagaaag	1195
HNMT	4	intron 2 + 2895	caatcagaaatgaagaaa A/G ctccaagaaaatttaagt	1196
HNMT	5	intron 2 + 3977	accaaacttggaggtgaaa G/A ttatgatgtatgttcagt	1197

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
HNMT	6	intron2 + 5296	ttacatagtgagttggag T/C cccaggattttatttcoct	1198
HNMT	7	intron2 + 13317	caaccctcatgaattcttag C/T tgggatgggtccctataaca	1199
HNMT	8	intron2 + 14682	gtatgtgagcaaatgagttc A/Δ ggaagatttaaatcccta	1200
HNMT	9	intron2 + 15406	gtctatgcattcatgcctcc G/A tctaaccagctgtctaccta	1201
HNMT	10	intron2 + 28943	atgtgacttaacttcaggt A/G tatcaatattccctgaatgt	1202
HNMT	11	intron4 + 49	cagaagaagagcttttcaga A/G tatatataatgaatctct	1203
HNMT	12	intron4 + (1942-1943)	tttgagaaaatttaaggta (A) tcttctatggcccacttcca	1204
HNMT	12	intron4 + (1942-1943)	tttgagaaaatttaaggta tcttctatggcccacttcca	1205
HNMT	13	intron4 + 2405	ccctgtgaccaagcagataa C/A ctatgctttatitaglcca	1206
HNMT	14	intron5 + (80-81)	cctgtgtttgaagaagctt (TT) atatattttgtcttcattat	1207
HNMT	14	intron5 + (80-81)	cctgtgtttgaagaagctt atatattttgtcttcattat	1208
HNMT	15	intron5 + 235	ctttcttttgggaastatg T/C ctittgtctctatatatga	1209
HNMT	16	intron5 + (702-703)	tacttacaggttgatttag (AT) acacagcagactctgtcttc	1210
HNMT	16	intron5 + (702-703)	tacttacaggttgatttag acacagcagactctgtcttc	1211
HNMT	17	intron5 + 749	ttcacacagacccactctt T/G aacaccatagtccacaaat	1212
HNMT	18	intron5 + 1101	gtggcagcctattctgtat T/G atattcatcaatcatcaga	1213
HNMT	19	intron5 + 1137	acagaaaaagtattgtagac G/A gaataacaattcattgaga	1214
HNMT	20	intron5 + 1348	aaggagcatgaatgtcca C/G aagtaacigagaactgatta	1215
HNMT	21	intron5 + 1673	caaaagaagaggagtaaga C/G tcaacatcagtttagctttt	1216
HNMT	22	intron5 + 2022	attttatttgggctttcta C/T gtctctctctctctaaagcta	1217
HNMT	23	intron5 + 2285	tgtcatatcaactttaa G/C atccagagtaaatgtggag	1218
HNMT	24	intron5+4159	taccagtggcccgcaacc C/T tcttatagtagtttaaal	1219
HNMT	25	intron5 + 4501	aagtatccacaaatctacta C/G tctgtttttcttcaatga	1220
HNMT	26	intron5 + 5251	cacacacacacacacaca C/G caaatggagcgcgcagaca	1221
HNMT	27	intron5 + 5802	gaaaagaaaaactgcttca C/T atcatgttgaacacaaagt	1222
HNMT	28	intron5 + 6189	tccaatccaccccttctcta G/C agcatatccctcagttacct	1223
HNMT	29	intron5 + 6297	gtcttgctcatctctttag T/A taatttgatcttggaaact	1224
HNMT	30	3'flanking + 458	tatgtcactctcaagaact C/T tataagaccagaagctctct	1225
HNMT	31	3'flanking + 993	ctgaanaagacactgaacc G/A ttaatcatactgatgtac	1226
HNMT	32	3'flanking + 1793	gtgggcacagacttttgg G/A ctgatatttcttattata	1227
GAMT	3	intron5 + 1411	ggtagactgggtccatccc G/A accagagagccaggtgcc	1228
PNMT	2	intron1 + 35	ctgaggacagggagacaaga G/T gtctcgggagtgaaagca	1229
CYP1A1	1	intron1+1590	ccactcttcaaaaggagta C/T atgtgacagcagctggaaat	1230
CYP1A1	2	exon2+160	gaatccaccagggccatggg G/A ctggcctctgtatggcaca	1231
CYP1A2	1	5'flanking-731	gactgggctaggttagggg T/G cctgagttccggctttgct	1232
CYP1A2	2	intron1+371	cttccctgtttcacactaa C/T ttttctctcttggaaatg	1233
CYP1A2	3	intron3+44	ataggcaggagaagccttga G/A acccaggttgtttgtcagt	1234
CYP1A2	4	intron5+81	tccctgtcaggaaactgttta T/C ataagtaagagggggacct	1235
CYP1A2	5	exon6+181	ctggccatcctgtacagca A/T ctggacttcagctgcggcc	1236
CYP1A2	6	exon6+295	cagctgcgcttctccatca C/T tgaagaagacaccaccatc	1237
CYP1B1	1	5'flanking-3669	tgtatcctgtgaagcatcac G/A gttatccttctctgcacatg	1238
CYP1B1	2	5'flanking-3149	tgcagcacttcccaacta G/C ttctctgtattttgagtca	1239
CYP1B1	3	5'flanking-1222	gggggaagccaccocccccc G/A agcgcctccggttccctta	1240
CYP1B1	4	5'flanking-376	ttccggagagcaagctcaag T/C cgcggagagggagggaggt	1241
CYP1B1	5	5'flanking-265	ctgggacacogtgcggcct C/T gattggaggtgctgtgatg	1242
CYP1B1	6	intron1+129	tgcggcagcgttgtccca G/A atgcaggaaaccgttacgag	1243
CYP1B1	7	intron1+379	tgaagtcaagccttctct C/T tctgtcccagactgggac	1244
CYP1B1	8	exon3+(799-800)	agcttctgggagatttttt (T) gagtcaagaacttaaggcc	1245
CYP1B1	8	exon3+(799-800)	agcttctgggagatttttt gagtcaagaacttaaggcc	1246
CYP1B1	9	exon3+1284	agtatagtggttccatga G/T ttatcatgaatttaagta	1247
CYP1B1	10	3'flanking+2226	ttcttttttttttttttt T/Δ aaaaattttctctatttct	1248
CYP1B1	11	3'flanking+(2226-2227)	ttcttttttttttttttt (T) aaaaattttctctatttct	1249
CYP1B1	11	3'flanking+(2226-2227)	ttcttttttttttttttt aaaaattttctctatttct	1250
CYP1B1	12	3'flanking+2230	ttttcttttttttttttaa A/Δ ttatttctatttcttaca	1251
PEMT	90	intron1 + (297-299)	attgtgagactcagaggt TGT/Δ ccgtgtagtcttgggatt	1252
PEMT	91	intron1 + 817	tcatgaagcctgttaaggcac A/G tcttgcgcccaagcagcttc	1253
PEMT	92	intron1 + 830	aaggcactcttgcgcccaa G/A cagcttcaatccagttctt	1254
PEMT	93	intron1 + 1035	gagttctctgaaggagctaa T/C accagttatgttttgaaga	1255
PEMT	94	intron1 + 1573	agtgaggcaggagagactaac C/T ggtgtgtgaggggtggct	1256
PEMT	95	intron1 + 1759	gatttttttaagaagaaga A/G gaaagaacatcaacatac	1257

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
PMT	96	intron1 + 2768	gcattctgtctccacagc C/A gggcacctccaggattcag	1258
PMT	97	intron1 + 2785	ggccggggcacctccaggt T/C cagaagtgactccagtg	1259
PMT	98	intron2 + 4598	ccgtgggttttttttt T/A ctctattcttgggtgctg	1260
NAT2	21	exon2 + 288	atgttaggagggtatttta G/T atccctccagttacaaata	1261
NAT2	22	5'flank - 2053	ctggttgcacacttttast T/C ccaggtgtcaggtttcaac	1262
NAT2	23	5'flank - 1299	gaatcaccagtgccggaggt A/G taacagtgaacccagacac	1263
NAT2	24	5'flank - 1145	ctgtagaacacaaagataat C/T ggaggcagttgtacatgcc	1264
NAT2	25	5'flank - 1036	ccttccacacaggtcccgag T/A tcatgtggcagcatgccaga	1265
NAT2	26	5'flank - 94	aaagatttgcataagagttc G/A cagaggcaaccigaggcct	1266
NAT2	27	5'flank - 643	atgtttatatattatattaa T/C attaatglaataaaattt	1267
AADA	1	5'UTR + 29	attaaagtacactattcagg C/T atcatgttaggtttactt	1268
AADA	2	intron1+138	gcgtggcctttgacastgt G/A ttacttagaagtgtgttg	1269
AADA	3	intron1+142	tggccttgcacatgtttta C/T ttggaatgtgttttttt	1270
AADA	4	intron1+1033	ttccagcagagacacacaca A/G gtaaacacccccagctaca	1271
AADA	5	intron1 + 1253	ttttttccctcatatttgc T/C gtctgtgtctacastgtga	1272
AADA	6	intron1+1366	ctctgttgcccttttaatta A/G ttaattcattcattactta	1273
AADA	7	intron1+1369	tgttagcccttttaattt A/C attcattcatttacttact	1274
AADA	8	intron1+2501	ggttacagaaagatgtgtg C/A ttggccaaasatgtatgt	1275
AADA	9	intron2+1971	aaatgaggttaagtaggag A/C attttttttttttttgtc	1276
AADA	10	intron2+1988	gagaattttcttttttt A/G tgcaggagaaatataacaa	1277
AADA	11	intron2+2341	aggtgacctttttttttt C/T atgcagacttaggtatct	1278
AADA	12	intron2+2546	gtctgacacagagagatcaa T/A ggcacaaagtgcagagcaaa	1279
AADA	13	intron2+2609	taggaggtttcactggaaac T/C tgaattcactgaggtatga	1280
AADA	14	intron2+2663	tataaatcacagtgtaaat T/C gttctgtgttttttaagta	1281
AADA	15	intron4 + 605	tgtgtcagtaaatattata T/C taagttaggtgaatgagaca	1282
AADA	16	intron4 + 821	tatatagtaggttagta G/T atcatglaattgtgagacta	1283
AADA	17	intron4 + 679	ttagagcttcagcgaattc A/G tataatcttcagatgttat	1284
AADA	18	intron4+1680	gttaaatgttgataaatat C/T acaatttgcacaaatatttg	1285
AADA	19	intron4+1748	atttagaagttctatcacatc T/C ttlatagtatattacacact	1286
AADA	20	intron4+1771	tatagtatattacacacttc G/A aaacacacaaatattttt	1287
AADA	21	exon5 + 238	caagtcactcttcaaat A/G ttaattggagttccctgtc	1288
AADA	22	3'UTR + 121	ttagaasttggttttttta A/G aatgtgtctagtttaagttca	1289
NTE	1	5'flanking - 535	ccgatctgtctccagattc C/T ttttaacttagactttctg	1290
NTE	2	5'flanking - 15	gttaatccccggaacaaace A/G gacggccttgcagggccac	1291
NTE	3	5'flanking - 748	agcatggcgcggggagag G/T gtggagggctgggagggac	1292
NTE	4	5'flanking - 690	tgaataatttaagggccg T/C gcttgcggagccggcggaa	1293
NTE	5	intron6 + 605	tcttgcatatacttagtg A/G ggggtctacatcaggggtt	1294
NTE	6	intron6 + 748	agctccagcctctctctc C/T ggggtttatctcagcatct	1295
NTE	7	intron6 + 987	gggtcgtgctctgggtccc C/T gtgctcatgtagtctacct	1296
NTE	8	intron6 + 1882	tggcctcaagcaatcctccc G/A cctcggcctcccaagtgt	1297
NTE	9	intron6 + 2222	gaatgtttttagtagacaga G/A agactgtctcgtggtttc	1298
NTE	10	intron12 + 166	tatctggtaccggaggaagt C/G tggcctgtctcccaaggcc	1299
NTE	11	intron13 + 69	atccaggtccacccgctgcc C/T gtcttgatttttaactctg	1300
NTE	12	intron14 + 8	agccccgcctcgggttaggc C/T tgggaacctgcccgtatg	1301
NTE	13	intron16 - 113	gccacccgcccctgcgctt T/C atattttttaacccttcc	1302
NTE	14	intron21 + 34	agggccggccggccagagc A/G tgcaggagatgtatccgg	1303
NTE	15	intron21 + 128	gaagaatcgtgcccctgag G/A gttcaaaccttaagtagga	1304
NTE	16	intron21 + 151	ttcaaaccttaagtaggacc C/G aggtgcagagcatctggag	1305
NTE	17	intron21 + 651	ccactgtctccagccggga C/T gacagagctagaacctgtt	1306
NTE	18	intron21 + 737	tggaaastgtctgtgatt G/T ttgttaggactctgggac	1307
NTE	19	intron21 + 1752	acagctggtctaggcttta G/C tgggaactgggaagcaac	1308
NTE	20	intron21 + 1788	gaagcaacagctgggtcaaa A/Δ gtgactttttttttttg	1309
NTE	21	intron21 + 1807	cactgcaacctgtgctctcc A/G ggttcaagtgattctctgc	1310
NTE	22	intron21 + 2065	ctgctctgttttatgttcag G/T tccccattagacagaggaa	1311
NTE	23	intron21 + 2336	agtcgtggggcacagagca G/A gaatttcagataagaggaa	1312
NTE	24	intron23 + 41	tggggaggggggggggg G/C ctggagcctcaaatcttctc	1313
NTE	25	intron23 + 71	caaatcttttcagacctgag T/C tcaagttctcgtcttcaac	1314
NTE	26	intron23 + 81	cagacctgagttcaagttct C/T ggcttccaaacacggagcct	1315
NTE	27	intron24 + 150	gtggggcggctgtgacctc A/C gccgtcgtattccagact	1316
NTE	28	intron29 + 37	gccttcagcaacctgtgacg T/C cactgggttgggggatg	1317

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
NTE	29	intron29 + 370	cgccccagtcaggagccc G/A tggggccggctggccctccg	1318
NTE	30	intron30 + 56	ecctcccgccacccacaccc G/A cacacgcgtggccacacaca	1319
NTE	31	intron30 + 358	aaaaatcacaaaattaac A/G ggcctgggtgggtgacctgt	1320
NTE	32	intron30 + 372	taaacaggctgggtgggtg T/C gctgtatccagctactc	1321
NTE	33	intron30 + 430	aaatcactgaacctgggg G/T tggaggttcagtgagctga	1322
NTE	34	intron30 + 655	gtgtcacaccagctatata T/C gcaaatgctttctcagg	1323
NTE	35	intron30 + 659	gcacaccagctatata T/C atgctttctcaggggcag	1324
NTE	36	intron30 + 760	tgaatatggcatttccaa C/T gcatgccagctgtccggt	1325
NTE	37	intron30 + 835	gcacacacgtataggtatg T/C ggcacctgtaccaggttaa	1326
NTE	38	intron31 + 40	tggtccctgcattgggtg T/C ggcataagctttgctacttaa	1327
NTE	39	intron31 + 41	gggtccctgcattgggtg G/A gctaatgctttgctacttaa	1328
NTE	40	intron31 + 1329	gtctgtcaagggcaggacag G/A ggaatgtaggcggatgtg	1329
NTE	41	intron35 + 31	aatgcttctgtgtgtt G/A gactgggacccacttctg	1330
DDOST	8	intron2 + 1299	atcttctgactgggtt C/T ggtcagtaactggtgtt	1331
DDOST	9	intron2 + 1581	gatactgttgggtgggaaa T/G gacagagagtgtaaacagt	1332
DDOST	10	intron2 + 2822	gtttctcaacaggtgtt T/G tgacgtttcagactggata	1333
DDOST	11	intron2 + 3392	cagaagcgtggggcctg C/T ggcctccctgtgtgtg	1334
DDOST	12	intron5 + 495	attgctgaaccaggaggg G/A gagggttcagtgccagg	1335
DDOST	13	intron6 + 226	ggactgcttgggtcacag C/T tctgtttgtccagatcc	1336
DDOST	14	intron8 + 303	aagagaataggctattg A/T gaatttgttagcagaga	1337
DDOST	15	3'flanking + 40	cacgcgtggagacgggca G/A ggaaggggttattaggatt	1338
MRP2	1	exon 1 + 77	catattatagaaggtctt C/T gtccagacgcagtcaggaa	1339
MRP2	2	intron2+192	atcaaatggcttggattt T/G gcataagaatgggtactct	1340
MRP2	3	intron 1 + 413	gataagttctagaactgca A/G ctatgatattgactagaag	1341
MRP2	4	intron2+3639	gtcatatccaccccccaat C/A gacccaataggatcaatgaa	1342
MRP2	5	intron2+3989	agtatgaaccgattttt C/T gggactggtgttctagtct	1343
MRP2	6	intron2+4078	aggtttccagatgtgtcc T/G aggcattcctgtgttagga	1344
MRP2	7	intron2+4171	cttattcttggctagttg C/T ttctaccacctttagctt	1345
MRP2	8	intron 2 + 5373	gttaagatatgtgaactca A/G aattttatcacagtgcaa	1346
MRP2	9	intron2+4436	ggactagtggaagaattga C/G ctctcctgaataatagatc	1347
MRP2	10	intron 2 + 3930	aaaactggcaggagaattt A/G ctggagctgcagtcaggact	1348
MRP2	11	intron 2 + 4257	gggtatggaaagttctg G/A gctgtggaggtgcggtgt	1349
MRP2	12	intron 3 + 772	ggtataaggcaagattttt A/T aaaaaatttaattgctaatc	1350
MRP2	13	intron 7 + 1658	ggactctaccagcttagt G/T cctgttttctaatctaaaa	1351
MRP2	14	exon 10 + 40	tggccagggaaggatcac G/A ttggagaacagtgaaactg	1352
MRP2	15	intron 11 + 1672	aacttttaagttcttaagac T/A ggaagggcctgtgtcctaggc	1353
MRP2	16	intron 12 + 148	ccctctacccgcccatg G/A cttttcctctttagacct	1354
MRP2	17	intron 2 + 1020	agtctgcgattacaagct G/C agccacctgcacagctctg	1355
MRP2	18	intron 2 + 5227	taaccataattatgtctct A/G tatgacatgaattcattgg	1356
MRP2	19	intron 2 + 5373	gttaagatatgtgaactca A/G aattttatcacagtgcaa	1357
MRP2	20	intron 2 + 5538	ttatgaggttaagcacatg G/T tcatgttttaaaagccttt	1358
MRP2	21	intron 13 + 180	catgagtttctgagccca G/C ttatctaatctataaatga	1359
MRP2	22	intron 13 + 1497	gtcagggtcccccctgtg T/C atagccagttcctctttaga	1360
MRP2	23	intron 15 + 169	atgagctgaagcaaggtt T/C tcagcccttcccctgtaa	1361
MRP2	24	intron 15 + 949	ttccaggtgacacatttct A/G cctaatttgggaatttaa	1362
MRP2	25	intron 15 + 984	tgttaatctagttcaatccc A/C ttatgaagaaggagggctc	1363
MRP2	26	intron 16 + 4059	catctgatgcacagttatt C/T aatttaagctccatttgtt	1364
MRP2	27	intron 19 + 10899	atgtatgggtattttatga G/A taagttatccatgctgtat	1365
MRP2	28	exon 22 + 51	caagcnaataggattttt G/A atattctcatcatccttgc	1366
MRP2	29	intron23+56	tactctgggtatcttctga C/T agggaggaaattattgtcc	1367
MRP2	30	intron 23 + 734	tggcccaactactgtactg G/A cactggggcactcaatgaat	1368
MRP2	31	intron 23 + 801	atggccagaccacacac T/G gatttttagtgtatctgag	1369
MRP2	32	intron 27 + 124	gggtccctaagtttcttt C/G ctctaactcaaggacctaa	1370
MRP2	33	exon 28 + 52	cagatggccaggcaaggc A/C agatccagtttaacaactac	1371
MRP2	34	exon 28 + 84	aacaactaccaagtgcgta C/T cgacctgagctggatctgtt	1372
MRP2	35	exon 28 + 129	agaggatcactgtgacat C/T ggtgcatggagaaggtagg	1373
MRP2	36	intron 29 + 154	ttcctagatggacacgtc A/G ttccaggaactttgaatgt	1374
MRP2	37	intron 30 + 91	gtgttaggtgtgctggca T/C agaattttccaggtctg	1375
MRP2	38	intron 31 + 170	gccaaattttccatcacgc A/G aetgaacgaacaggtta	1376
MRP2	39	intron 26 + 154	ctggctcatcttttaccga T/C ggaactattcttactcttc	1377

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
MRP2	40	3'-flanking + 739	gigaattttttataagct C/T gttctccttaaaatttattc	1378
MRP2	41	intron 3 + 1145	acatcctttcccccagtc C/T tcggttagtgagcatttct	1379
MRP2	42	intron23+432	tggcagtagagcagggtag G/A aggtattattctgcagaggaa	1380
ABCB1	1	5'flanking-196	gcttggagccatagtcag T/C actcaaatattttttatct	1381
ABCB1	2	5'flanking-18	tactcttaccctgtgaag T/C agaactgaagaaatctact	1382
ABCB1	3	intron1+71660	cttctggaggaaagggct A/C gaaatataccaaatccaag	1383
ABCB1	4	intron1+80091	gaaataatttcaagttctg A/C aataatcatgacctatag	1384
ABCB1	5	intron1+103126	gataatcatcgaattctc T/C gtgtctcaagaaaggctat	1385
ABCB1	6	intron1+103148	tgctcaagaaaggctatg C/T gataattgaatttctctag	1386
ABCB1	7	intron1+108428	aatttatttcatctatctg A/G tcaccatttcacacaactca	1387
ABCB1	8	intron1+112042	cataagttgaattgtccca A/G tgattcagctgatgcgctt	1388
ABCB1	9	intron2+491	gcctctgtgcttcagggg G/Δ actagaggttagtctcacct	1389
ABCB1	10	intron4+36	atttaactattcaaatattt C/T ggaatttgacatctcctta	1390
ABCB1	11	intron5+1596	ttagctcttctactgcttca T/C agtgaagaatcaaatatt	1391
ABCB1	12	intron8+1789	aaacactctgaattataac C/T gctctgggaaccacagctca	1392
ABCB1	13	intron14+24	agttgtccttgcctttgcc T/C ttttagaggtagcaaaata	1393
ABCB1	14	intron14+81	tgcaagaaagttaggaaact C/T tataatcgggaaggga	1394
ABCB1	15	intron15+38	caaaccaacctgatttata A/G caataagacatttctact	1395
ABCB1	16	intron17+73	gtttgttggctagggctac A/G gtggagtggaacaaagaga	1396
ABCB1	17	intron18+564	caacagtaaaagttcaact G/A aaaggatgtctctgttta	1397
ABCB1	18	intron18+2062	tttccttgaggaaagttat C/T ctctgttcttctgagttca	1398
ABCB1	19	intron18+2293	ccacatcaggttttccocag A/G cacttgggacagttgaa	1399
ABCB1	20	intron20+557	aaacccctaaccattgacac G/A tggtaatttttctggga	1400
ABCB1	21	intron21+24	cgtgcctcttctactggt G/A ttgtcttaattggcattt	1401
ABCB1	22	intron21+2725	ctgacctgttttggctgac A/G ggttttcttctccctca	1402
ABCB1	23	intron21+4725	tcttggattataaagatcca A/G agagataggaatgttaatt	1403
ABCB1	24	intron22+8507	tgcacttgggaanaaanaaa T/C atggaattgttaaatata	1404
ABCB1	25	intron22+8537	tgtaaatatacttttttt T/A aaaaaaaggacacatttat	1405
ABCB1	26	intron22+8565	aggaacatttattcagcat T/C atgacagactattacattt	1406
ABCB1	27	intron22+8952	caccttggttcatggtttg G/A caaagtactggcctgaacca	1407
ABCB1	28	intron22+9520	caccaacaaatattcttttt A/G caagtgggtggcctctggt	1408
ABCB1	29	intron22+9836	agactctgacttagacatga C/T ggcaagggaagagagactt	1409
ABCB1	30	intron24+377	taaaatcacagtgttttga C/A taagtcttgaagcctttgg	1410
ABCB1	31	intron24+1493	ggggaggtgtccagcacga A/Δ catggagagctggacttgat	1411
ABCB1	32	intron24+1495	gggggtgtccagcacgaac A/T tggagagctggacttgat	1412
ABCB1	33	intron25+342	tgcacgctgtattcttggg C/T tcaagcagctctctgctct	1413
ABCB1	34	intron26+134	cttggataaagttctgagac C/G taataagttcttcaagtg	1414
ABCB1	35	intron26+1272	gtccttcaattttgttga A/G cttaaaacaggactctaaa	1415
ABCB1	36	intron26+1394	tatttaagtgtgtttaaag A/G ttgtctataatgaatttga	1416
ABCB1	37	intron26+(1987-1988)	aaggcttgaagagtgaaag (AAG) gaggctatttgcctccagac	1417
ABCB1	37	intron26+(1987-1988)	aaggcttgaagagtgaaag gaggctatttgcctccagac	1418
ABCB1	38	intron27+59	gcagcctctctggcctatag G/T ttgattataagggctggt	1419
ABCB1	39	intron27+80	ttgattataagggctggt T/G tccagaagtgaagaaat	1420
ABCB3	1	intron3+8	tctcctttggcaggtagggt G/A tggcagctgggtccatttg	1421
ABCB3	2	intron4+104	cttcaacogtatgccaggac C/T tggagatgctttctctgt	1422
ABCB3	3	intron10+219	gcagcagtggtgtccctcc A/G tggcagccccgtcaggtcc	1423
ABCB3	4	intron11+(317-319)	atggtagccaggtgagtg GTG/Δ tccatctatctctgtctt	1424
ABCB3	5	exon12+19	agctgcaggactggaattcc T/C gtgggatcgcacagtgctg	1425
ABCB3	6	exon12+(356-357)	aggtgggtgggtgggt GG/TGGTGGGTGGA ggtg	1426
ABCB7	1	intron1+220	acggggcaggggttctggg C/A agaggacacctggagcgtg	1427
ABCB7	2	intron1+480	agtttaactccttctgacga G/A gctgtcttctgtaggcca	1428
ABCB7	3	intron1+(512-513)	gataggccaaaaccgtaact AT/Δ ctttcaaaacatagaccgc	1429
ABCB7	4	intron1+1690	agttctcaataaggcagat G/A aagttagataaaatttga	1430
ABCB7	5	intron1+5309	aattaatatcattattgct G/A tattgttgcagtgttatct	1431
ABCB7	6	intron1-11274	tgcttctttcaagccagcc A/G gcttcaaaaaaagttagct	1432
ABCB7	7	intron1-11085	caggttttcagggtcatgt A/G gacctgaagaaatagag	1433
ABCB7	8	intron1-10037	attctcttctcaacttct T/C ttattacatttctcatcat	1434
ABCB7	9	intron1-21	ccactctgaacattccct G/A ctttttcttctgacag	1435
ABCB7	10	intron3+(135-136)	ttctctatgaaaaaaaa (A) catatttaattgacctagtt	1436

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ABCB7	10	intron3+(135-136)	ttctctaagaaaaa catattaattgacctagtt	1437
ABCB7	11	intron3+333	aaaacaatttggtgtg G/A tttgtttcaagtttatgtt	1438
ABCB7	12	intron12+524	taaccactctgccccagta G/T gaaacacagtgccgaacca	1439
ABCB7	13	intron13+1543	alcctgtgagtgaggagc G/A tatggctagcataaatataa	1440
ABCB7	14	intron13+2400	tgttacccttactgctcatt C/G tcattcttccaccctgctat	1441
ABCB7	15	intron15+2201	ctccttctaaccttagcaa G/C agtctggagatttactatc	1442
ABCB8	1	5'flanking-2272	ggcttaggcctgaaggctga T/C gttggggccagtaacctga	1443
ABCB8	2	5'flanking-2070	agctatgaaaaaagaccc G/A tcttctagaggtagcaaaa	1444
ABCB8	3	intron1+25	aaacggaaaaacctactcag A/C gccggccattgaccgccgg	1445
ABCB8	4	exon2+308	tgctggcttggggtagcc G/A tctgtgtgaggtttcccca	1446
ABCB8	5	intron2+334	ccccacttaaaacatttgt C/G cctctgtctcccatcca	1447
ABCB8	6	intron4+12	cctgctccggtactgccagc G/T gcaggtgcagagtggagt	1448
ABCB8	7	intron5+547	agttcatagcattctcgtc G/A gccccctcaggcctgctgt	1449
ABCB8	8	exon7+57	ggcaatgtgcggactgtgcg A/T gccttgcgcattggcgaacg	1450
ABCB8	9	intron9+1231	tttcgcagctcagtgaca C/T cctcgcgtgccctttctg	1451
ABCB8	10	intron9+2164	cctcttgaggctccttctag C/T gctgctaigtggagattct	1452
ABCB8	11	intron9+2645	ttctgcctggtgcttcccc C/A ggtgctttagcaagtgt	1453
ABCB8	12	intron9+2646	tcctgctgtgtgcttcccc G/A gctgctttagcaagtgt	1454
ABCB8	13	intron9+3229	caggccgagcaggagctcc G/A tgggtcagctggctccctt	1455
ABCB8	14	intron12+(113-114)	tcctccactgccacaaggg (GG) ccttcttctgtggacaac	1456
ABCB8	14	intron12+(113-114)	tcctccactgccacaaggg ccttcttctgtggacaac	1457
ABCB8	15	intron13+128	tgtctcggagagacctggc C/T gtcttcacatgctcctagct	1458
ABCB8	16	intron13+305	ctcaggtctcagagaagctc A/G tagtggaggtgctgagctc	1459
ABCB8	17	intron14+135	acagtgtgtcagggaagc C/G agaaccacagccaaaggga	1460
ABCB8	18	intron14+159	accacagccaaagggaagc A/T gtctgtgtgtggagcaggg	1461
ABCB8	19	intron15+747	gttgagccttggctctgt A/G aggggacagagggaact	1462
ABCB8	20	3'flanking+333	cctatccctggctcaccoc G/A ggaccacagctcccctctt	1463
ABCB8	21	3'flanking+1168	cctctttcagggtgtgat G/A cagtgcattgatgagcagc	1464
ABCB8	22	3'flanking+(1719-1721)	tagaccgaggagccggccc GTC/A ttctaacctgcctcggcc	1465
ABCB9	1	intron1+ 69	aggtgcacggccaggccag G/C gtggggggcgtctgggcac	1466
ABCB9	2	intron1+8873	tggccacagcagtgaggcc T/C ggaactacctcaaggcttc	1467
ABCB9	3	intron1+8940	accagctcagcctgccagc G/A tgcacacggccacaaagctg	1468
ABCB9	4	intron1+11410	agatccaaagggtccagagg T/C tggatgtgacccctcgtgc	1469
ABCB9	5	intron1+12863	gggaagccagtgccacaa G/A gctctgagcttcaactcca	1470
ABCB9	6	intron1+19731	gccaaagtgtcaagtcagc G/A agggagggcctgacaggg	1471
ABCB9	7	intron1+29649	cagaatccagatgccgtaa T/C gttgttaaaagcctgcaca	1472
ABCB9	8	intron1+31793	ggccagccggggggggtag C/T ggccagaccgtgggcaaaa	1473
ABCB9	9	intron1+37537	agagtcacaggttgggtg C/A cccggggaaggtggcatcta	1474
ABCB9	10	intron1+38293	taccagccctgtgcttcag G/A gaccatgtgacctgcaact	1475
ABCB9	11	intron1+44661	cccaggtgctgcttccac A/G gcaggttgccgtcctgcag	1476
ABCB9	12	intron1+49576	aaagtggccctgtgctgt C/T cctgaagccctaaagcacc	1477
ABCB9	13	intron1+64669	ccacagacaagccggtagc G/A cactcgcagctcaacacac	1478
ABCB9	14	exon2+448	cctgtttttggccctgttc G/A tggagctacatttcacto	1479
ABCB9	15	intron7+3364	ggtaccagagtggtgtag A/G gttggacaggaacgctgtc	1480
ABCB9	16	intron11+113	ggcccccggagctctccca G/T actatcagcctcctggctg	1481
ABCB9	17	exon12+370	cccagcctgcagcactgaa A/G gacgacctgcatgtccat	1482
ABCB10	1	5'flanking-424	tcggtctgcgcctccgcc C/T ggtctgcggcgtgagaaag	1483
ABCB10	2	exon1+491	acaaagggcggttgccccc G/T cagcggccgagctccggag	1484
ABCB10	3	intron1+37	ccattccctccggccggcc T/G ctcttctccacagcgggg	1485
ABCB10	4	intron1+217	actggttgagattttaca C/T ttgtttctgttgacacac	1486
ABCB10	5	intron1+405	gcgtttatactttttttt T/A aaccaaaccacattttt	1487
ABCB10	6	exon3+185	agggccggggccaggcttc C/T gtagcatcagatgatgt	1488
ABCB10	7	intron6+1269	caaatccaaactgtgcctt C/G cacagaatgggttgaaaaac	1489
ABCB10	8	intron9+632	cccaactcacttgggtgag G/A gcaagtgatgtgaggt	1490
ABCB10	9	intron10+2373	tacctcagggcactcagaca G/C cctcaccatcagaggctca	1491
ABCB10	10	intron11+108	tccttttctgtttttgtt T/G ttttttttcttgaggtg	1492
ABCB10	11	intron11+2379	cattgtttttatgtattc T/A gttgtgcatccatcatca	1493
ABCB11	1	5'flanking-(2596-2595)	tgtgttttagagctttctct (TT) gagacattttgtcaaggtt	1494
ABCB11	1	5'flanking-(2596-2595)	tgtgttttagagctttctct gagacattttgtcaaggtt	1495
ABCB11	2	5'flanking-1746	agctgaagtgaattagcac G/A atcaactcagttactacact	1496

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ABCB11	3	5'flanking-(326-314)	aggggaaggtttaaagga (T)9-12 gctctgtatgttttaagt	1497
ABCB11	4	5'flanking-135	agagaggttcccaagcacac T/C ctgtgtttgggttattgct	1498
ABCB11	5	intron1+511	aaatagatgcaaaaaaa A/Δ tgagctgtggtgcattgtt	1499
ABCB11	6	intron1+581	aattcagtttttaggtcac C/T caagccagtgagggtcacat	1500
ABCB11	7	intron1+(1938-1951)	aaagacgttttaagggttt (A)10-13 gaaagaaaagaasactgtag	1501
ABCB11	8	intron1+4517	ggttcccaacatctcatct G/A ataasaaaataatttgcca	1502
ABCB11	9	intron1+5651	aaagagaatagggttagtga T/C tagtattcctgtgcttaag	1503
ABCB11	10	intron1+(12200-12201)	aagagtggtctctagcccc GT/Δ gtttgattggggcacttac	1504
ABCB11	11	intron1+13023	glitgctactttgattaaa G/A aagaagaagagataataat	1505
ABCB11	12	intron2+739	cctgcctattctgaccta C/T actggggaacagatgtg	1506
ABCB11	13	intron2+(921-922)	tattttagtgcataaaagt (CAGATCTTCTTCAGCT AATTTAGAAATGT) tgctgtccatttgatattca	1507
ABCB11	13	intron2+(921-922)	tattttagtgcataaaagt tgctg	1508
ABCB11	14	intron3+644	agccacacgttctcttcttgc G/A tgggaagttaaaaaatggg	1509
ABCB11	15	intron3+2231	agtgaacctgagattgagct A/G tactgaactctctagaagag	1510
ABCB11	16	intron3+2406	aaaggggtgtctttaaatcc T/C tatgtttttctcatcaggt	1511
ABCB11	17	exon4+10	tttctcatcagggttcaaga T/C gagaagaaggtgatgccgt	1512
ABCB11	18	intron4+434	ccattttatagttatttcca A/G tgcccccacacagtttatcta	1513
ABCB11	19	intron4+518	gtagatgagtagctaaaaac G/T aaagtacgtctgaaataa	1514
ABCB11	20	exon5+120	ggcacaaatgacagatgtttt T/C attgactacgacttgagtt	1515
ABCB11	21	intron5+320	gggaagtgaacctgaattt T/C acttgatlatcatctccaag	1516
ABCB11	22	intron5+16076	agaagaggttaacagtaagcc T/G cctgattacagcacacatc	1517
ABCB11	23	intron6+303	atttgccgtgtgtttgtg G/C gggcagttgagtgctttaa	1518
ABCB11	24	intron7+1141	aaaggattcagcaggcatga A/G gaaagaagaagctttgcaaga	1519
ABCB11	25	intron8+2463	ccattggctaataagcaatga A/C ctatgacatggtctaaetta	1520
ABCB11	26	intron8+2677	tcaatgatgttacagtga A/C tctaatattgtttaaaccc	1521
ABCB11	27	intron8+2699	ctaattattgtataaaccca T/A gccacatgttaaatgaatct	1522
ABCB11	28	exon9+24	gtgtcgaatttaacgacta T/C gagctgaagccctatgccaa	1523
ABCB11	29	intron9+108	cacctgggtctgtggccctcc A/G gagggaagtactgttcaaga	1524
ABCB11	30	intron10+2475	taatactccaaaccacgga G/A ttatttcattaaagacatg	1525
ABCB11	31	intron10+2478	tcattccaaaccacggaatt T/A atttcattaagaacatgata	1526
ABCB11	32	intron10+2711	tttacagattggaagaagcca C/T tgaagtgttcaggtccaga	1527
ABCB11	33	intron10+3539	agtgcctgttaattgtatca C/G ttgtgcacagagaaaaatg	1528
ABCB11	34	intron10+3623	tgcaagaaggtgttcttcca T/C gaccttcctgagttcagaa	1529
ABCB11	35	intron10+3661	gaattcattataaaaaata A/T cactaatggagcgtgcat	1530
ABCB11	36	intron10+5100	gggccactctttggcttggc A/G atagactgtggccaatgaaa	1531
ABCB11	37	intron10+5292	gctatttgtaggaacatct G/A ggcagatcaggttagccttc	1532
ABCB11	38	intron10+5912	gagtaattcagtgaaaaa A/Δ taangtggatttttaataca	1533
ABCB11	39	intron12+116	ttttccagtaataaggaat G/A gagggtcttctctgaag	1534
ABCB11	40	intron12+326	gataaatgacaaggcaatta G/C aacaatcaggaagcacaggt	1535
ABCB11	41	intron12+335	caaggcaattacaacaatca A/G gaagcacaggttcttccaa	1536
ABCB11	42	intron12+2572	cctcatccttgccaatgttt C/T cttttactggttttgatgg	1537
ABCB11	43	exon13+23	tctaaatgacctcaacatgg T/C cattaaccaggggaatga	1538
ABCB11	44	intron13+70	atggcagttatgtatcaaa C/T agaaaggtgtagcatcatt	1539
ABCB11	45	intron13+(1578-1579)	ttattggcctctatttttc (C) tggccattgtcgaagtga	1540
ABCB11	45	intron13+(1578-1579)	ttattggcctctatttttc tggccattgtcgaagtga	1541
ABCB11	46	intron14+32	catacttccctgggagaac C/T aagaggtcatagaaggaaaa	1542
ABCB11	47	intron14+80	cacaattatacatttctt C/T tctgtatgttcccaagtcac	1543
ABCB11	48	intron14+439	tattgtgtaaaaaaatctt A/G ttgtatctcattctaaag	1544
ABCB11	49	intron14+(1262-1263)	cagcctttgcattatattt (T) gctgtgtgtctaacaggag	1545
ABCB11	49	intron14+(1262-1263)	cagcctttgcattatattt gctgtgtgtctaacaggag	1546
ABCB11	50	intron14+1283	gctgtgtgtctaacaggag A/C aaagagacacggttgcic	1547
ABCB11	51	intron14+1339	tgagatagatttaggacc G/A tgaccaatttttttttgg	1548
ABCB11	52	intron14+1359	gtgaccaatttttttttgg T/C tgaasaaatttttttgaat	1549
ABCB11	53	intron14+1480	tattgattgacaaataccc G/A tctgggaaggatattct	1550
ABCB11	54	intron15+370	ccttttcaatgtctgcaca G/A cctatttaagatatccca	1551
ABCB11	55	intron16+(550-559)	aaagtttagtttctatca (T)9-12 gctactctgatggactct	1552
ABCB11	56	intron17+188	tttctctcccaattcctgg T/G ttttggtagcttctcatc	1553
ABCB11	57	intron17+194	tcccaattcatgggtttt T/G gttagcttctcatcttctg	1554

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ABCB11	58	intron17+(197-198)	caattcatgggtttttggtt (T) agcttctcactctcttggg	1555
ABCB11	58	intron17+(197-198)	caattcatgggtttttggtt agcttctcactctcttggg	1556
ABCB11	59	intron17+(289-296)	ttagaaggggactctttt (A)7G(A)4 tctgttttagtttctct	1557
ABCB11	59	intron17+(289-296)	ttagaaggggactctttt (A)12 tctgttttagtttctct	1558
ABCB11	59	intron17+(289-296)	ttagaaggggactctttt (A)10 tctgttttagtttctct	1559
ABCB11	60	intron17+1070	tcagacttgggttttccat C/T ttcttcttgagaacaagt	1560
ABCB11	61	intron17+1651	tgttaaatatctcattgta T/C atctgacggatttttctg	1561
ABCB11	62	intron17+2226	ccctaagctctcctcatca T/A gcacctgttctcaccagt	1562
ABCB11	63	intron17+2979	cctctcttcttctcagc T/A ctacttttcaactgttggct	1563
ABCB11	64	intron17+3288	aetcccatctcctaccta T/G ccactctcctcgaatctt	1564
ABCB11	65	intron17+3289	atcccatctcctccttag C/T catctcctcctcgaatctt	1565
ABCB11	66	intron18+97	aatatgagttttctaggtat A/G tatctagcagttttcaagt	1566
ABCB11	67	intron18+98	atatgagttttctaggtat T/C atctagcagttttcaagt	1567
ABCB11	68	intron18+892	ctctgaaggttctgataca C/T ctattttgtttggaatcaa	1568
ABCB11	69	intron18+2681	atgtatgagatcaagtcagg A/G tcaaatatagacacccata	1569
ABCB11	70	intron18+3780	ggacctctcttggggcaat C/G gttccagaaaatctgtgtat	1570
ABCB11	71	intron18+5741	ctcaccgggtataatacaac C/T gtacgaaggttttctttt	1571
ABCB11	72	intron18+(5882-5883)	tgcgtattcctcctcagtgag (C) tttttctcagccacgca	1572
ABCB11	72	intron18+(5882-5883)	tgcgtattcctcctcagtcag tttttctcagccacgca	1573
ABCB11	73	intron19+10022	tggctaggttaaaaaaaa A/A gagattcaactataattgct	1574
ABCB11	74	intron21+322	caagattcaactactcctccc C/A aggggttgggttaacagggc	1575
ABCB11	75	intron22+257	ctgttcaatttctctctgca T/C agtgattcattccaccctcc	1576
ABCB11	76	intron22+552	taattatacttctccttg G/C ggggttaagtgggttgta	1577
ABCB11	77	intron22+569	tgggggttaagtgggtg G/A gtacataaacactctcaaa	1578
ABCB11	78	3'flanking+243	aaacaccacagagtgacata G/A aactaagggcggcaggatc	1579
CYP4B1	1	5'flanking-333	gaacattctcagtgctgt A/T tgaagacagtggttatta	1580
CYP4B1	2	5'flanking-18	gagcagctgaaggcaggtca G/T atgaaggctaggctgga	1581
CYP4B1	3	intron1+341	tcceaaacctctgtagta C/T atagaagtgccatccatt	1582
CYP4B1	4	intron1+542	cctatgggtgctcaggagc C/T gtgacaccttccagggtca	1583
CYP4B1	5	intron1+2856	gaggactttgcacatagtag G/A tgcctcagctatattgtg	1584
CYP4B1	6	intron1+6086	tttggacttaagactggg G/T cccgtgctagttgtgtgac	1585
CYP4B1	7	intron1+6598	ttttgggttgggggggg G/A cccatagtaggggagacgt	1586
CYP4B1	8	intron1+6660	acctaagggttgcctcctg A/G agggagcagtgctcagggg	1587
CYP4B1	9	intron1+7242	ccctgttctccttaactca T/C gctggactgttcccttgg	1588
CYP4B1	10	intron2+107	gctgtgtactaagctcgg C/G agctgaggttccaccctac	1589
CYP4B1	11	intron3+361	atgtgtgggtgtaggacca C/T ggctgtgtaccagagctgt	1590
CYP4B1	12	intron4-492	aaaggctttcacatctaaaa C/A gtgtctcctcttttctgt	1591
CYP4B1	13	intron4-315	ggattactacatatacacc A/G tgcggggagctcaccacct	1592
CYP4B1	14	intron4-157	ctccccacctctctgata T/C tccagcaggatggaggcag	1593
CYP4B1	15	exon5+22	acaagttggagagaaagct C/T agagggttaagctcttgac	1594
CYP4B1	16	intron5+125	cccaggagccttagcttgc G/A gggagacaggacctgctat	1595
CYP4B1	17	intron5+(287-289)	tgtctaagccaatccctcct CCT/A accctctgttagcaggag	1596
CYP4B1	18	intron6+54	gcttgggttctcctcctgg C/T cctctatgccccctccct	1597
CYP4B1	19	intron7+(99-100)	agctcttaagcatttcccc (TC) ttctctcagcaaatataacc	1598
CYP4B1	19	intron7+(99-100)	agctcttaagcatttcccc ttctctcagcaaatataacc	1599
CYP4B1	20	exon8+114	tcctgtttctcactgcat G/A gccctgtaccctgagcacca	1600
CYP4B1	21	exon8+139	tgtacctgtgaccagcat C/T gtttagagaggaggtccgc	1601
CYP4B1	22	intron8+247	agaaagttgtcaacaggag C/T tgataatttgtgtctact	1602
CYP4B1	23	intron8+366	tgtgggttgcaacagagctg A/G gacagctgggagagccagtt	1603
CYP4B1	24	intron8+650	cctttgcttgggtcagaca C/A cctgcttctctctgggt	1604
CYP4B1	25	intron8+844	tcatatgtgagaatcccc C/A ccacgggtatccagacaca	1605
CYP4B1	26	intron8+1767	tcacattcaagaatgtct G/T gttgtgtctgtgagggat	1606
CYP4B1	27	exon9+53	tgtcatcaaggagagcttc C/T gccctctccccctgtgcc	1607
CYP4B1	28	intron9+652	agtcgggtgtgtctgagc G/T ctctgtcactgtgaggtgc	1608
CYP4B1	29	intron9+774	cctgttaccacacctctgt C/T tgcacacaggaagcctgac	1609
CYP4B1	30	intron10+33	tgggtgtgagatcagacag G/T gtggggactggaggggtca	1610
CYP4B1	31	exon12+224	ccagatggctcaggtgtga C/A ctccctggccaccacctcc	1611
CYP4B1	32	exon12+270	ctgggttggaggagttgg G/A cccctgcttccaggaggt	1612
CYP4B1	33	3'flanking+129	tctgtgtctcaggtcacgt G/A gtgtccaggtcaggt	1613
CYP27A1	1	intron1+295	agggggagctgtcttggga A/G gaggtggcagaggcaatg	1614

Table 1

GENE	NO	LOCATION	SEQ	SEQ ID NO.
CYP27A1	2	intron1+17503	cagtcataaagcctctgt C/T ctcttagagaaggaggac	1615
CYP4F2	1	intron1+(145-146)	ccaagccctggcaacctca CA/Δ gtgattcaggctggccttt	1616
CYP4F2	2	intron1+193	tttaatcagttctctctct C/T ttccattctaatgtctta	1617
CYP4F2	3	intron1+324	ccctgtctacctccggcac T/C gcccgctcctgcctctccac	1618
CYP4F2	4	intron1+367	tccttgaggctccctggccc G/C ttctctggcctcaggatct	1619
CYP4F2	5	intron1+402	ggatctcaccgtccatcccg T/C ctgccctcaggatgtcca	1620
CYP4F2	6	exon2+35	gcctgtctggctggcctc T/G ggccagtgccagcatccct	1621
CYP4F2	7	exon2+166	cgggttttccacaaccccc A/G agacggcaactgttttggg	1622
CYP4F2	8	intron2+125	ggcagagaagcagaggagc A/G tcttactcttctctgtt	1623
CYP4F2	9	intron2+440	gggcctgtctccacttccac T/C acaccgaaggcacctttct	1624
CYP4F2	10	exon3+48	gttcgactcagctgtggc C/T acctaccacaggccttta	1625
CYP4F2	11	intron3+701	agaactccacccacgttggg T/A cctttctctgacctgtg	1626
CYP4F2	12	intron3+742	cttccactgttggacgggc G/A aggtgagcaggggaatfg	1627
CYP4F2	13	intron3+1020	gcttagctttctccatgtc G/A cttttctctcaagggtggc	1628
CYP4F2	14	intron3+1039	cgcttttctctcaagggtg C/A cttttctctcatgtccaac	1629
CYP4F2	15	intron3+1040	gcttttctctcaagggtg C/G ttcttctcatgtccaacg	1630
CYP4F2	16	intron3+1920	ccacctgtctaacctctgtt G/C ctgtttctcatgtctggg	1631
CYP4F2	17	intron3+1945	ttgtctctgtctggcggt T/A ctctacaatggctttat	1632
CYP4F2	18	intron3+2621	agcattctgtagaatgctga G/A ctgtgctcagggttgogga	1633
CYP4F2	19	intron3+2665	tgttgatcgtgtaggagc A/G gtccaaggcatgtcggaac	1634
CYP4F2	20	intron6+194	gggttggaactgtgggtgt G/T gtccagagctgtgagggac	1635
CYP4F2	21	intron7+67	tgtgaagtgcagatgaag G/A atttgaactgttaagagg	1636
CYP4F2	22	intron7+2811	ttccaaggaaattgccatt T/G aattctcctgtaactcaggt	1637
CYP4F2	23	intron7+(3096-3097)	gggttgggttgggttgggtt G/T ttactgccttctctccagg	1638
CYP4F2	23	intron7+(3096-3097)	gggttgggttgggttgggtt ttactgccttctctccagg	1639
CYP4F2	24	intron8+145	gggtgtgtctacacctgggt G/A ctgaagcagcccgagacc	1640
CYP4F2	25	exon9+44	ctctcctgggtcctgtacca C/T ctgcaasgcaccagaata	1641
CYP4F2	26	exon11+48	gaaccatcaccaaccgct G/A tggggccggaccctgagtg	1642
CYP4F2	27	intron12+108	tgttccaaagtccagctctc C/T ttccctcacctcctctggag	1643
CYP4F2	28	intron12+285	gcattgggtatccaggcacgg A/T taccctctctctattctc	1644
CYP4F2	29	exon13+238	agtggaagcctagaattacc C/A taagaacctgttccacagtc	1645
CYP4F2	30	exon13+342	tgtgctgaattgttcatggc G/A gccctattccagtgccaa	1646
CYP4F2	31	exon13+563	tagtgaactgtcttttata T/C gaatttccagacaggcca	1647
CYP4F2	32	exon13+707	aaatgttccggaccctagata G/C tgacgaaggtgacccagcc	1648
CYP4F3	1	intron2+258	cattaatgcacctctgggg G/T ctctggcaggggttggg	1649
CYP4F3	2	intron2+916	ttaggacatgtctgagtc C/T acactgtctccacaaact	1650
CYP4F3	3	intron2+3417	atccagggtctcacagctgt C/T acttctctcttggcttag	1651
CYP4F3	4	intron2+4090	gagagcatgaattgggtct G/A tgttttctctccagattca	1652
CYP4F3	5	intron3+89	tgtgtgctcctccaggggtc G/A cgtgccatgtgcagacagg	1653
CYP4F3	6	intron3+243	tcaagtctgtgtacggcta C/T gtctgtcacctgtatatt	1654
CYP4F3	7	intron3+502	gggtctggggccagggtcc G/C taagtgaactgtctgagaca	1655
CYP4F3	8	intron3+755	ttttgtggcctgtcaggac A/T tgtgaacacatgtcagttc	1656
CYP4F3	9	intron3+855	gggacagacagggtgtcta G/A gtcttgtgaaggcattctg	1657
CYP4F3	10	intron3+970	cctgacatagctctacgtg C/T catgttaggcaggttcattg	1658
CYP4F3	11	intron5+122	gggggtttattataactgat C/T gttagaggactgtatgaat	1659
CYP4F3	12	exon7+159	gggtcacagactcacagatg C/A cgtcatccaggagcgcgcc	1660
CYP4F3	13	intron7+2107	caggttgccagtgattttt T/Δ ctcaagaagttttcatcaag	1661
CYP4F3	14	intron7+2255	gaccaagaagggtctaggag T/A gcaaggtgggttgggttc	1662
CYP4F3	15	intron8+132	cctcaatgcaaggttgtgt A/C caccctcgggtgtgaagca	1663
CYP4F3	16	exon9+59	taccacattgcaagcaacc G/A gaataccaggagcgtgtcg	1664
CYP4F3	17	intron9+13	attgaatggtagtgcagg G/A ctgtgacctgttctgagc	1665
CYP4F3	18	intron9+36	gggtgccctgttctgagcct G/C tctctgtgtctgttcccc	1666
CYP4F3	19	intron9+167	accatcctgactgtctggg C/G aaaggttataggcccttagg	1667
CYP4F3	20	intron9+369	tccttaattctacccttcc G/A tccagtcagggtattataa	1668
CYP4F3	21	intron9+458	tcattatccatccagctct T/C gttagcaaatctctcata	1669
CYP4F3	22	intron10+46	ctctcgtgtggaagaggg A/C cctcaggcaggagcatig	1670
CYP4F3	23	intron10+63	gggcctcctcaggcaggagc C/A ttgtcctgactgcccccttc	1671
CYP4F3	24	intron11+14	ccctgaggtcggggccccc C/G tctctgttttttccattcc	1672
CYP4F3	25	intron11+84	gatcaggagaatccaacatc G/A cctcctccaagacacacac	1673
CYP4F3	26	intron11+113	caagacacacaccctgtct T/C tccaaggctggcggactggg	1674

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
CYP4F3	27	intron11+164	cgcaaccccttcttggctc T/G cctccaggctctatgacccct	1675
CYP4F3	28	intron11+165	ggcaaccccttcttggctc T/C cctccaggctctatgacccct	1676
CYP4F3	29	intron12+156	gaaaagcccacagagtagg G/A ttgggttggctcctagaagga	1677
CYP4F3	30	intron12+253	gagctcggctaggctcag G/T atatgcaagccacatgggg	1678
CYP4F3	31	intron12+346	ttgggtcccaggccaggtt A/C ccggttggggccaggga	1679
CYP4F8	1	5'flanking-61	accatgtttacccatcattg G/T tcttgagctccccagcccc	1680
CYP4F8	2	exon1+67	gtggcagcatccccgtggct G/T ctcctgtgtgtgtggggc	1681
CYP4F8	3	intron1+707	taocgacaggtattcaca T/G tatttccacettatccactg	1682
CYP4F8	4	intron1+857	acacccctacccctcacatc G/A tgacacagctgggcccagaag	1683
CYP4F8	5	intron1+907	tgccatctccacccctcccc G/A tgcagggtcatctctttat	1684
CYP4F8	6	intron2+668	ttggcacttccaccatag T/C tcatgccccttctgtccag	1685
CYP4F8	7	intron2+818	ggcacagagccatggctca G/A gcccacaaatgcigagtac	1686
CYP4F8	8	intron2+1079	tatgcttgggtgttcagaa C/T atgtggaccatgaggagc	1687
CYP4F8	9	intron2+1194	ccggccccctttagccccc C/A accctccttcttctctctgc	1688
CYP4F8	10	intron5+45	aacatgggatggagtgagg G/T gtgggttggggagagcaaa	1689
CYP4F8	11	exon8+(19-20)	ggccatgacacacagggcag (GCCAG) tggcctctcctgggtctgt	1690
CYP4F8	11	exon8+(19-20)	ggccatgacacacagggcag tggcctctcctgggtctgt	1691
CYP4F8	12	intron8+222	tttatttccccactaacttg C/G tatgcaagcttagtaaatc	1692
CYP4F8	13	intron8+334	cttgagagattaacggcaaa A/T accgcaatgacttttgacc	1693
CYP4F8	14	intron8+1999	ttctaatgacattattctc T/C tgcctttagctatgactag	1694
CYP4F8	15	intron8+4184	caggagggcggtgtatgctc C/T ctggataattgttgggtgt	1695
CYP4F8	16	exon9+119	ecgtgtgtctccagacagc C/T gactcatcccaaggtgcc	1696
CYP4F8	17	intron11+282	gggttgggggttccgggct G/C gtctcgtgcgcagtggggcc	1697
CYP4F8	18	intron11+340	tgacgtcagacettccacct C/T ggccccaggaactgcacg	1698
CYP4F8	19	3'flanking+35	atcacctacotttgaccaa T/C taccttttcagatttcggt	1699
CYP4F8	20	3'flanking+83	ctgtgttggccctgtgctt G/C agtcccgaggatggccagta	1700
CYP4F8	21	3'flanking+90	ggccccctgtgctcagtcac A/G cggatggccagtagggggcg	1701
ALDH1	1	intron1+564	cattattttctcagccaa T/C tgttgcattggagcagatg	1702
ALDH1	2	intron1+710	gttctgagagtaactctgaa C/T ttgctcttttcacactgct	1703
ALDH1	3	intron1-3868	ccctttttatccagaata C/G agcctaactcttctctcig	1704
ALDH1	4	intron2+2933	taagtatgctatactatatt T/C gatagatatactatactata	1705
ALDH1	5	intron2-1646	caatgtgattaaactgaatgc C/T gcaaatatgcaatgtatag	1706
ALDH1	6	exon3+54	caggcttttcagattggatc C/T ccgtggcgtactatggatgc	1707
ALDH1	7	intron3+157	taggcccttaacattgaac T/G atttcaaatgaatctgc	1708
ALDH1	8	intron3+339	tgactctctagaaatgat G/A ttggatttattcaagcatt	1709
ALDH1	9	intron3+655	agcagttagatgagtcagag C/A ataataagttggggaggg	1710
ALDH1	10	intron3+735	gaagccaatttaacataaac C/A aataccaagatcaggttcca	1711
ALDH1	11	intron3+863	gcaagatggtaaatcaag G/A accatttattatcacaatat	1712
ALDH1	12	intron3+1757	agatgacaaagatttctctc T/A ttcaaaaattccctagcaca	1713
ALDH1	13	intron5+90	ttctctaaaacagatggatg C/A ttatgtatttgaatgtg	1714
ALDH1	14	intron6+213	caggaaagccaaacacaaagg T/C ttgggttccaaacagtaact	1715
ALDH1	15	intron6+1323	ttttgaaataattcttata C/T tglacattttaaactttta	1716
ALDH1	16	intron7+638	gcaaaaggaagtggtggag G/A atactgtaccatgcaaaaaa	1717
ALDH1	17	intron9+(1462-1463)	aatggaattctatgttttt (T) gttgtgattatttctatc	1718
ALDH1	17	intron9+(1462-1463)	aatggaattctatgttttt gttgtgattatttctatc	1719
ALDH1	18	intron9+1757	tgactagaaatttggttct A/G taatgaatgaatccagt	1720
ALDH1	19	intron12-1383	aatccacttattactctcc T/G gagagcttcaagtgcctata	1721
ALDH1	20	3'flanking+40	tttaagtaacagttttgt T/C acagtgatttctctgtca	1722
ALDH2	1	intron3+1766	aaatttgggtcctatcctgc C/A tggcccccttccctccctc	1723
ALDH2	2	intron8+52	gaaggtagccctggccacct G/C tgttggcctccagccgatc	1724
ALDH2	3	intron8+69	cctgtgtgtggtccagcc G/A atcctgtcgtcccccagtg	1725
ALDH2	4	intron9+5197	gctttcttatgaccttggc C/A atttccagttgtctgttg	1726
ALDH2	5	intron11+114	gagctgggtcagtttctcc T/C gggtcagggtgtgtgtcga	1727
ALDH2	6	3'flanking+411	ggatagatttctgcctcc T/C tctgtgtgtgtgaacagct	1728
ALDH2	7	3'flanking+(432-433)	tctgtgtgtgtgaacagct TC/A ttttcatgcatattctttt	1729
ALDH2	8	3'flanking+488	ccaaataagatgtgttgaa G/T gtttcatgcatatttctgt	1730
ALDH7	1	5'flanking-1455	ctgcctgtccacccacag C/T agottgcacatcatccccc	1731
ALDH7	2	intron1+464	catgaatgactctgggaag A/G atcattcttgcaatggact	1732
ALDH7	3	intron1+2269	aaatggatccacacagaa G/C agacctccctcaccggtca	1733
ALDH7	4	intron2+1349	actgagcttctgccaccggc C/T gcttgcggcttcatgaga	1734

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ALDH7	5	intron2+1820	tccgtgtggaaggcaaccttc C/G cccagcctcagtggttagga	1735
ALDH7	6	intron2+2046	aacctcaggcgtgcctcag C/G caggagccagcctggcccc	1736
ALDH7	7	intron2+2939	aagcacgcactgaacatga G/A tgagtgaatgaacaaatga	1737
ALDH7	8	intron3+7	tgccnagaacctgtgagc C/T ggcgggctgagggcgag	1738
ALDH7	9	intron4+36	gccccttcgggtacaccttc T/C ccgtcagggcctcaggccc	1739
ALDH7	10	intron6+(116-117)	attctctctctctctctct CT/Δ ggaaccagctggagcagto	1740
ALDH7	11	intron6+263	cagacctcactagtgacct T/C gctgccccccaggctcttag	1741
ALDH7	12	intron6+1298	gtagacagagctggactcca T/G ccttggtgataaggatcc	1742
ALDH7	13	intron6+1411	ggcagggtcacagcagagg C/T gggaggagccaaagggttg	1743
ALDH7	14	exon7+185	acctcgtggcccccgacta C/T gtctatgcagccctgagat	1744
ALDH7	15	exon7+339	tgcggcattgctgggtgc G/A gctgtggccattggggccc	1745
ALDH7	16	intron7+249	ccagggtctcagggtcagc G/A tgctaatgaactcccatc	1746
ALDH7	17	intron7+277	atgaactccatccaccac C/T ggctatcctgaaggctgta	1747
ALDH7	18	intron7+498	gaccaaggctcggggattct C/T tgtgtccacagccctgag	1748
ALDH7	19	intron8+14	caggcaggtgggggtcggc C/T gggctggcagggtcaggag	1749
ALDH7	20	intron8+49	caggagcccccggtggcag C/T accagtggtggcagcgggg	1750
ALDH7	21	intron8+111	tcaggactttggagtgtag A/T cctctggctctgtctctgc	1751
ALDH7	22	intron8+3219	atcctgaggggtcaggcc A/G gccctcagcacatcgtttc	1752
ALDH7	23	exon9+33	gtgtgacccagaccagcag C/T gggggctctgtgggaaca	1753
ALDH7	24	intron9+948	tcacagcccccgagctgac C/A cttttgtggccgtggccc	1754
ALDH7	25	intron9+1067	aggctcccaagcctgggtc C/T ctctggccccaccactct	1755
ALDH7	26	exon10+137	ccgcaatcgccgcgcgcct G/A aggtgtcgtgtggccat	1756
ALDH7	27	exon10+397	cgtcccaaccctgagagcc G/A agtgggaaggcatgggaac	1757
ALDH7	28	exon10+1198	ctcttccccatgctgctcat C/T ctctcggccccaccactc	1758
ALDH7	29	exon10+1475	cagggtggacotgatttc G/A tctcgtctctctgtgctga	1759
ALDH7	30	3'flanking+15	cctggcaatactatcatctc A/G gtgattgtctttgtgcat	1760
ALDH7	31	3'flanking+60	caacaggactctggaccaag G/C ccttgcgttgggttaacaat	1761
ALDH8	1	intron1+98	agggaaagggatgtgtgccc G/A tggcccttgggtcaggggg	1762
ALDH8	2	intron1+157	atggctcgagggtccatggg T/C acgggcttgcctcaggagag	1763
ALDH8	3	intron1+354	totgtggcagacaaggatt C/G ggtcggggcaccagggtc	1764
ALDH8	4	intron1+851	tatgacagggtccatcaggcc T/G caacttctgtgtgtctt	1765
ALDH8	5	intron1+894	ctcagcatctgccccacag T/G gcttttgacacgttggttc	1766
ALDH8	6	intron1-463	aaagaacctctcagatccct C/G gtttagtcccaaggagg	1767
ALDH8	7	exon2+61	gccttcaactgaggcgac G/A cggccggccgagttccggcc	1768
ALDH8	8	intron2+8	ggccttcataagggtggcc A/G tggaggtggggccccggc	1769
ALDH8	9	intron2+23	ggccgtggaggtggggccc G/C ggcagggtcggagcagcgt	1770
ALDH8	10	intron2+(180-181)	ttcactcctgaacactcaca (A) gccacctgtgatgcaggct	1771
ALDH8	10	intron2+(180-181)	ttcactcctgaacactcaca gccacctgtgatgcaggct	1772
ALDH8	11	exon3+72	gactacgtctcagaacct T/G caggcctggtgaaggatga	1773
ALDH8	12	intron8+375	ctgcagcatcctaacctcac C/T gtccgactcaaggctgccg	1774
ALDH8	13	intron8+463	aatcaacccccatggcaccoc G/A accgtcactgagagggtct	1775
ALDH8	14	exon9+33	atgctggagcggaccagcag C/A ggcagcttggaggcaatga	1776
ALDH8	15	exon10+428	aggtgtcctcaactcaccoca C/T cctccccaattccagccctt	1777
ALDH9	1	exon1+121	actgtgtgggtatggcggg G/A tggtagggagagtgtgtgt	1778
ALDH9	2	intron1+67	cgcgatttccagccagcc C/G ccgttctgtgttctgcag	1779
ALDH9	3	intron1+103	tgcagcttgacttgagcac A/G agacagtgacagtggaggt	1780
ALDH9	4	intron1+1818	gaatttttggaaaaaa A/Δ tgttccctttaggttgctt	1781
ALDH9	5	intron2+5891	tcaggacagggaagtaaga G/A gtttaccattctaatcttct	1782
ALDH9	6	intron2+6398	atcaaaaacacttctctgat T/G atcgtctctgaacctgcct	1783
ALDH9	7	intron2+9677	atgacgtgagtlitgtgt G/A tctttttgttttctgtcct	1784
ALDH9	8	intron2+9991	gggagagtgagggaacctac C/T ctggcttctaactcttcat	1785
ALDH9	9	intron2+10198	ttgtcagagacettgttat A/G atccttactgtactatcag	1786
ALDH9	10	intron2+10256	ttagttagaacttttttt T/Δ gtaaggatggagatctag	1787
ALDH9	11	intron2+11382	catattceattctttatgt T/C ctttagaocaaagaaaggca	1788
ALDH9	12	intron2+11455	taaaccttlaagctcatcat C/T ggaccatctatgaatttct	1789
ALDH9	13	intron2+12044	atttaagtgaagctattt C/T tagtttaaaattgagcag	1790
ALDH9	14	intron3+334	ctatttagcaacttttttt T/Δ gacagtgtataaagtttca	1791
ALDH9	15	intron3+368	gttttcaacattgatattg G/Δ aaggttgtagggccclagga	1792
ALDH9	16	intron4+191	ccctcaaggagcttatagtt T/A aggtgtacacactctgtc	1793
ALDH9	17	intron4+557	tagaaaattgtatgtt G/A aaagcattactgttaggaca	1794

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ALDH9	18	intron5+830	agttcaagatgattttag G/C ttcaggccctagttagctta	1795
ALDH9	19	intron5+838	atgatttttaggttcagg C/T ctgattgacttagcatgcaa	1796
ALDH9	20	intron6+120	agaaaagtgcacaaatagt A/C caaagaattcccatgtacct	1797
ALDH9	21	intron6+2569	ettaaaatcigtcttaata T/C tttttggggagaggacac	1798
ALDH9	22	intron8+1414	ccgatcttcaaaaaatagc T/C ggggtgtgtgtgtgtgtgtgt	1799
ALDH9	23	intron9+664	aaagttcacatttttttt T/A ataacttcaggtcaagagc	1800
ALDH9	24	intron9+2170	taatgcacacatttttttt T/A ctctatagggacatccacg	1801
ALDH9	25	exon11+587	aaaacaaaaacaaaaaaa A/Δ cctgttctcttataggctc	1802
ALDH10	1	intron1+39	gggtgtggggaaactggccc G/T cgcgcgcactgtgtgactg	1803
ALDH10	2	intron3+2491	tgccgcgaagaattggcac T/A gctgagttctacatgcagtt	1804
ALDH10	3	intron3+2595	ttctgtacatcaactgtga T/A ggttgaggccagttctgtgt	1805
ALDH10	4	intron3+2775	taccgctttgccctgacca G/A ggttaaatcttcaataact	1806
ALDH10	5	intron3+3424	eggcaattctgcacacacccc G/A cgtctcagcattttccctg	1807
ALDH10	6	intron3+3676	atgttgagagattgtgtgt G/A ttgacgtttaggttttttt	1808
ALDH10	7	intron4+481	tagaaaaaagaggtttcag G/T tctctctgtctaatacgggt	1809
ALDH10	8	intron4+769	atcctgotttatacctgaac G/A tcttgacggcagagccaaaa	1810
ALDH10	9	intron4+796	aggcagagccaaaagccaca A/G ccaggagagtcgtgtaccgaa	1811
ALDH10	10	intron5+254	attgtgtgtgcatatactt T/G ttttaaaaaagttaataat	1812
ALDH10	11	intron6+137	aatcctgctttctgtgtat T/C gtacctgtagctttttgtat	1813
ALDH10	12	intron6+923	eggctaataatgtaagag G/A aagggcctatcctgattagc	1814
ALDH10	13	intron7+331	tgtttttctgtatgaatcc A/Δ caggcattgtgtgaataca	1815
ALDH10	14	intron8+643	tttagaacatgacctgctg C/T cctccacatgtgagatga	1816
ALDH10	15	intron8+666	ctccacatgtgagatgact G/A actcagctttttttttccc	1817
ALDH10	16	intron9+2129	tgttttcatitttaaaaaa G/T gttgactttggaattcatg	1818
ALDH10	17	exon10+(1894-1895)	tgtgtgtgtctactaataca CA/Δ tctgttcaaatgaacata	1819
ALDH10	18	3'flanking+31	gtttttgcaacttttttt T/Δ ctcatitttaaaattcttagc	1820
ALDH10	19	3'flanking+106	gtgtgtgtgtgtgtgtgt G/A gtgctatagtaaataggtt	1821
ALDH10	20	3'flanking+1630	aaaagcacgtgggaacaca A/G ttaatcatgtcttaccgtat	1822
ABCC7	1	5'flanking-834	gctaaaacactccaagcct T/G ccttaaaaatgcgcactggg	1823
ABCC7	2	5'flanking-729	cctccttgcagattttttt T/Δ ctcttctagtcgtgtccta	1824
ABCC7	3	exon1+125	tagcaggagccccagcgccc G/C agagaccatgcagaggtogo	1825
ABCC7	4	intron1+6200	ctatgtgagacgttaagaag G/A tagaggtggccaagaaggaa	1826
ABCC7	5	intron1+7538	agttctcttcttagcatgg C/A ctacagaggtgcacttaoct	1827
ABCC7	6	intron1+13519	gaacttaaatctttagtca T/C acaattgtgtctacatactg	1828
ABCC7	7	intron1+14110	attcacagatattttttt T/Δ aatttggggaaagtgtgt	1829
ABCC7	8	intron1+14293	ggcaggcagatttctgctc C/Δ tataaccagagcttatcag	1830
ABCC7	9	intron1+14316	taaccagagcttctcagag C/G atttatgtcccaaaagagaa	1831
ABCC7	10	intron1+14433	cagaataacaatgatggcto G/A gaaaataatgggtatttctg	1832
ABCC7	11	intron1+14824	acgttttgacagtgcacaa G/C tttctttcttaagcttaa	1833
ABCC7	12	intron1+23401	aatattttgaaatcacta C/G ggtatcctgcatagtgattt	1834
ABCC7	13	intron3+879	gaaaatttcaggtctatca C/A ccccatgaaaaatcacetta	1835
ABCC7	14	intron3+922	acttatcttaacaaagatga G/C tacacttaggccagaatgt	1836
ABCC7	15	intron3+933	caagatgagtcacttagg C/T ccagaatgttctctaatgct	1837
ABCC7	16	intron3+13704	tttttcaaatataaaaaaa A/Δ tcaggtgatctgttaaatg	1838
ABCC7	17	intron3+13758	tattaaagaacatgatgctt A/G aaacagattagggaacta	1839
ABCC7	18	intron4+240	ctctgtgtgtgttttttt T/Δ ctctatgtcatgttatcatt	1840
ABCC7	19	intron4+376	ttatgttcagcaagaagagt A/G taatatatgattgttaatga	1841
ABCC7	20	intron4+586	tgtccagacaagagcccaa T/C tgcagagccctcatttaggt	1842
ABCC7	21	intron4+1089	tttcaatctgaacattttac G/A taagtgaagactttgttaga	1843
ABCC7	22	intron4+1615	aaagttaggtgtgtgtgt C/T tcttcttcttctcaatgtt	1844
ABCC7	23	intron4+1946	aatacaacaaacttgagct T/C tgcctatacttttcaagaat	1845
ABCC7	24	intron6+783	tatctaatgttttgagtcac A/G tagcaatttgttgaatccc	1846
ABCC7	25	intron6+(1128-1131)	gattgattgattgattgatt GATT/Δ tacagagatcagagagctgg	1847
ABCC7	26	intron7+(731-732)	gtagcaatgagaccattttt (T) cttaggttagctccatgtt	1848
ABCC7	26	intron7+(731-732)	gtagcaatgagaccattttt cttaggttagctccatgtt	1849
ABCC7	27	intron7+1434	gaatgtttgtttgaacctg T/C ataactgtgcatgaattgt	1850
ABCC7	28	intron8+752	cagctctcttctcagctcc A/G ttccttcaattatcaccta	1851
ABCC7	29	intron8+1109	tatggcaagacttcagtat G/A cgtggacttaattcttctt	1852
ABCC7	30	intron8+1312	atgaagcattcatittttt T/Δ ctccgtccaatgttgatta	1853
ABCC7	31	intron9+(6521-6522)	gtgtgtgtgtgtgtgt (GT) ttttttaacagggttttgg	1854

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ABCC7	31	intron9+(6521-6522)	gtgtgtgtgtgtgtgtgtgt ttttttaacagggtattggg	1855
ABCC7	32	intron10+2119	gaacactttatagtttttt T/G ggcacaaagatctagctaaa	1856
ABCC7	33	intron11+3867	tttttctcaagaaattaga A/Δ ggggggagaattgtttta	1857
ABCC7	34	intron11+11844	tgaatcaaaatcatctaaaa A/Δ gctttcagaacaccgacttt	1858
ABCC7	35	intron11+12144	atattcaacaggtttacata T/C acttacaacttcatacatat	1859
ABCC7	36	intron11+20975	gtgtggatagtaaatgccag G/A gtaaatcacatagcatctaa	1860
ABCC7	37	intron11+27057	atggaagagaaggttttagta G/A gggggagggaaggagggtg	1861
ABCC7	38	intron11+27131	gagagagacttttttttt T/Δ aaggcagaggtttactacct	1862
ABCC7	39	intron13+152	gtattaaactcaaatctgac T/A gccctactgggcagggttc	1863
ABCC7	40	intron13+287	tttgcagtaactgtgcttg T/C gatataatattacttaattia	1864
ABCC7	41	intron15+(85-86)	etacatatatgcaacacac AT/Δ aaatgttatatacacat	1865
ABCC7	42	intron15+106	taaatatgtatatatacaca T/A gtatacatgtataagtatgc	1866
ABCC7	43	intron15+3341	ggaagtataaattgttaaat A/C actgagaccacaacttaca	1867
ABCC7	44	intron15+5556	tgtattgactaataagtaaat A/T attttgggcagctttatga	1868
ABCC7	45	intron15+5919	tgttagttctatgtggaac C/A gtgggaaataattttatat	1869
ABCC7	46	intron17+2479	caaaaaggatggaagtcag A/C ggaagaggagaccctatgt	1870
ABCC7	47	intron18-81	oogtatgcaaaaaaa A/Δ gaataaatcactgacacac	1871
ABCC7	48	intron19+751	cattaataaataacaaatc A/G tatctcttcaagaatggca	1872
ABCC7	49	intron19+820	tgacatttggatagatta T/C tctaattttagttttttcag	1873
ABCC7	50	intron21+1532	ttacctttaacttttttt T/Δ agtttgatcagctctctta	1874
ABCC7	51	intron21+1607	atgcttttgggttgggtct G/T ataattgtatagaattgtt	1875
ABCC7	52	intron21+11260	atgtggaacaaatcatgacta T/C atgcttttacttctctat	1876
ABCC7	53	intron22+(130-131)	agaatcaatattaacacac AT/Δ gttttattataggatcat	1877
ABCC7	54	intron23+1828	ctgtcctaagtttaaaaag A/Δ aaaaacaaagggaakaggaa	1878
ABCC7	55	intron24+(7100-7112)	cctttacaacactcttagaca (T)12-14 agtttaacatgttacaac	1879
ABCC7	56	intron25+237	actcttcccccttgcaaca C/T atgatgaagcttttaatac	1880
ABCC7	57	exon27+115	gggtgaagctcttccccac C/T ggaactcaagcaagtgcag	1881
ABCC7	58	exon27+334	ggatgaataaagtttttt T/Δ aaaaagaacacatttggtaa	1882
ABCC8	1	5'flanking-1099	aaagggctgaaggggtctt T/C cttttgtgtccctgactg	1883
ABCC8	2	5'flanking-(424-422)	cacccacacccacccacac CAC/Δ aagllaacgttctgccccac	1884
ABCC8	3	intron1+1212	agcctggcaacatagtgag A/G cccccccgccctttotaca	1885
ABCC8	4	intron2+1003	aggaggactgtgaatccag C/A ctgcatgttttgggtcgggt	1886
ABCC8	5	intron2+1253	caatcactaaggagaatc C/T agtaaccagcaagatgaga	1887
ABCC8	6	intron2+1382	cccagactgcactcctgcag T/C gctgcctgctcctgtgtt	1888
ABCC8	7	intron2+2371	tttcagagctgtctggaat T/A tagggggcaggtggggggg	1889
ABCC8	8	intron3+1957	cctacccttagccagggg C/T cccacatagatgaatgg	1890
ABCC8	9	intron3+(2088-2089)	agagaacccctcattaacca (CCA) gggcgtgctgaccagtctc	1891
ABCC8	9	intron3+(2088-2089)	agagaacccctcattaacca gggcgtgctgaccagtctc	1892
ABCC8	10	intron3+2204	taaagcacagttatcaocc G/A tggatggatttgccttttc	1893
ABCC8	11	intron3+2286	ttatctcccttgaaggag A/G ctcacagagccagaaatc	1894
ABCC8	12	intron3+2312	cagagccagaaattctagaa C/G agggaaagtggagggggg	1895
ABCC8	13	intron3+2356	cttgaactgcaggagcaga A/G ggaatgggtattggagaa	1896
ABCC8	14	intron3+2359	tgaactgcaggagcaga A/G aatgggtattggagaaatgg	1897
ABCC8	15	intron3+2370	gagagaaggaaatggatt G/A ggagaatggcagccctcca	1898
ABCC8	16	intron3+2382	tgggtattggagaatggcc A/G gccctccaagggtctggt	1899
ABCC8	17	intron3+4910	ggggacagccttcagctgtg G/A aattctccctgctctaga	1900
ABCC8	18	intron3+4969	catttctccagctcctgaggc A/G ttagagcagaaggccgatgc	1901
ABCC8	19	intron3+5003	ccgatgcttctgcccctcat C/G ctatgtctcctctgcaggga	1902
ABCC8	20	intron3+5019	ccatctaatgtcctcctgc A/C gggaccacaaggtggatggca	1903
ABCC8	21	intron4+14	ggtgaggtaagcaggccac C/T tggccagggtgggtggga	1904
ABCC8	22	intron4+187	agacactgcactctgcccac G/A tgtgctctaccagggtcc	1905
ABCC8	23	intron4+204	cacgtgtgctctaccaccag G/C tccagaggaggagggggt	1906
ABCC8	24	intron4+254	gttcgtgaggttggggat G/A actttcgttagaaagggaag	1907
ABCC8	25	intron4+357	tgtatcatatcgtcacgct G/C gtaaatgaatgaatagtt	1908
ABCC8	26	intron5+92	ggcattaggtaaaatcctg G/A tgggacaaaagggaactg	1909
ABCC8	27	intron6+4205	tcgtgaaagtacatgggg G/A catgaagatcattggctga	1910
ABCC8	28	intron6+5519	gattccagggaatgttaa A/C aggaaccggtcttcttaaac	1911
ABCC8	29	intron6+5575	ctgaccagtagccagccag G/C ggggcaagtttccatccccc	1912
ABCC8	30	intron6+6587	gttgccatctgagatcttgc G/T ggaagtacacaagagacct	1913
ABCC8	31	intron6+6747	ttccactggccttttctgct C/T agtaattgctacattacagg	1914

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ABCC8	32	intron9+191	gaggagcgtccctccggg A/G ggacaggaagcggcctggc	1915
ABCC8	33	intron10+1963	cccaggagtcacacctccct T/G tgtccagctagaccatggg	1916
ABCC8	34	intron10+2724	cctgggacatgtttttctat A/G taacacagcatcaaaagatg	1917
ABCC8	35	intron10+2938	gcccgcacaggaactccac G/C tgtccaagtacactaggag	1918
ABCC8	36	intron10+3094	tccgaggatgtgtttttt T/Δ cctccgttagtcagcagtg	1919
ABCC8	37	intron10+3368	tcctgctcatatgcggcacc A/G tcagactctgggcaagcaa	1920
ABCC8	38	intron10+8897	ggtttgattaaagcctca C/T gggcagagaattcgccatc	1921
ABCC8	39	intron11+308	tgtgtattgagaagtatg G/A gaataccagacagaaagct	1922
ABCC8	40	intron11+1171	gccctctcatttccctcca G/A tgcctgagcgtttccagtg	1923
ABCC8	41	exon12+7	gcctctgtccacagactttc G/A tgggcccagtcagcttctc	1924
ABCC8	42	intron12+356	accaagaataggccatccc G/T tcccacgtgtgtcccat	1925
ABCC8	43	intron12+934	tgggttcaaagatggaatgg G/T gcataactcagcaaatat	1926
ABCC8	44	intron12+1370	ggagggaggctggcaggg G/G atgaaggcagagcctgttg	1927
ABCC8	45	intron15+412	ggagggtgggcccagagtg C/T gttcttgggaccacaagga	1928
ABCC8	46	intron15+688	actccccggcccactcac A/G tctgccacttccctccctg	1929
ABCC8	47	intron16+4464	actcatcccaagtattgac G/A agaaagagggtggactcg	1930
ABCC8	48	intron16+4574	ttgaagatcttaagtgttt T/C tggctcactcatttcgcaa	1931
ABCC8	49	intron16+5011	agctaaagcacaacagcct G/T tgacctggcaagcattocca	1932
ABCC8	50	intron16+7808	tgtcctactttttttgac C/G ctataacttccgtactcg	1933
ABCC8	51	intron16+7730	ccagctcctagtgggtgga G/A ggaaggacatcggttgggg	1934
ABCC8	52	intron16+8369	ttgcaaaactgagtagggcc T/C ggagagcttactgtgtgctg	1935
ABCC8	53	intron16+9708	tgcacttgcgcctacttat T/G ccagacccaatgattgggc	1936
ABCC8	54	intron17+651	tatagttaatgggctctg A/G gtccctcaaaccttccctc	1937
ABCC8	55	intron17+692	cccttacctctcaaaaaac A/G cttggatccccctagagg	1938
ABCC8	56	intron17+1541	ctcaggatcttctggagg C/T atggttcactcccactgag	1939
ABCC8	57	intron18+580	actaagcagatttctaccaa C/T tgcacctcccactcccctg	1940
ABCC8	58	intron18+658	gaacaagccctgagaatgc C/T ttccgacccccctactccg	1941
ABCC8	59	intron18+660	acaagccctgggaatgct T/C ccgcaacccctactccggc	1942
ABCC8	60	intron19+93	gcccttccatgatcaccca T/C acccagccatctcactccc	1943
ABCC8	61	intron19+123	tctcacccccagggtctta T/C ctgcactccagccctccat	1944
ABCC8	62	intron19+219	cataggggagagggcaggaa C/T ggaagggaaggagagagccc	1945
ABCC8	63	intron19+845	tagtattaacctgccaaa C/T gctgtgtgaagtgtgacct	1946
ABCC8	64	intron20+338	tcccctccacaagcttagac A/G aacaggattctctgtgaet	1947
ABCC8	65	exon21+10	tttggtagcagggcatcaac C/T tgtctgtgtgtcaagccag	1948
ABCC8	66	intron21+192	caaggatgacacaatgccc C/Δ attgcaagacttcagatgag	1949
ABCC8	67	intron23+17	gaagggtgggtatctcagg A/G tggccaagcagccacccctg	1950
ABCC8	68	intron23+67	gttctgtcgaacctgaact C/T ataaaggtcttctgtcctt	1951
ABCC8	69	intron26+268	gtgagcgtctgcacatccaa G/C taagattgttttctcctcc	1952
ABCC8	70	intron26+308	cgataagtggtgttaattg C/T ccatccccccatgagttc	1953
ABCC8	71	intron26+348	cagctccctgcccctccctc A/G ctctctctctctcagccagc	1954
ABCC8	72	intron26+807	gacagctgtgagtcaggcc G/A gggcggcagctgagaaggc	1955
ABCC8	73	intron26+834	cagctgagaaggcggcagt G/C gtcagatgggttgagaac	1956
ABCC8	74	intron28+(118-121)	ccctcaaaaaataaaaaaaa AAAA/Δ cagaatgaaggaaatagaa	1957
ABCC8	75	intron28+1348	tgggttaagcgaagacggg G/A ttgaacgctttgagtttgt	1958
ABCC8	76	intron29+1253	ctcttagggatgtgtctca G/T taagaagagcagagcaag	1959
ABCC8	77	intron29+1589	cagatccagcttctgttaa A/G cagctcagctcagggccaaa	1960
ABCC8	78	intron29+2322	gogccctacactcctataac G/A cgcacatgcccgtatgcaca	1961
ABCC8	79	intron29+2348	atgccctgatgcacacacat T/C ttcaacacgcacttactcta	1962
ABCC8	80	intron29+2418	agacacgtcacctcccaca C/T gtctccacctgggggtgtg	1963
ABCC8	81	intron29+2494	tcagtcctcagacacatg C/A cctctctccacgagagaca	1964
ABCC8	82	intron29+2735	gcccgaaggagagtgatga C/T ggcagcccggttgatcaga	1965
ABCC8	83	intron30+386	gtcctctgggctccagcctt C/T gcagccctgtgtgtgtc	1966
ABCC8	84	intron33+93	ggcttcgcagtcacctgtg G/T ccttcaggcccgaggcctc	1967
ABCC8	85	intron33+358	agggacctggggcgagagag C/T gaggccacctgtgtattgag	1968
ABCC8	86	intron38+54	cccaggacaggaactggct G/C ttgtggcctgactcagtga	1969
ABCC8	87	intron38+466	aggacattctggcacatgc C/Δ tcatcctctctcacaagcc	1970
ABCC8	88	intron38+529	tggcccccacccgggtgtt A/G tccccaccactctgacccgc	1971
ABCC9	1	intron3+38	tgttgttctccttaagag C/A tattgtttttcccccaaa	1972
ABCC9	2	intron3+305	gctggccttctgcttgcag T/A agttgtatttaagaatcag	1973
ABCC9	3	intron3+320	tgcagaagttgtatttaag A/G atcagagctcttgtgaggag	1974

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ABCC9	4	intron3+631	ttctgtggaatcagaggct G/C tctaaatattcttaattt	1975
ABCC9	5	intron3+8644	tggacgcactcaacattttc A/G agttattactccttcaactc	1976
ABCC9	6	intron4+757	eggetatcatgaacactga A/G tcttagtaaaactctctt	1977
ABCC9	7	intron4+1022	tactgtggaattttttctt G/C acagagatattgtttttca	1978
ABCC9	8	intron5-1217	cagtggttagatgtgtttct A/G ttgccatcatctacaaat	1979
ABCC9	9	intron6+(106-107)	tatgagttgttcaaataggc (T)7-9 cagagaattgaatgtttct	1980
ABCC9	10	intron6+1347	tcagtcgtattcctactaaa A/Δ caaaattttgaagttaigt	1981
ABCC9	11	intron6+1618	ctttttatttctgtcttacc G/A ttttactaagggttgatata	1982
ABCC9	12	intron6+1835	cttttaataaatgcaaacgt C/T acacctgtctatataaaga	1983
ABCC9	13	intron7+407	cctatagaatttttctttc T/G tttttctcaaaaaattaaa	1984
ABCC9	14	intron7+423	ttcttttttctcaaaaaa C/T taaatgtttgtatttatt	1985
ABCC9	15	intron8+743	ttctgtagatgaagcttaag A/T gctagatcttatttgaaaaa	1986
ABCC9	16	intron8+850	tttttaacttattgtttgcc T/G tttcattttttatagaaaa	1987
ABCC9	17	intron9+585	cgaatttgcgtcttttaga A/T aatctttgcaaatataaaa	1988
ABCC9	18	intron9+1394	attttttcttctgaagtat G/C agtctgagagctgactgag	1989
ABCC9	19	intron12+1167	atttgaagacttttaaat G/A agataattgtctgtgtct	1990
ABCC9	20	intron12+1195	tgtctgtgtcttatattct A/G ctgagaaactagaattat	1991
ABCC9	21	intron12+2123	ataagtcctctcccggtt G/A attgacittagagcatttc	1992
ABCC9	22	intron12+(2653-2656)	caaaaacagaataatgaag TAAC/Δ tattatctaaataataaaa	1993
ABCC9	23	intron13+(3043-3044)	aacatactctctctctct (CTCTTT) aagtcaaaatatttagtat	1994
ABCC9	23	intron13+(3043-3044)	aacatactctctctctct (CT) aagtcaaaatatttagtat	1995
ABCC9	23	intron13+(3043-3044)	aacatactctctctctct aagtcaaaatatttagtat	1996
ABCC9	24	intron14+85	ttctgtgaagtgctccaaa T/A tttgcttttaattgtttt	1997
ABCC9	25	intron14+275	agtgtcacatgtattttt T/C ggtattctctattttatcaa	1998
ABCC9	26	intron14+453	ctcatttcaaatgtgctat T/C tggactctcccaggcttg	1999
ABCC9	27	intron14+3709	atccctagtgatgtacact G/A agcttgcctccactttct	2000
ABCC9	28	intron14+3813	ctgatttatatttagatga C/T ttcccaagttcacacatcta	2001
ABCC9	29	intron14+4000	ttctttactcaatgtagc A/Δ ccaaatcagaaggtgacatt	2002
ABCC9	30	intron16+1466	atcccaactgatttaattac A/G ttgtgtagctgtgcaacca	2003
ABCC9	31	intron16+5357	atttggagaagaaattata T/G aaccttcccaactgaatt	2004
ABCC9	32	intron17+1368	aatcctgtgtttttttt T/Δ ctttttcaattttcagtagg	2005
ABCC9	33	intron20+98	aagtaactcaaggaaagatg G/A ttaactgtgaactgtlaa	2006
ABCC9	34	intron22+28	ctcatagttaagaaggttc A/C gagcccaattcagaagatt	2007
ABCC9	35	intron22+194	tgaacctataaattctaat G/Δ ccatctttggatgagtgca	2008
ABCC9	36	intron22+1370	ccaggagcaaaaagaatga C/T gtaacttaaggattggac	2009
ABCC9	37	intron22+1487	agcaagccagggaaggaagtc G/G attgaattgtattagaat	2010
ABCC9	38	intron23+(455-462)	atagccatgaaggataagaa AATTAGAA/Δ tgccatttgt	2011
ABCC9	38	intron23+(455-462)	tatgtttcag	2011
ABCC9	39	intron24+(460-465)	aactctttcttctcatctgc TTTAAAA/TTTTAA gcaagccttg	2012
ABCC9	39	intron24+(460-465)	aaggagagtg	2012
ABCC9	40	intron24+595	gcctgcaaaaataatgaagaa A/G acaatctgtctgacattga	2013
ABCC9	41	intron28-926	aaatatttcagaatttggg G/A tgtgagcattgcccctat	2014
ABCC9	42	intron29+2692	cttgaagtctttttttt T/Δ aaagtaatgaattttctaa	2015
ABCC9	43	intron29+5464	agacaacactgctttttt G/A ttttcaaatcaacgacag	2016
ABCC9	44	intron29-1830	aactgctgaaggaaaaaa A/T tcatattgctgttaatttt	2017
ABCC9	45	intron31+102	tgtttttgtttccacttca G/A tatccagaataactctctat	2018
ABCC9	46	intron33+877	aecatggaaactatagtaaat A/G tagttttttgggttcaga	2019
ABCC9	47	intron36+1281	aatttacaattttttttt T/Δ gcaggagaatttttgcasa	2020
ABCC9	48	3'flanking+197	aattgagctcatgcatgtgt T/G ttcaaatatatacatgcaaa	2021
CES1	1	5'flanking-983	tatttctttagccagcgtta T/C caaatgtgttttagtaatt	2022
CES1	2	5'flanking-814	tcacattgcttgacatcac A/C cctactgctctccacccta	2023
CES1	3	5'flanking-248	agtcttgcgaagggtgacacc G/Δ ttatgccacaagcagttggg	2024
CES1	4	intron1+22	tgaagtccttctgaagtcaaa T/Δ atgcggggcaacttttgaaa	2025
CES1	5	intron1+30	ttcgaagtcasaatgcggg G/T caacttttgaatctctgtt	2026
CES1	6	intron1+1662	aagggaatccctgagctag C/A atgaccagcccagtggttc	2027
CES1	7	intron1+1726	cctccctgaagtcctcagca A/C tcttagctgttctctcgccc	2028
CES1	8	intron1+2716	tgttccaaggaggttcatc T/G cagtatttttgaattagc	2029
CES1	9	intron1+(2747-2749)	tgttaattagcaacaacaca AAA/Δ gaaagaagctaaatttga	2030
CES1	10	intron1+3288	ttatttgtcattaaagaaa A/Δ ctcaagcgttagcctggca	2031
CES1	11	intron1+3691	gagaatttgggacacccctt T/G ttcatctctctatccagcat	2032

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
CES1	12	intron1+3819	tccttcttgcatttatttt A/G gctggatgttttatgcctc	2033
CES1	13	intron1+3880	aaccagctcaatgggttagg G/A aggcattgatcgtcatccc	2034
CES1	14	intron2+74	gagtcaaggcagtcctcga T/G gggctgacctttgtctg	2035
CES1	15	intron2+552	atggagggtgttccatca C/A cctggccaaagctgggaagaa	2036
CES1	16	intron2+885	cagatatttagatggtaag T/C attatgaigtaatatattgt	2037
CES1	17	intron2+2001	ttggcatgtcagggtgcga G/A actcatgtagaatcactcc	2038
CES1	18	intron3+2119	cgctgagtcgatgaatagtc T/G aggcctgagggtgatggag	2039
CES1	19	intron4+127	taaggcatccagccoccttc G/A taattggacactacccacc	2040
CES1	20	intron4+347	tcctgcatgacacttagcag T/G cagccagcaggtaagggt	2041
CES1	21	intron4+(1984-1985)	tggtgctgaaggctctgc (C) tgacatctctgtccccacc	2042
CES1	21	intron4+(1984-1985)	tggtgctgaaggctctgc tgacatctctgtccccacc	2043
CES1	22	intron5+766	gggtggcagagggtcagc T/C cactactgattcctcagtc	2044
CES1	23	intron5+825	ggagtagatctagcctgaa T/G agcgagtgagtcactgaccc	2045
CES1	24	intron5+828	gtagatctagcctggaatag C/T ggtgagtcactgacccac	2046
CES1	25	intron5+868	ctcctgagcatgaactctcc T/A cccctccactctgctcag	2047
CES1	26	intron7+68	acttcttattcagctgtc C/G tcttggccaggagcagtttc	2048
CES1	27	intron7+681	cctccaaatcaacaatcca A/G ttatcgctctgtctagtt	2049
CES1	28	intron7+885	aggaactatccaagagaaa T/C acattcatatacttcgcagg	2050
CES1	29	intron7+2151	gtcgtgtaactgaatct C/G aggagttgagtcctcaggc	2051
CES1	30	intron7+2470	atatgatatacgaattcac G/A ggtgagtcgggaagaaacct	2052
CES1	31	intron8+128	cgtgtttgtttctgagccc A/C gagagggtgagtcactcacc	2053
CES1	32	intron8+2618	ccgtatggcaacacatgagt T/G gggctctctatactgtga	2054
CES1	33	intron8+2665	aaaattattatcaaaaggt G/A aaacctaaatgaagacatg	2055
CES1	34	intron8+3785	ccatggccatggccatgcc G/A gtctatggactggtctcac	2056
CES1	35	intron8+3791	cgcatggccatgccgtcta T/C ggtactggttcacccctcag	2057
CES1	36	intron10+222	gtggctggagaagctgaat C/T gctcccccgggtctggtgt	2058
CES1	37	intron10+230	gagaagctgcatgctcacc A/C gggcgtggtgtcactttt	2059
CES1	38	intron11+1177	ctagcaggtgccctgacaca C/G ctttgacacaggaaggagcag	2060
CES1	39	intron11+1311	ggcctatgctctgctgtga A/G ctatataagagttcccatc	2061
CES1	40	intron11+2025	ttctcatttggagtgctaag A/G ttaaaattagcataacact	2062
CES1	41	intron11+2029	catttggagtgctaaatta A/C aaattggcataaaccttcca	2063
CES1	42	intron11+2317	catcacaaaagctctttct T/G ctatggttgctctgagttt	2064
CES1	43	intron11+3887	caaatatttggctctaatto C/T gcttccacctcagacagcta	2065
CES1	44	intron12+2311	ggcctctgggcatctcact G/A tgcagcttaggcgccttgc	2066
CES1	45	intron12+2331	gtcatgcttagggccttg C/G ggcctctgttttttcagaa	2067
CES1	46	3'flanking+71	aacggtgatgaagaggcga T/C gtgagaaggaaagtgcttt	2068
CES1	47	3'flanking+362	ttgcattggcaattactgacc G/A ttgcacaggcctgcaacacc	2069
CES1	48	3'flanking+581	atttctggattctgttagta C/T gtgaaagctctaaagcatg	2070
CES1	49	3'flanking+1348	aaatctctgctggagaga G/C agcaagcatgcagatcaac	2071
ABCB4	33	intron22+767	acagtggtctgagcataga A/Δ cctgtgcaatccaccagca	2072
AADA	23	intron2+46	tgtcactgaggtagttcgca A/G acatttlaactaagttctcag	2073
AADA	24	3'flanking+208	aatgctaaaaaasasasaa A/Δ tcactgtggtactttggga	2074
ABCA4	1	5'flanking - 1005	tgccatcataagcagaact A/G tctctctctcttggagct	2075
ABCA4	2	5'flanking - 819	gtctagagcttttcaagag A/T acacattctgagatttgagg	2076
ABCA4	3	5'flanking - 680	agcccccacccattgcagg G/A tggatgacagtaatggcc	2077
ABCA4	4	intron1 + 208	tgcccttcccaggaaaggt G/A ttctctgtctcagccaca	2078
ABCA4	5	intron1 + 234	ctgtctcagccacatgaa A/G tcttttgcctaccgtgctg	2079
ABCA4	6	intron1 + 510	agctcacgatcaagtcacag T/C ttaactggacacattattt	2080
ABCA4	7	intron1 + 1527	gcttaacaaccagctcaaa G/A agagcagcatggacacgct	2081
ABCA4	8	intron1 + 2077	caggactgtgctgctgcc T/G aaatgagccattcctgtg	2082
ABCA4	9	intron1 + 2174	ccctctcaatctggcctt G/C ctggcatgggtggagctc	2083
ABCA4	10	intron1 + 2246	gtccccaggagatggagcc A/G ctgggctgaggcccttggc	2084
ABCA4	11	intron1 + 2364	ttctgtctggcagcctccc G/A atggctcccacctgtacc	2085
ABCA4	12	intron1 + 4243	ctccctgggtatgcctgta C/G gcagttaagcgtcaaggaca	2086
ABCA4	13	intron1 + 4287	atgccctctgggagggga A/C gctgagcatgattttggaag	2087
ABCA4	14	intron1 + 4309	ctgagcatgattttggaagc C/T ggcagaagaggtatttga	2088
ABCA4	15	intron1 + 4416	tgacgacccgcccccgc C/T ccgcaasacacacacact	2089
ABCA4	16	intron1 + 4996	tttaccctggacaggcag G/A ccaagctgctgtgctccctc	2090
ABCA4	17	intron1 + 5007	aacaggcagccagctggc T/C ggtccctcctcgtatcaca	2091
ABCA4	18	intron1 + 5080	gtgtgtgctggtttcttag C/G aagcaccatggttccagtt	2092

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ABCA4	19	intron1 + 5152	gggagatgaacgttaagtga G/A ggcaggcctacaaggttga	2093
ABCA4	20	intron1 + 7110	ccactggatctgcttttga A/G tcaagagtcttaagctcca	2094
ABCA4	21	intron1 + 7290	gattttgttggtctttgca T/A ggaacacagtcattattca	2095
ABCA4	22	intron1 + 7483	totgagcctctttccttaac T/C gcagagtgaatggtacaga	2096
ABCA4	23	intron1 + 7497	cttaactgcagagtgggtg C/T tacagagaatctttactac	2097
ABCA4	24	intron2 + 1067	tcaagcagcagcagcaactg C/A gtggagtcttttgaactaa	2098
ABCA4	25	intron2 + 1106	aacactcctatgccctctc G/A gcacaaatgacgtgtcccc	2099
ABCA4	26	intron2 + 1119	ccctctcggcacaacatgac G/A tgtcccccttgcttccct	2100
ABCA4	27	intron2 + 1243	caccagcagcaggagctggc A/T cacatgagatgctctgctt	2101
ABCA4	28	intron3 + 26	tgttgatccctaccatgc A/G gggaggaggttgcacacc	2102
ABCA4	29	intron3 + 101	agcatggagcactgagtgt C/T ttgtgcttctgctgagccc	2103
ABCA4	30	intron3 + 330	tgttgggtggagtgaatca T/C tttaggagaaactcagtt	2104
ABCA4	31	intron3 + 470	tgaagtcaagttacaaagt C/G aagttactcttctggagaa	2105
ABCA4	32	intron3 + 634	tgaacacaaatgacccctct T/G ccaagaaaatggccacata	2106
ABCA4	33	intron3 + 1016	ccttggggagctcagtag A/G ttcttcaggagagcctgc	2107
ABCA4	34	intron3 + 1554	gaaagttgggttcatgttt T/C gcactcacattatgagtga	2108
ABCA4	35	intron3 + 1686	ctagacattctcacagagcc A/G agggcagcaaggcgggctc	2109
ABCA4	36	intron3 + 1823	ttcactctctccatggacc A/G gtctccctgctctcaatg	2110
ABCA4	37	intron3 + 1938	caaatctcgggaacaatc G/A gtttgaccagctttattct	2111
ABCA4	38	intron3 + 1951	acaaatcgggttgaccacgc T/G ttattctcctgtccatca	2112
ABCA4	39	intron3 + 2063	ggctgtcagagcctacctgc G/T tgaatgggtggaaggcagg	2113
ABCA4	40	intron3 + 2079	ctgcgtgaatgggtggaagg G/A caggtctcagagaattgggt	2114
ABCA4	41	intron3 + 2188	agacacacagagcagctggac C/T gagaggcagcagccctgc	2115
ABCA4	42	intron3 + 2214	ggcagaccctgccaaaact G/A ggagactgaatgctcgtc	2116
ABCA4	43	intron4 + 2717	cgctctctgcacagccacc T/C gggagagatgcccagttt	2117
ABCA4	44	intron4 + 2802	attctcagcagggagggtta A/G tggtaaaagcccaggaatg	2118
ABCA4	45	intron4 + 3182	ccccagagccacagcagccc C/G tgtctcctgggtgtgttct	2119
ABCA4	46	intron4 + 3515	agtataataaagcaggagc C/T atagcccccactctcaaga	2120
ABCA4	47	intron4 + 3907	aggggagtgacagtgggcac C/A actctcaggggaecctattac	2121
ABCA4	48	intron4 + 3923	gcaccaactctcaggaaccc A/G ttactgtgagagaagccact	2122
ABCA4	49	intron4 + 3952	agagaagccactgtgccact G/C tctgtcgaacttcaagacc	2123
ABCA4	50	intron4 + 4125	ggctgtccagcacacagggg C/A aggcctctggccactgggg	2124
ABCA4	51	intron4 + 4637	aatcacttgcccaaggtca C/T cttaactgttaggtgttct	2125
ABCA4	52	intron4 + 5319	acctctagggtctccagag A/G cccaagaacagaaaccttc	2126
ABCA4	53	intron6 + 2266	cacccttcagacctcagac G/A ggtcctggggcttcttcttc	2127
ABCA4	54	intron6 + 2857	ccagaggagaaagtctctgc G/A tagtcggcctcagttaccca	2128
ABCA4	55	intron6 + 2861	aggagaaagctctcgttag T/C cggcctcagttacccagga	2129
ABCA4	56	intron6 + 3078	gcaggcatteaatgggact T/G tgcctttattgtctcctggc	2130
ABCA4	57	intron6 + 3375	ttcaatgccaaatggttct C/G attacaagaagaggggaa	2131
ABCA4	58	intron6 + 3412	ggaaatctcagtaaccac C/T gtgaagcctctaccacact	2132
ABCA4	59	intron6 + 4635	ctttcgggtggtattgcta C/T gtcaagtgtctgggaagcc	2133
ABCA4	60	intron6 + 5576	ccactaatatgcatttctta G/C taagcgtctcactatcac	2134
ABCA4	61	intron6 + 5925	aaaaagcattttgctcttat A/G aaagccagcctctttttag	2135
ABCA4	62	intron6 + 6916	cccagacaacccaagcagag A/G cctcttagggccggaatcat	2136
ABCA4	63	intron6 + 6993	agcacaggatcaaggcctaa A/G ggcctcttagactgacctca	2137
ABCA4	64	intron6 + 7242	ttgcccttttgatctgtgac T/C tttttccagaaatagttt	2138
ABCA4	65	intron6 + 7454	atggagggtcctcctgggac T/C aggcagttatcagagatga	2139
ABCA4	66	intron6 - 264	aaacagcaatttagaatcact T/C tgaatagttagatattta	2140
ABCA4	67	intron6 - 86	agggggggggagttttcaa A/G catataggagatcagactgt	2141
ABCA4	68	intron6 - 32	tatacctacaacatata T/G atttaaaaaattgtttact	2142
ABCA4	69	intron7 + 828	gatgtgggaaggttagagaa G/C agccattgtactaatgctc	2143
ABCA4	70	intron7 + 1019	aggctcttgactgtctaga T/C agcaagtctaacttttgc	2144
ABCA4	71	intron8 + 374	gtaaacacggctgtgggtg C/T ttttacaacacaaatcgt	2145
ABCA4	72	intron8 + 874	tgatgagctgttatttggt G/A ggtacagcctattaatttag	2146
ABCA4	73	intron9 + 605	tctgtctctgtctgtct C/T tgtctgttttaggccaact	2147
ABCA4	74	exon10 + 1268	aacttttgaaagactggaac G/A cgttaggaagttgttcaaag	2148
ABCA4	75	exon10 + 1269	acttttgaagaactggaac C/T gttaggaagttgttcaaag	2149
ABCA4	76	intron11 + 5236	ggcctggcagagatgaata C/T tattcagagttcacagtga	2150
ABCA4	77	intron11 + 5270	cagtgattttcatttca A/G tatatttgattttcaggtct	2151
ABCA4	78	intron11 + 5687	atcatgtaatgtactttaga C/G tcagatatataaatattgt	2152

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ABCA4	79	intron11 + 7136	gacttcccaacttaccttag T/C ggagctgtatgacacatagaa	2153
ABCA4	80	intron11 + 7180	acgctcataaatgcttctct G/A ggctgtaaaggttgaaattt	2154
ABCA4	81	intron11 + 7701	gttagacgcaggcattacct C/T gtggcttggccccagtgta	2155
ABCA4	82	intron11 + 8073	ggggtgtttgccacatcca T/C tggcattttccaaaaggaac	2156
ABCA4	83	intron11 + 8586	cagctgctgcgctggagag G/A gctcaaacotottccgccag	2157
ABCA4	84	intron11 + 8893	agcaaatgaccccttgact C/T cttttccactagtgtgct	2158
ABCA4	85	intron11 + 9257	gaatgaggtcactgtctga T/A ggcaggtggcttcccatga	2159
ABCA4	86	intron11 + 11234	cccaaatattttgttttc G/A ttttaggaattaaattcag	2160
ABCA4	87	intron11 + 11641	aagaaacaaacatttatga C/G aacttttggtgtgtgacctg	2161
ABCA4	88	intron11 + 11808	tggattttttaagaata C/T caattccatttcttttaac	2162
ABCA4	89	intron11 + 11923	aagatcattattaatctc A/G tcagcgtggttcacttaag	2163
ABCA4	90	intron11 + 12055	tgaacaattccatgggacc T/C gcccccaggcagtgaggct	2164
ABCA4	91	intron12 + 305	tcacocctgtgtcggagggt G/A tgagtgaactatccaaagccc	2165
ABCA4	92	intron13 + 1461	ttgggtttcagtgcagcat G/A tagctgtctactcagatccc	2166
ABCA4	93	intron14 + 1237	aaggccacaaagtctaaag A/G gatgaggaggagcgtgagc	2167
ABCA4	94	intron14 + 1268	ggagctgagccctgtctct T/G atctaggtttccctgttct	2168
ABCA4	95	intron14 + 1309	ttccatcctcagctctgt T/C cttttccagtaccacatg	2169
ABCA4	96	intron14 + 2979	tcactctgtgtggtagcaa C/T ctcaaaaaatcaagtata	2170
ABCA4	97	intron17 + 23	gagtcctttaaaacacaaat C/G ttaattgtttgaatacaactc	2171
ABCA4	98	intron17 + 204	tgctgggcccgtgtgtatca T/G gaatggcgtatcatggtga	2172
ABCA4	99	intron17 + 715	gggactccctagagctgaa G/A tactctccatctgtttgtt	2173
ABCA4	100	intron18 + 1282	ggaagtgaagaacccaagc C/T gcttcagaaattcatgagg	2174
ABCA4	101	intron18 + 1531	gtctaccccttaggaccatt G/A taagagtacattgggtaat	2175
ABCA4	102	intron19 + 1802	actgctacccagaggagcaa C/A gccctgagctcatgccccgaa	2176
ABCA4	103	intron20 - 195	acagattttccattgtatg G/A atgaactatgtaagccatcc	2177
ABCA4	104	intron23 + 755	ctgctcccccgtgggttcc C/T tatgtccatccacgggaggg	2178
ABCA4	105	intron26 + 497	ctgagttaggtctagatggg G/A acactttgtaggaigagga	2179
ABCA4	106	intron26 + 702	tatcaaatataactcagacg T/G cagctcctctggccccttga	2180
ABCA4	107	intron27 + 156	cctgctttccaaaccccttat C/T ttagttcttggtaacatgaa	2181
ABCA4	108	intron27 + 385	tttaagaacagtgagtcac G/A tgacttgcctttgaaatgc	2182
ABCA4	109	intron28 + 299	gacatgccaatcagaccacg C/T gagtgttcaggcagcctacc	2183
ABCA4	110	intron29 + 168	ctccttcacacttgtgtgc A/G gggacattcaactcctcta	2184
ABCA4	111	intron29 + 497	gctgtcaataaggaccacaa C/T agactaatccaattcctc	2185
ABCA4	112	intron29 + 567	agctgtaggaataaaaagg G/A agacaaaacagatccacaago	2186
ABCA4	113	intron29 + 577	aataaaaaggagagacaaac G/A atccacaagctagagatggt	2187
ABCA4	114	intron30 - 2494	aatcacagctcatctgtgc A/G tcataggatocccaaaagaa	2188
ABCA4	115	intron30 - 2169	aatgtaacagcacaagctct A/G gaaaaggcagggccgttcc	2189
ABCA4	116	intron31 + 535	ctactgtgaattatctct T/G tgatcactgcccctttggat	2190
ABCA4	117	intron31 + 957	gagttctcagcagcaaatct C/A cagtatgaatttttgatt	2191
ABCA4	118	intron32 + 445	tcagagggttagaacctca C/T caagtggagctcaggagcc	2192
ABCA4	119	intron33 + 48	aggatttttgacttgctaa C/T taccatgaatgagaactct	2193
ABCA4	120	intron35 + 129	tgtttagtcaggcacatatg A/G acatccgactttcaataag	2194
ABCA4	121	intron35 + 209	ttcccccacatttatgtgg C/A aagtaagttacatttggtt	2195
ABCA4	122	intron36 + 3209	ttgaggcctccacacccac G/A gcaggttgccccctgaggaa	2196
ABCA4	123	intron36 + 3542	cttgccagggaggttaggca T/G ggggtgggtagggagcta	2197
ABCA4	124	intron37 + 304	ctggggcagccattcccca A/G cccctcaccagctctgact	2198
ABCA4	125	intron37 + 525	taaatttgaatgagtaatto A/G tccatctgggctcagtttc	2199
ABCA4	126	intron37 + 766	tgttcaggtctggagacc T/G cctatgaattgtacaggct	2200
ABCA4	127	intron37 + 856	aaaaaccatgaagtgtca A/G ggcaggcatcattatctcca	2201
ABCA4	128	intron38 + 62	tagtagagtatgtttgtc G/A agcagagccaggggcaagca	2202
ABCA4	129	intron38 + 761	tccttggcgaagttaattct G/A atgaagagactgggtgtct	2203
ABCA4	130	intron38 + 1315	cagagtcagactctggaag G/T cggggggataagaacacagc	2204
ABCA4	131	intron38 + 1316	agagtcagactctggaagg C/A ggggggataagaacacagcc	2205
ABCA4	132	intron38 + 1526	ccaacatttctaagcacc G/A ccttcaaaaactgttattt	2206
ABCA4	133	intron38 + 1561	gtttttcatgttaattatc C/A gatcacagctgctatgaa	2207
ABCA4	134	intron38 + 1562	ttttttcatgttaattatc G/A atacacagctgctatgaaa	2208
ABCA4	135	intron38 + 1674	ccagctgaacaccacgtgcc G/A ggtgtgtgtgatataaaca	2209
ABCA4	136	intron38 + 2867	tgcctgctagacaaagggg A/G agctccgccactagaagac	2210
ABCA4	137	intron38 + 2874	ctagacaaagggaagctcc C/T gccactagaacactgcagg	2211
ABCA4	138	intron39 + 123	gaggggaccttctggggctg G/A aggtgtcctgcagctggag	2212

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ABCA4	139	intron40 + 1904	gacactgtacagccagccca A/G tctgaccccttttctcat	2213
ABCA4	140	exon41 + 5814	ggaaataaactgacatctt A/G aggtacatgaactaaccac	2214
ABCA4	141	intron41 + 122	atttggttccagtttttg T/G aggtcatcatccctgtgtt	2215
ABCA4	142	intron41 + 287	tctgcagagcatgggtcagc C/T tcgagatgtctactctca	2216
ABCA4	143	intron41 + 411	cccttcccccctctgtct C/A accctgtctcagttctcagt	2217
ABCA4	144	intron41 + 443	gttctcagtcgggtttctt G/A tatcttcagattatccag	2218
ABCA4	145	exon42 + 5844	cgtatcttcagatttacc A/G ggcacccctcagccagcagt	2219
ABCA4	146	intron43 + 328	ttttagcctattctctatc A/G aatgcaccattgtctccat	2220
ABCA4	147	intron43 + 345	taaaatgcacacattgttc C/G cattacccctccacacat	2221
ABCA4	148	intron43 + 370	acctccctccacacatttt A/G caaacgtttcagggagttt	2222
ABCA4	149	intron43 + 376	ctccacacattttacaaa C/T gtttcagggagtttactgag	2223
ABCA4	150	intron43 + 670	ttaacagagctggcccta T/G ggcagagacagagagatga	2224
ABCA4	151	intron43 + 701	ggagagatgagctctcactc A/G tctgctcttctctggctgc	2225
ABCA4	152	intron43 + 822	gttaggtgctgctgacatc G/A tccagcatctgctgactgg	2226
ABCA4	153	intron43 + 915	ggcagagcagctcctgagca C/T gcttcaatggctcagcagg	2227
ABCA4	154	intron43 + 1242	actgagctggacgtagaaa G/T aaactataggttaagacac	2228
ABCA4	155	intron43 + 1671	tagagaagtttacttccatc G/A ggacacatgcatctttcta	2229
ABCA4	156	intron43 + 2036	ttgagggtactcagtaatt G/A cttttttctgctgatttt	2230
ABCA4	157	intron45 + 176	gtgtttgttcacacagctc C/T ggagaaaaaacagtcacgc	2231
ABCA4	158	intron45 + 193	ctccagagaaaaaacagtc C/T ggacacagcctgacttggga	2232
ABCA4	159	intron47 + 238	cccaagctctcgtatgggc A/G tctgacagagcatgcag	2233
ABCA4	160	intron47 + 269	atgcatgcagacccctgctg G/A gatggaggagctgctacc	2234
ABCA4	161	intron47 + 326	accatttatctcaacagatc C/G gggacgttggcctatttac	2235
ABCA4	162	intron47 + 715	aagtcaactaagctggttgt G/A ggaggaacagcacatacc	2236
ABCA4	163	intron47 + 734	tggggagaaacagcacataac G/T cacttatctatgctgaggt	2237
ABCA4	164	intron47 + 931	ggacactgcagatgatcta T/C agaaatagcagcatgtagg	2238
ABCA4	165	intron47 + 1260	acactctctgtggaccac A/C ctcatccaagagaggttaac	2239
ABCA4	166	intron48 + 1663	tctcgtctctctcttaccctc T/C aggtgttggtaattttgt	2240
ABCA4	167	intron49 + 127	agagagcccccacccacca C/T ggtccctaccaagctccac	2241
ABCA4	168	intron49 - 1545	gcagtttaattccaaactttt C/A tcccttatggtgagatcat	2242
ABCA4	169	5'flanking - (1441-1400)	gtaaatctcagttgaatcag (TCA)14-16 atttttcagctggttctg	2243
ABCA4	170	intron1 + (4712-4720)	ggggggcgggactatagcc (A)8-10 cagcctaattcaaggtgag	2244
ABCA4	171	intron1 + (7295-7304)	ttgttggtttgcaatggat CACAGTCAT/Δ ttattcactc	2245
ABCA4	172	intron2 + (951-952)	ctgtctcatcagactcttct TT/Δ acctctcccggaggacca	2246
ABCA4	173	intron3 + (2642-2653)	cctgggtgcagagcagat (A)10-12 tagcatgatatattact	2247
ABCA4	174	intron4 + 5202	cacaaagcatctgacacccc C/Δ atocagccctgcttaacttt	2248
ABCA4	175	intron6 + (3029-3044)	cactaanaaacaanaatttac (A)16-18 cctgaagaattgacagga	2249
ABCA4	176	intron6 + (5138-5139)	ttcatgacagatcagatgtt (G) cttttatgatttacaaga	2250
ABCA4	176	intron6 + (5138-5139)	ttcatgacagatcagatgtt cttttatgatttacaaga	2251
ABCA4	177	intron6 + 5985	tttcttttttaaaaccccc C/Δ agactaggagaaggtctgtc	2252
ABCA4	178	intron6 + 6094	gggacggacagaaaaagacc T/Δ agtttctgttgccaaaga	2253
ABCA4	179	intron6 - 161	tattttttcaatttaataa A/Δ gattttttgtttcaaaag	2254
ABCA4	180	intron7 + (809-810)	ggcccgatctgcacactga (TG) tctggaaaagttagagaaga	2255
ABCA4	180	intron7 + (809-810)	ggcccgatctgcacactga tctggaaaagttagagaaga	2256
ABCA4	181	intron8 + (472-484)	atcttccccacctttcacta (T)10-13 ggtcttctatgggttaaagg	2257
ABCA4	182	intron9 + (48-71)	gtacccctggacccctccagaa (GT)11-13 gagagagatgtgcttctc	2258
ABCA4	183	intron9 + 554	ataggggcagaaaagacaca A/Δ ccaaaagttctctctcactt	2259
ABCA4	184	intron10 + 11	catgatcagatgaaggggg G/Δ ttgagaggtggggggggg	2260
ABCA4	185	intron11 + 4242	ggagaggaaatggtgttagt G/Δ cctcctgtaaataggcccg	2261
ABCA4	186	intron11 + (13743-13753)	tgctctttttgggtgagtg (T)9-11 cctctccaggaagaagaaa	2262
ABCA4	187	intron13 + (636-637)	cgaggtgagaggttggagg (G) ctcatgttcattatagatg	2263
ABCA4	187	intron13 + (636-637)	cgaggtgagaggttggagg ctcatgttcattatagatg	2264
ABCA4	188	intron18 + (569-570)	tgtcgcctcatctctctc TT/Δ aaactagttctgtatttctc	2265
ABCA4	189	intron20 - (304-297)	tataacctgactttttttc (A)7-9 ggattgcttttttaacata	2266
ABCA4	190	intron22 + (1236-1246)	gctgaattagttcccttggg (T)9-11 agttaactcctgattttgc	2267
ABCA4	191	intron26 + (4626-4635)	gataatcaatgctgttaagg (A)9-10 tggcattagagatccagacc	2268
ABCA4	192	intron33 + (115-116)	taaaacccgtctgtttttt GT/Δ ttcatgttttttagggccc	2269
ABCA4	193	intron36 + 1078	taagcagctatcacitaa A/Δ tacaanaaccagagattatca	2270
ABCA4	194	intron37 + (290-291)	ccttgaccaaaagcctgggg (T) cagccattccccaccctc	2271

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ABCA4	184	intron37 + (290-291)	ctttgacacagcctcgggac cagcctcccaaccctc	2272
ABCA4	185	intron38 + 896	ataaaagagagagagaaa A/D gaggcagctcgcaggac	2273
ABCA4	196	intron38 + (1209-1210)	atggaacccctgagactct GT/A ttccagactctttagatt	2274
ABCA4	197	intron38 + 1322	ctcttgagagagcggggc G/A atgagacacagcccgcca	2275
ABCA4	198	intron38 + 3107	agcccccacgtcgtgagag A/D agggagtgaggttcccc	2276
ABCA4	199	intron40 + 152	ttttccaaatcaccagct A/D agagtcaggttcacatgg	2277
ABCA4	200	intron43 + 330	ttatgacttctctctctctct G/A gacacatgtctctctct	2278
ABCA4	201	intron43 + 1354	ttatgacttctctctctctct G/A ttatgacttctctctct	2279
ABCA4	202	intron43 + (1305-1306)	ttatgacttctctctctctct AAAG/A caccacgtccacaccccta	2280
ABCA7	1	5'flanking - 1558	agaaatgttgcctccctctctc C/T tctgcatctctctcagag	2281
ABCA7	2	5'flanking - 1594	aatgttgccctccctccct C/T ctgcatctctctcagagcc	2282
ABCA7	3	5'flanking - 1180	gcccagtgagtgagagac G/A tggcccaatagagagctct	2283
ABCA7	4	5'flanking - 480	agagctgagtgagtgagac A/G gctgacacacacacacac	2284
ABCA7	5	5'flanking - 0	ctctctctctctctctctct G/A ttccagactctctctctct	2285
ABCA7	6	intron5 + 31	ctccagctcagagctcagac G/A gcttccacacacacacac	2286
ABCA7	7	exon + 563	ctctctctctctctctctct A/G gcttccacacacacacac	2287
ABCA7	8	intron6 + 103	ctccagctcagagctcagac A/G gcttccacacacacacac	2288
ABCA7	9	intron6 + 166	ctccagctcagagctcagac A/G gcttccacacacacacac	2289
ABCA7	10	exon8 + 955	ctccagctcagagctcagac A/G gcttccacacacacacac	2290
ABCA7	11	intron8 + 421	ctccagctcagagctcagac A/G gcttccacacacacacac	2291
ABCA7	12	intron8 + 443	ctccagctcagagctcagac A/G gcttccacacacacacac	2292
ABCA7	13	intron8 + 447	ctccagctcagagctcagac A/G gcttccacacacacacac	2293
ABCA7	14	intron8 + 448	ctccagctcagagctcagac A/G gcttccacacacacacac	2294
ABCA7	15	exon10 + 1184	ctccagctcagagctcagac A/G gcttccacacacacacac	2295
ABCA7	16	intron10 + 10	ctccagctcagagctcagac A/G gcttccacacacacacac	2296
ABCA7	17	exon11 + 1388	ctccagctcagagctcagac A/G gcttccacacacacacac	2297
ABCA7	18	intron12 + 115	ctccagctcagagctcagac A/G gcttccacacacacacac	2298
ABCA7	19	exon13 + 1424	ctccagctcagagctcagac A/G gcttccacacacacacac	2299
ABCA7	20	intron13 + 55	ctccagctcagagctcagac A/G gcttccacacacacacac	2300
ABCA7	21	intron13 + 78	ctccagctcagagctcagac A/G gcttccacacacacacac	2301
ABCA7	22	exon14 + 1851	ctccagctcagagctcagac A/G gcttccacacacacacac	2302
ABCA7	23	exon16 + 2153	ctccagctcagagctcagac A/G gcttccacacacacacac	2303
ABCA7	24	intron16 + 34	ctccagctcagagctcagac A/G gcttccacacacacacac	2304
ABCA7	25	intron18 + 8	ctccagctcagagctcagac A/G gcttccacacacacacac	2305
ABCA7	26	intron18 + 181	ctccagctcagagctcagac A/G gcttccacacacacacac	2306
ABCA7	27	exon17 + 2385	ctccagctcagagctcagac A/G gcttccacacacacacac	2307
ABCA7	28	exon17 + 2421	ctccagctcagagctcagac A/G gcttccacacacacacac	2308
ABCA7	29	intron20 + 166	ctccagctcagagctcagac A/G gcttccacacacacacac	2309
ABCA7	30	exon21 + 3027	ctccagctcagagctcagac A/G gcttccacacacacacac	2310
ABCA7	31	intron22 + 1388	ctccagctcagagctcagac A/G gcttccacacacacacac	2311
ABCA7	32	exon23 + 3417	ctccagctcagagctcagac A/G gcttccacacacacacac	2312
ABCA7	33	intron23 + 147	ctccagctcagagctcagac A/G gcttccacacacacacac	2313
ABCA7	34	exon26 + 3528	ctccagctcagagctcagac A/G gcttccacacacacacac	2314
ABCA7	35	exon28 + 4046	ctccagctcagagctcagac A/G gcttccacacacacacac	2315
ABCA7	36	intron30 + 81	ctccagctcagagctcagac A/G gcttccacacacacacac	2316
ABCA7	37	exon31 + 4239	ctccagctcagagctcagac A/G gcttccacacacacacac	2317
ABCA7	38	intron32 + 1	ctccagctcagagctcagac A/G gcttccacacacacacac	2318
ABCA7	39	intron33 + 54	ctccagctcagagctcagac A/G gcttccacacacacacac	2319
ABCA7	40	intron34 + 245	ctccagctcagagctcagac A/G gcttccacacacacacac	2320
ABCA7	41	exon36 + 5057	ctccagctcagagctcagac A/G gcttccacacacacacac	2321
ABCA7	42	intron38 + 65	ctccagctcagagctcagac A/G gcttccacacacacacac	2322
ABCA7	43	intron40 + 154	ctccagctcagagctcagac A/G gcttccacacacacacac	2323
ABCA7	44	intron40 + 277	ctccagctcagagctcagac A/G gcttccacacacacacac	2324
ABCA7	45	exon41 + 5582	ctccagctcagagctcagac A/G gcttccacacacacacac	2325
ABCA7	46	intron41 + 266	ctccagctcagagctcagac A/G gcttccacacacacacac	2326
ABCA7	47	intron41 + 389	ctccagctcagagctcagac A/G gcttccacacacacacac	2327
ABCA7	48	intron41 + 891	ctccagctcagagctcagac A/G gcttccacacacacacac	2328
ABCA7	49	intron41 + 894	ctccagctcagagctcagac A/G gcttccacacacacacac	2329
ABCA7	50	intron41 + 898	ctccagctcagagctcagac A/G gcttccacacacacacac	2330
ABCA7	51	intron41 + 1001	ctccagctcagagctcagac A/G gcttccacacacacacac	2331

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ABCA7	52	intron41 + 1051	actcatgctggctccacca G/T accatggccccgcccatcac	2332
ABCA7	53	intron41 + 1131	tgcctctgccccatgccatt A/G tgcctctgctccacactcaa	2333
ABCA7	54	exon44 + 5985	gaagcgtctcgtcgcgcct G/A gccatcatggtgaatggcg	2334
ABCA7	55	intron44 + 201	ggcgaggaccaggagcgct G/C agccggggctctgggtgg	2335
ABCA7	56	intron44 + 233	ctgggtgatttagaagaca C/T aatcagggtgctgttgagt	2336
ABCA7	57	intron44 + 313	agttaggaggaggcctggtt A/G gggcgggggccataggaaa	2337
ABCA7	58	intron44 + 337	ggcggggccataggaaagt G/C ggcgggggtattttgtgt	2338
ABCA7	59	exon45 + 6133	tggcgggcgggttccctggg G/T cggagctgcggaggcacat	2339
ABCA7	60	exon45 + 6159	ctgcggaggcacatggagg C/T cgcctgcgttccagctgcc	2340
ABCA7	61	intron45 + 27	acggcgccggggtcgggctg G/C gggaggcgggctggggcca	2341
ABCA7	62	3'untranslated + 6580	aaggctggagggaagccg G/C tggtaaacctgtgtcatgt	2342
ABCA7	63	3'flanking + 108	caagctgagtggtgcacatac G/A ggcgaagtgcggttcatac	2343
ABCA7	64	3'flanking + 376	cttacaggagccgggtgtcc C/T gggcacaggccaggccgg	2344
ABCA7	65	3'flanking + 687	cagcaggagagacttggggg G/A gggagagagttcacactgc	2345
ABCA7	66	3'flanking + 688	agcaggagagacttggggg G/A gggagagagttcacactgc	2346
ABCA7	67	3'flanking + 1169	cctcagctgacccacttca C/T ggggctgcaggcggtgat	2347
ABCA7	68	intron9 + (398-422)	ctgaactaccacgtctctc (T)22-26 aagagatggagttcaactct	2348
ABCA7	69	intron12 + (175-184)	gggactctgagggtctgtt (G)8-10 actctgagggtctggggcc	2349
ABCA7	70	intron30 + (81-87)	ccctctggagctctcccg (C)6-7 ggcctcagctcccttccc	2350
ABCA7	71	intron34 + (349-361)	agaaagagaaagagagaaag (A)12-14 cagaatgtgctttgggtga	2351
ABCG1	1	5'flanking - 1772	cctgggcttcagcaggggcc T/C cacacctgcaatgggtcct	2352
ABCG1	2	5'flanking - 1754	cctcacacctgcaatgggt G/T ctggggagagggtgcagtg	2353
ABCG1	3	5'flanking - 1450	tcacaagcccgagatttggg T/C tttgggctcttttggat	2354
ABCG1	4	intron1 + 4	ctgggtggaggagaaaggta G/A gggggcggctcttttgt	2355
ABCG1	5	intron1 + 576	agctcaggaggtgtctgaa C/T gccacacagtcaggagttt	2356
ABCG1	6	intron1 + 1426	aattctcttcttaacttca A/G gaattttttatagaanaat	2357
ABCG1	7	intron1 + 2342	agagcctgcaatggggccgc G/A agggacctgcacactca	2358
ABCG1	8	intron1 + 2399	gggggtttgacagacaggat A/G tctctgtctgttccagctg	2359
ABCG1	9	intron1 + 2406	tgacagacagatatctct G/G tgtgttcagctgtcggtt	2360
ABCG1	10	intron1 + 2911	ccctctctgtgccactgtt G/C tcccaacacagcctgtct	2361
ABCG1	11	intron1 + 4363	tataatagattcctagcaga A/G aacataattgtagaggaac	2362
ABCG1	12	intron1 + 4752	gctttcagagccattcaca C/T aagggtctctttttatgg	2363
ABCG1	13	intron1 + 5026	ccaggtctgtgggtttcag G/A ccaaaaggagcgtgcaag	2364
ABCG1	14	intron1 + 5532	gggttaaatattccggcg G/T gccaaagtcaattatctga	2365
ABCG1	15	intron1 + 5681	gctaaagtgcaggaaggca T/C catgaataatctcttcagg	2366
ABCG1	16	intron1 + 6290	tcacagcagattcatgag T/A gaatttttagcccgctgt	2367
ABCG1	17	intron1 + 6386	agatgtctccctccagccag C/T acattttctccctgagca	2368
ABCG1	18	intron1 + 6758	acctcatgtgtgtgtccccc C/G ctgccttctctctactgctt	2369
ABCG1	19	intron1 + 7029	tgggtcagattaaatatat C/T tgaaggactaaaccgtaaa	2370
ABCG1	20	intron1 + 7176	ttgtcacaattgtgaaaaa C/G gcaaaaagatgggtttcag	2371
ABCG1	21	intron1 + 8243	gcctgagagcgtggcagta G/A gaagggtccagtgaggac	2372
ABCG1	22	intron1 + 11224	tctgttttagaggaagaaat G/A ggcagcatcatttttcaac	2373
ABCG1	23	intron1 + 11371	ggcctctcttggagccctt T/G tctctccagccctgctct	2374
ABCG1	24	intron1 + 12420	gggatttcgaatctcaaac T/C ctgagctctgtgtttccc	2375
ABCG1	25	intron1 + 12484	gggttgcctccaggaagat G/T tttgtatgttcttttctg	2376
ABCG1	26	intron1 + 12955	ctgggttgggtggagccac A/G gtctcacactattggcagg	2377
ABCG1	27	intron1 + 12985	ctattgcagctgtgcaaca T/C ttttttggatttgcataa	2378
ABCG1	28	intron1 + 20041	acatggcgggttcccttct T/C cctcggaatggcctggaatt	2379
ABCG1	29	intron1 + 20046	gcggccttcccttctctc G/A gaatggcctggaattcagtc	2380
ABCG1	30	intron1 + 21058	acaagactlagaatttgacc G/A tgattttaaactattctaa	2381
ABCG1	31	intron1 + 26189	ttcttggatgtgcccagca C/T ggggcaagggtttgatag	2382
ABCG1	32	intron1 + 27453	atcatgtgtttggggaaa G/C ctgggacccacttggtaca	2383
ABCG1	33	intron1 + 28098	cagggaaggagacagctgtg G/C tctgtcttagagttaggcc	2384
ABCG1	34	intron1 + 29670	ccttcagttgtaataggag A/G agggcgacagaggagctg	2385
ABCG1	35	intron1 + 29810	attgttctctgtttttt T/C tgtgttgacttcccttba	2386
ABCG1	36	intron1 + 36220	cagatccctgtgtgtgg G/T aggtataggagaggtttt	2387
ABCG1	37	intron1 + 36341	aaacagggttgagttctcc G/A taaggacaggagaccttcc	2388
ABCG1	38	intron1 + 36370	aggagccttccacatct G/A gcaagaattctctttttc	2389
ABCG1	39	intron1 + 36662	cagactaatgcacattct G/A gattgagctgactgtattga	2390
ABCG1	40	intron1 + 36914	tgtaaaagatggagaagac A/G cagtgtcgttctgtgtgag	2391

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ABCG1	41	intron1 + 37029	tgtgactcatggccctctgcc A/G ggggactgggctggccctgc	2392
ABCG1	42	intron4 + 1186	tgaagaagaaatggatgagt G/A gaaccacaagagagaaat	2393
ABCG1	43	intron4 + 1200	aagaaatggatgagtggaa A/C ccaaaagagagaaatgtgg	2394
ABCG1	44	intron4 + 2041	aagcagagggttttccaccc G/A gagactcaagagctgtctcc	2395
ABCG1	45	intron4 + 2490	gtgtgaagtagagctgagc A/T cacggggagccctccatcc	2396
ABCG1	46	intron4 + 2552	atggccttggggcactgcct G/A ctgtgcccagccagctt	2397
ABCG1	47	intron4 + 2822	cagcagactccgtgctgaag T/C cacagaaagccagcccttg	2398
ABCG1	48	intron4 + 2850	agccagggccctggcctgcc G/A gagctgaagaccagagaca	2399
ABCG1	49	intron4 + 2919	gcctccagggtagctaca C/T gggaccggaagccagatggc	2400
ABCG1	50	intron4 + 3506	ggcagctgggctgcccaga T/C cctccctggagcccccgcg	2401
ABCG1	51	intron4 + 3538	cgcccgccrfaagcccccag G/A ggggctgggctacaagtg	2402
ABCG1	52	intron4 + 3554	ccagggggctggagctaca A/G gtgaccttgaggtttttg	2403
ABCG1	53	intron4 + 3721	ccagctcatggcaggggtg C/T gggggaaagccaccacag	2404
ABCG1	54	intron4 + 3852	ccaccagggccactcagtcgg C/T caagagcgtgcccagctgt	2405
ABCG1	55	intron4 + 3921	gaagaccagcagctgatgcc A/G gctgggaagggctctgcc	2406
ABCG1	56	intron4 + 3979	accaccagccttttcaga C/T agccctccagagctgtttc	2407
ABCG1	57	intron4 + 4291	gagccgctggagtaggtcc G/A ctgtgatggctcccaggg	2408
ABCG1	58	intron4 + 4922	gaaccaccagaaattgtgc A/G tctctcagtgctcattca	2409
ABCG1	59	intron4 + 4988	tattgactggacaccttctc C/T gtatgggacactggctagg	2410
ABCG1	60	intron7 + 672	atcagtaacggctcactaac G/A gatcgtctgatggggccg	2411
ABCG1	61	intron7 + 840	attcatttctcactgctg T/C ctgaccagagagcggaggt	2412
ABCG1	62	intron7 + 891	tggccactgttgggggtg G/A ggtaccagagggccctgga	2413
ABCG1	63	intron7 + 997	tgtgctctgttttggcct C/G atctagggaggtgtgtggcc	2414
ABCG1	64	intron9 + 1616	ctgggggagaaagagata A/C agtctagagctgctgtcac	2415
ABCG1	65	intron9 + 1630	aggataaagctaaagactg C/T tgcacagagtcagggtcc	2416
ABCG1	66	intron9 + 1674	gcttccaaagccgcacccg G/T gttgttctctgacggagga	2417
ABCG1	67	intron9 + 1689	ntccgggtttctctcagc C/T gagagggcttttggaaagc	2418
ABCG1	68	intron10 + 446	tggctgacagtgaaacagc G/A gctgcttctccagaaactta	2419
ABCG1	69	intron10 + 581	atgcagagtttcaagagg C/G agactcaggaagagtaaggc	2420
ABCG1	70	intron13 + 243	accgggagagccatggcagg A/C ccaagtgttctggacgttg	2421
ABCG1	71	3'untranslated + 2370	gcctctcagctgagtgctg A/G cagtcagagctgtgtggca	2422
ABCG1	72	3'flanking + 1124	ctcagaactacatcagtgga G/A gtcagtgttgaagcccca	2423
ABCG1	73	3'flanking + 1252	atggggccacagccctgcc T/C cagaagcagctttgtctcg	2424
ABCG1	74	3'flanking + 1433	gggggaagagcttgggaacc A/G tggggctgttggtctgaa	2425
ABCG1	75	3'flanking + 1513	tgaaggtgaactggagtag G/C tgaagattctcagttgacg	2426
ABCG1	76	intron1 + (19909-19944)	ccgatgagggggatgggg (CACCAGGCAGCAGACTCTGA TGAGGAGGGGAGGGGG)caccagggccagacttga	2427
ABCG1	77	intron1 + (19909-19944)	ccgatgagggggatgggg ca ccaggccagactctga	2428
ABCG1	78	intron1 + (25136-25137)	catgaacttgcctgaccata (G) cccgtgaggagctaggct	2429
ABCG1	79	intron1 + (25136-25137)	catgaacttgcctgaccata cccgtgaggagctaggct	2430
ABCG2	1	intron1 + 152	tcatttgaaggtgggtatgc G/A gtttaaaactgacagttcaa	2431
ABCG2	2	intron1 + 614	agctagtcaataaataac G/A ccagagtagtaagggagaga	2432
ABCG2	3	intron1 + 10002	cctcatgaatggatatacg T/A cccaacatctctcttctgat	2433
ABCG2	4	intron1 + 10123	aaagtgttcccttgggtgc G/A tataccaaatccctgcata	2434
ABCG2	5	intron1 + 10768	ataggataattgagaacag G/A gctgaagaactctgcagga	2435
ABCG2	6	intron1 + 10791	ctgaagaactctgcaggaaa T/C gaaatagttccctgcttt	2436
ABCG2	7	intron1 + 10792	tgaagaaactctgcaggaaet G/A aaatagttccctgcttta	2437
ABCG2	8	intron1 + 14183	tcacttaaggctttgcagg T/G gctcaggccacagaaagaga	2438
ABCG2	9	intron1 + 14934	aaagtgtctttaaatttcc A/G tcttgagtcagtgagctatt	2439
ABCG2	10	intron1 + 14955	tcttgagtcagtgagctatt G/T aaattcagaaataagttat	2440
ABCG2	11	intron1 + 17251	clgtttgggaacagcaactc A/C atcataggcagagagaaagt	2441
ABCG2	12	intron1 + 17347	atttcaaacctgtttccaa G/A ttgttaagctcatcttaagg	2442
ABCG2	13	intron1 + 17626	gaaggtgcatacaacttcc T/G acataaagcttgagctata	2443
ABCG2	14	intron1 + 18271	aaatgaagctgcicattgcc A/G cacatttaaaatggacttg	2444
ABCG2	15	intron1 + 18369	ctattgctttctgtctgca G/T aaagetaaaaaactctccaga	2445
ABCG2	16	exon2 + 34	algtcgaagtttttatccca G/A tgcacaaggaacaccaat	2446
ABCG2	17	intron2 + 36	tgaanaagacagcttttta A/G tttaacctacagtgaaactca	2447
ABCG2	18	intron2 + 4230	caaccctaattggaggcc C/T gggcgtgtgtgattggaaag	2448
ABCG2	19	intron2 + 4518	gttgacagaacttttatgtg A/C gggacactgacctgcatgca	2449

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ABCG2	20	intron2 + 6278	atgtatgtaccacgcttca T/C attcttaaaaggatgacccta	2450
ABCG2	21	intron3 + 10	ggcaaatctctgtgagtata A/G gagagataagtaagcggtt	2451
ABCG2	22	exon5 + 421	tgcgggtgagagaaaactta C/A agttctcagcagctcttcgg	2452
ABCG2	23	intron6 + 3158	actattctagtgtattotag A/G ttgtcaatacaacacactga	2453
ABCG2	24	intron6 + 3203	tccattctctttttataaa A/G gcattgaattttaggtttgt	2454
ABCG2	25	intron6 + 3287	tcaggctgaactagagcaa A/G caactcaaaaggcaagaatag	2455
ABCG2	26	intron7 + 179	ttcattttitgagcaccagc T/C tegtattttaggtatctttct	2456
ABCG2	27	intron9 + 5677	gcacttggacttgcgttgc T/C acatacttgcattgcctcgc	2457
ABCG2	28	intron9 + 5974	tatacataaatgggtgtg A/T taagtttttatctctaattg	2458
ABCG2	29	intron10 + 1908	gcagctctttgcagcctat G/T ttgtctgtctggaaggctga	2459
ABCG2	30	intron10 + 2094	ccctggggctgagggtatct G/A gattatttccagacttgccta	2460
ABCG2	31	intron11 + 20	tgtgtagtggtctttgtct A/G ggaacggggcgtgccacag	2461
ABCG2	32	intron11 + 1447	tgtttctcaaggaaagcccc C/T gtcaaaagaggaagaaagc	2462
ABCG2	33	intron12 + 49	atgtcttttacttgcctat G/T ggtgaagtcagctgcacctt	2463
ABCG2	34	intron12 + 1566	tatgcatttacttggacaga C/T acacatttggagaccgagg	2464
ABCG2	35	intron13 + 40	gctotgatagaagattgtt C/T ttctcttatttcttctctgc	2465
ABCG2	36	intron13 + 1823	ttactgaacggcgctgact C/T ttagtatttgcatttttag	2466
ABCG2	37	intron14 + 497	ctaatagaacacacacagca T/C gaagatgttgcattgtaaat	2467
ABCG2	38	intron14 + 815	taactcttttgaacttctt A/G aaatttaaaactgttttaoct	2468
ABCG2	39	intron15 + 110	ccaggggcactgaattttt C/T ggcctcagcttttctatcc	2469
ABCG2	40	intron15 + 566	gcgcctatgcatgtgtgt T/A gtttttaatttaacttggaa	2470
ABCG2	41	intron15 + 639	aaacagaacacacttgaaat G/A ttgagaaacacacccgttt	2471
ABCG2	42	intron15 + 1197	taagtatctgggattacagg C/T gccaccaccacacccctgct	2472
ABCG2	43	intron16 + 520	catcaattcaggtcaagaaa T/C agaagatttggcacacaa	2473
ABCG2	44	5'flanking - (998-995)	tgtgggagctcactactcc TCAC/Δ aagccttgatggccogttt	2474
ABCG2	45	intron13 + 405	ctgctagtattttttttt T/Δ aacttttttaattattgtt	2475
ABCG2	46	intron13 + (692-702)	tcaatatgttttctgattatc (T)9-11 aatgttacttactactaet	2476
ABCG2	47	intron15 + (645-650)	aaacacttgaataaatttgg (A)7-8 ccccgttttccataatgtt	2477
ABCG4	1	intron1 + 84	ggccttgggttcccatgttc G/A gaagctcttgcceccagtg	2478
ABCG4	2	intron2 + 77	gaacacagaaggtatttcga A/G agggcattgacccccatct	2479
ABCG4	3	exon6 + 679	tgtgtccctcatgaagtcc G/T ttgcacagggggccgtacc	2480
ABCG4	4	intron7 + 95	ggccctctagggttagat C/T tacccttgcctgtccttccc	2481
ABCG4	5	intron7 + 158	cttgcctttgggaagtgg G/A tgaatctaaactgagctct	2482
ABCG4	6	intron8 + 106	ccccaggggcattgcaacca A/G tegtgtctaggaagaacct	2483
ABCG4	7	intron8 + 1089	aggtacacaaacttaattgta C/G aagatttctcttagacctgg	2484
ABCG4	8	intron11 + 1113	acgttagacagataaagta T/C ggtcatatggcaaggagga	2485
ABCG4	9	intron11 + 1120	acaggaataagttggtcat A/G ttgccaggaggaagggagac	2486
ABCG4	10	intron11 + 1173	gggggcagcgttgacacaga A/G ttggaggcaggtggacac	2487
ABCG4	11	3'untranslated + 2758	gagtgcaggcacataactg A/C gaacagggccattcacacct	2488
ABCE1	1	5'flanking - 158	aactcagattctggcacct C/T cagcagctgtcttgcgaac	2489
ABCE1	2	intron9 + 237	ctgaatttatatgcaaatc C/T gtgctttatagggaagcaga	2490
ABCE1	3	intron9 + 4203	ttgtgtaggagctgataca T/G taatttgacatagagattg	2491
ABCE1	4	intron10 + 1811	ccsagaacttcagctttct T/C ttcaacttaaatattggaac	2492
ABCE1	5	intron17 + 2301	atatcagaacacagatgta T/C gtcagagaaggtgtacag	2493
ABCE1	6	3'untranslated + 1810	tggatgattgactgactct G/C agaatttggataagccattt	2494
ABCE1	7	intron1 + (5349-5363)	tttgtctgggttgggtggg (T)13-16 gagagctgggtctgactca	2495
ABCE1	8	intron1 + (5845-5854)	tacattttgcasaatttata (T)9-10 gcagataacttttactct	2496
ABCE1	9	intron5 + (836-851)	taatttcaatgattctgta (T)14-16 aggatcctctgactggcag	2497
ABCE1	10	intron8 + (1153-1169)	tctttcaaatattatttgc (T)13-17 catagtttcatgtttgata	2498
ABCE1	11	intron9 + (1023-1024)	ttgctcttttcaaatctct (T) attcattggcccgacagctcg	2499
ABCE1	12	intron9 + (1023-1024)	ttgctctgttttcaaatctct attcattggcccgacagctcg	2500
ABCE1	11	intron9 + (2338-2346)	agtgtatggacacctgggg (A)8-9 ctagttaaggaaagtaata	2501
ABCE1	13	intron9 + (3213-3221)	ttccaattttcaattgttacc (T)8-9 ctggcagattactcctgaa	2502
ABCE1	14	intron10 + (284-299)	ttcctctgatttggctct GCAGTATTACTGTAGT/Δ atttg	2503
ABCE1	15	intron10 + (840-853)	ttattttcaaatata	2504
ABCE1	16	intron16 + (1163-1172)	tttttggttctttctttc (T)13-14 aatttggaggaatctttt	2505
ABCE1	17	intron16 + (1372-1382)	gattagaactcaggttaaa (T)9-10 gttttgcacaaatattac	

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
CHST1	3	intron1 + 3900	gccctgccccactcccc G/G ttccggccctccagccctt	2509
CHST1	4	intron1 + 6520	cctccccagaggagctggg C/T acactgggcccgttgtgt	2510
CHST1	5	intron1 + 7534	attgtgtgtgcatatcgc T/O cacatggagagtgctctag	2511
CHST1	6	intron1 + 7911	ttttccttgggaagaaaaac G/A ccttgcgttttatgcattt	2512
CHST1	7	intron1 + 7963	aaaacattcatggggatta G/C tgcgtgctacgtcagatca	2513
CHST1	8	intron1 + 9173	ggcctgccacagatcaggcc G/A aggtggggacagaaatgcc	2514
CHST1	9	intron1 + 9701	cccagaattctgaalacagc A/G gcgatgcaggactacagg	2515
CHST1	10	intron1 + 12132	aacagatccacaggaccag G/A agcasaggggaggaacatgc	2516
CHST1	11	intron1 + 12465	atgcagggaaggcgctggc G/A caaaactgtcaactgagata	2517
CHST1	12	intron1 + 12561	atgcctccctgtccactttc G/A ctttgagtttcaggatctc	2518
CHST1	13	intron3 + 529	ccatggctgcagggttctt T/G catgctcagggatgaggt	2519
CHST1	14	intron3 + 617	agggagacagggagagga C/A cacttgaggaacagggcc	2520
CHST1	15	intron3 + 798	aagaggcttccagctgtc C/T gcaggtaaatcctggggg	2521
CHST1	16	intron3 + 818	caggttaaatcctgggtgc A/G agaatgtttgtcagctcc	2522
CHST1	17	3'flanking + 762	ataactggtacaggtttact G/C gtgtctacatggcagagaa	2523
CHST1	18	intron1 + 7874	gtttcccttgccttgcct T/A cattttcctcactcattt	2524
CHST1	19	3'flanking + (335-349)	cacactgccacactggcta (T)12-15 gttttttgtagagcggg	2525
CHST3	1	5'untranslated - 294	tcacgctgcccagccggcc C/G gcagcgcctccatccctccg	2526
CHST3	2	intron1 + 96	gcctccagggcggcggccca G/A actttggaggagaggggg	2527
CHST3	3	intron1 + 4467	agggagagtgaggcagagc C/G gggcagcggagggaggtga	2528
CHST3	4	intron1 + 4853	ggatgagcactgcccagctg A/G tccctgccaccttccacag	2529
CHST3	5	intron1 + 4965	tcactgcagaggggacaca G/C tgaccaggacgaagttag	2530
CHST3	6	intron1 + 5046	ggcctgtccatcttggacc C/T ctggttccatccagtgct	2531
CHST3	7	intron1 + 5300	ccttttctctctagggcct A/G aagagatgacagatgctgc	2532
CHST3	8	intron1 + 5354	agcgcgtggactccacagc G/A ggttggggggggccctggc	2533
CHST3	9	intron1 + 5428	gacacgcttcacgctctgt C/G tctattgcccaaatctggc	2534
CHST3	10	intron1 + 5621	ctgtggcttccctgggacct A/G ggaatttatcactgaggt	2535
CHST3	11	intron1 + 6555	gggtgggacactgctgaag G/C ttctgttctgctgttttc	2536
CHST3	12	intron1 + 6990	aaacacactgggcacacccc G/A tcccgcactgtgactaac	2537
CHST3	13	intron1 + 7133	ctggggcctgtctgcagg T/G ttgtgtgtctgaagggcc	2538
CHST3	14	intron1 + 7161	gtctgaagggcccccagaa T/C agaatctagaacctgccag	2539
CHST3	15	intron1 + 7199	cagtcaggaagcagtgctac C/T caccagagatgaagaactg	2540
CHST3	16	intron1 + 7316	cttgcactgtgtgagtgcc C/T tggggtagcgtgcccagga	2541
CHST3	17	intron1 + 7367	gacaggaaccccaccccgag T/G gatgtcggcccttgacct	2542
CHST3	18	intron1 + 11412	gttgcacttctgtattcct C/T tgcgtcacttgctctttgt	2543
CHST3	19	intron1 + 11591	ccctggaggccctcactgc G/A gtgacttattaccagcatg	2544
CHST3	20	intron1 + 12541	accacacagcatgaatgg G/C ccagcccccgcctgcccgt	2545
CHST3	21	intron1 + 12672	gtgcccacgctggggctgt G/C gggtcgggcatggcaggg	2546
CHST3	22	intron1 + 14809	ggatgttaggtttgggct C/T ggccttaaggatgggtga	2547
CHST3	23	intron1 + 16161	gatgtgttcaggcatgtc G/A ttgggtctttaaccaccac	2548
CHST3	24	intron1 + 16385	tatttagcatgtggtttca A/C ctittctgttttcaaaagg	2549
CHST3	25	intron1 + 33638	gacttggccacgtcctgg G/C catgaatctgtgtatgtc	2550
CHST3	26	intron1 + 33878	agcaagaaagtgtctcccc C/T acgcccactcaggcataa	2551
CHST3	27	intron1 + 34680	agcacacatggagctttccc G/A cagtgggttcagcgtccc	2552
CHST3	28	intron1 + 35145	aggaagccgaagcctcact T/G gctgggcttgcctgacct	2553
CHST3	29	intron1 + 35340	tgtgaagtgttcccacagt T/C ggtggccctgtgtccaccg	2554
CHST3	30	intron1 + 35436	gccactcatgtatggagca T/G tgccttttttcttctctt	2555
CHST3	31	intron1 + 36150	ccatagagagggctgggct G/T aggaagccagggaagcagga	2556
CHST3	32	intron1 + 36194	ggttggggaggccagcagg G/A gtgtgggctcagcggggag	2557
CHST3	33	intron1 + 36561	ctctgtgttctgtcaat A/G tgcagagtctggcaaaac	2558
CHST3	34	intron1 + 37602	ctggacagcaacttaaaaa A/T agaatgttccctggaggg	2559
CHST3	35	intron1 + 37725	ggatagccaggcagctccc C/T gacccgcacctgctttt	2560
CHST3	36	intron1 + 37734	gcagctccccgacccgca C/G ctgcttttcccccctctcc	2561
CHST3	37	intron1 + 38208	gccattctagatggagtc C/T gactttgggtgcttgca	2562
CHST3	38	intron1 + 38219	cgatcccgactttggg T/C gcttgacttgggaaggga	2563
CHST3	39	intron2 + 255	ctcagctgtgaaggttag A/G caagatacttaacattctg	2564
CHST3	40	3'untranslated + 2202	acacctcagaggagcctgtg G/A ttaacattgtaggattatt	2565
CHST3	41	3'untranslated + 2569	agccctcatctgaggtagg C/G caagaggaaagtacagagt	2566
CHST3	42	3'untranslated + 2717	ctggaattcctcttagggc C/T ctgggaaggtattgcttaa	2567
CHST3	43	3'untranslated + 2753	cttaacgcaggatgctgg G/A tgtttgtttcgggctttta	2568

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
CHST3	44	3'untranslated + 2800	gcttggctgtctttctgttt C/T atggctgtgttttgccttt	2569
CHST3	45	3'untranslated + 3283	ccgagggctgcccgctctg C/T ttctgttttctggacaatt	2570
CHST3	46	3'untranslated + 3327	ctgtcagatcacggccattg T/C aaaccacaggggtgcattt	2571
CHST3	47	3'untranslated + 3787	gttcccaatgtggaggtcgg A/G gggctggagctggggggg	2572
CHST3	48	3'untranslated + 3860	ggccctgtctaattgtggacag T/C agactttatccctcttctt	2573
CHST3	49	3'untranslated + 4915	ccagatgtcatagaagcca G/A tctctgtcacatacaccgca	2574
CHST3	50	3'untranslated + 4993	taaaagcaattttggctttt G/A tcttctgcaatacatgcac	2575
CHST3	51	3'untranslated + 5223	ggagggagcttcagcaggag G/A tcttcccaagaggttatt	2576
CHST3	52	3'untranslated + 5370	tcataactgtaatcccagca G/T ttggggaggccaagggtggg	2577
CHST3	53	3'untranslated + 5545	ccattcccaagtcagaaag T/C gaagccagatclcaaggct	2578
CHST3	54	3'untranslated + 5859	caaaagcacaaagcagaatt G/C gcaacttcacttgcctca	2579
CHST3	55	3'untranslated + 5870	cagaattggcaacttcc T/A tgtctcaaggtctccaagat	2580
CHST3	56	3'untranslated + 5971	ttccaaggctacagacatgg C/T gccatctccacaggcctagc	2581
CHST3	57	3'untranslated + 6208	atttcattgtcgtatgtac G/A agacaccccttcacggca	2582
CHST3	58	3'untranslated + 6223	tacgagacaccccttcac G/A gcatacactgcatgtatg	2583
CHST3	59	3'flanking + 281	agacaggaggttggccag C/T ggtcaggggctggggatg	2584
CHST3	60	3'flanking + 997	acctcttaagattttgagc C/T ggtgcctgtatcccaacct	2585
CHST3	61	intron1 + 22595	cggagcgggaaabaa A/ Δ gaataagaagaaagggt	2586
CHST3	62	intron1 + (35423-35424)	gctcatgtcacagccactc AT/ Δ gtatgggcaattgccttt	2587
NDUFV1	1	intron3 + 670	ctgggtgagtgagggtgca T/C ggaattgaagaccagtcct	2588
NDUFV1	2	intron6 + 160	tgtgcggcccccagccctga C/G catgcctccctttggagcc	2589
NDUFV1	3	intron9 + 27	accaccccttctgctagcac G/A gagggtgggtggcatcaagg	2590
NDUFV1	4	3'flanking + 1111	tgtaggctgaggtcagcccc A/G atccagtcacaaagccccc	2591
NDUFV1	5	3'flanking + 1658	gaatcggaagtgctctgtg G/A gcaaccaccatgctccgggc	2592
NDUFV1	6	3'flanking + 1713	gatctgggaggaggtgaca C/T agggctgagctgggtgaag	2593
NDUFV1	7	intron4 + 214	tgggttaaattttttttt T/ Δ gcttcaaaatagatttt	2594
NDUFV1	8	3'flanking + (772-774)	tgaactcgggttcagggtc TTC/ Δ ctgtgaacactgttttgaa	2595
NDUFV2	1	intron1 + 526	ggaaatgtcgtctaaataa C/T ggtatcaactaactctgaa	2596
NDUFV2	2	intron1 + 6689	tcgttgatggtgattgt T/G tgaacaacagaagaattca	2597
NDUFV2	3	intron1 + 14767	ccaaatgcctgcccagag G/T gtggcaggaaaggtacaaag	2598
NDUFV2	4	exon2 + 86	aaggaaattgcataagacag T/C tatgcgaatggagctggg	2599
NDUFV2	5	intron2 - 29	cagaagatctactctctaa T/G gaagctggatacaactttt	2600
NDUFV2	6	intron2 - 168	tttactttgtaactact T/C atcaaatgtgttttggca	2601
NDUFV2	7	intron4 + 677	aaaccacatctctattgatt G/A tgaatgaatcacataacca	2602
NDUFV2	8	intron4 + 2295	tatgattcaacttcaaaag A/T gttatgtatgaaataga	2603
NDUFV2	9	intron5 + 102	caactctgccattctattg G/A atctgtacttacctagtaat	2604
NDUFV2	10	intron7 + 5466	tgtgaagaggctttaagata A/C caaagtctcagctttcagga	2605
NDUFV2	11	intron1 + (13562-13563)	tactcttaaaattactcctt (CTT) ttattataagtalacgtct	2606
NDUFV2	11	intron1 + (13562-13563)	tactcttaaaattactcctt ttattataagtalacgtct	2607
NDUFV3	1	5'flanking - 606	aatttcgactaacgttgggg A/G cgaactcttctgtaataaa	2608
NDUFV3	2	5'flanking - 222	cgccgcgccccgccacag G/A cccagcgccccggggcac	2609
NDUFV3	3	5'flanking - 111	tggccccaggaggagcactt A/G gccctactgggtgcgcgc	2610
NDUFV3	4	intron1 + 137	ttggccgctgaccccgctc C/T ctggcccgagactgaccgc	2611
NDUFV3	5	intron2 + 152	tatacaagacacagatcta T/C aacagattttgaccaaca	2612
NDUFV3	6	intron2 + 6304	ttcacagatgaaggggtcc G/A aaattttgtcaagaagac	2613
NDUFV3	7	intron2 + 6433	tcgccttgccttctcctc T/G tccagctcctctgattctga	2614
NDUFV3	8	intron2 + 6563	cccttgaaacagagccccc C/T gatttaacgtatcagcaaaa	2615
NDUFV3	9	intron2 + 9819	actatcttctgtgcgcctg G/A cagagccaccttgccagagc	2616
NDUFV3	10	intron2 + 9858	aggatgcagctctttaaat G/A agacatogtttttgctaac	2617
NDUFV3	11	intron2 + 11673	cttgtaggtaagcgccctgt A/G tgtgagccaagtcatcata	2618
NDUFA10	1	5'flanking - 1734	tgcaccttgaaactgtttact T/C tctgtabccatttaacctt	2619
NDUFA10	2	5'flanking - 1492	aaaacatccacgcaaacagg T/C tgtgagagttacgtctcg	2620
NDUFA10	3	intron3 + 370	aagactgtcatgtgccctg G/A agacagagatgtgggtgcca	2621
NDUFA10	4	intron3 + 2485	ttgtttttttcttctctg G/A aatgcagtgatcagttgaca	2622
NDUFA10	5	intron4 + 236	ctgtgaagcagattggagc C/T ctggacctcaacacacgca	2623
NDUFA10	6	intron4 + 1742	tgtccgcatctgctgagtg C/T tgcgtgaagctgaggactgg	2624
NDUFA10	7	intron4 + 2090	ggctgggggaagcagatca T/C gttgctgaagacaggtgg	2625
NDUFA10	8	intron4 + 3054	cagctgattactactgaa A/C cgggataaagtcagcttgat	2626
NDUFA10	9	intron4 + 3066	ctactgaacgggataaag G/T agctgatgatttcagctg	2627
NDUFA10	10	intron4 + 3377	gtcacagtttaagctgct G/A tttaactctgtgaagtagc	2628

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO
NDUFA10	11	intron5 + 46	aagcatctctatttgaatg T/C agatcagcactaaaagccct	2629
NDUFA10	12	intron8 + 1465	gcacgcccagttcctgta C/T aggcctcatatccagcgtgc	2630
NDUFA10	13	intron8 + 1809	cctggaggccacaggatggc C/A ggggactcaacttccctct	2631
NDUFA10	14	intron8 + 11226	gttgtgtgactgtgtgggc A/G tctacactctcgggctcag	2632
NDUFA10	15	intron8 + 11319	atcttgcccttccctcctgco G/A tctgttcaggctgaatcct	2633
NDUFA10	16	intron8 + 11386	ccataatcctagcttgaacc C/T tctttttccctgtgaccc	2634
NDUFA10	17	intron8 + 12301	acataattattgttaacatg C/T cgttaccagtgacattct	2635
NDUFA10	18	intron8 + 13361	ccaggccactgattgcttgc G/A cattttctagcattttctta	2636
NDUFA10	19	intron9 + 183	ttctgtgtgggaagctgat G/A agtctctcagatgacagccc	2637
NDUFA10	20	intron9 + 6669	aataaiaatgaccctttctg G/T aaattctagaattcctttt	2638
NDUFA10	21	intron9 + 8028	gaggacattccacagaaagt G/A tgactattagagcagaggt	2639
NDUFA10	22	intron9 + 10742	ctggaggaggggtgagc C/G agttcagccagcactgggt	2640
NDUFA10	23	intron9 + 10985	agaaagggttacacaggagc A/G cacttctcaggagtggtgt	2641
NDUFA10	24	intron9 + 10989	agggttacacaggagcacac T/C tctcaggagtggtgtgagc	2642
NDUFA10	25	intron9 + 12601	ctgtgaatcctctcactgc G/A tgaaggcctggctccctct	2643
NDUFA10	26	intron9 + 13908	cacattgttatgaaccaag C/T ctggaattcagtgtagaaga	2644
NDUFA10	27	intron9 + 13911	attgttatgaaccaagcct G/T gaattgcagtgtagaaga	2645
NDUFA10	28	intron9 + 14064	tctgtcattatgaaccct A/G tcagataaatttaaacag	2646
NDUFA10	29	intron9 + 14184	tggctttgttgggaacagc G/A agagatacagaaccgacgt	2647
NDUFA10	30	intron9 + 16487	cttgaagctgactgttccct C/A ctggaagctgactgttccct	2648
NDUFA10	31	intron9 + 16779	gccagcgtgactgtttag G/A ttctctatgacattcagacc	2649
NDUFA10	32	intron9 + 17663	ttccaaatcacccagaaact T/G tgcagtattttgaagctct	2650
NDUFA10	33	5'flanking - (1668-1659)	gtaaaattgttttaactaga (C)9-11 ttcttaaccaggtataaa	2651
NDUFA10	34	5'flanking - (1355-1334)	ctgtatccatttgaaggcac (A)15-21 tgcagaagaaacaggcaaa	2652
NDUFA10	35	intron1 + (46-61)	tggcgggtggcagggtggc GGGGTGGCGGGGTGGG/Δ gag	2653
NDUFA10	36	intron4 + 2486	ctcactggaacttttttt T/Δ aatttaattttlaaatttt	2654
NDUFA10	37	intron7 + (1600-1601)	cacttccattctgactgtta (A) cgggtgacttcttctgccca	2655
NDUFA10	37	intron7 + (1600-1601)	cacttccattctgactgtta cgggtgacttcttctgccca	2656
NDUFA10	38	intron9 + 1054	ggcgtgctgttttccctt A/Δ tctgtcctgtgacaggtgtg	2657
NDUFA10	39	intron9 + (8161-8172)	tttctcgtttctggagac (T)10-12 aatgtgaasattgtgtt	2658
NDUFA10	40	intron9 + (8646-8647)	aattccccctgttctct (TT) ctgtagacattttaacccta	2659
NDUFA10	40	intron9 + (8646-8647)	aattccccctgttctct ctgtagacattttaacccta	2660
NDUFA10	41	intron9 + (16503-16523)	ccttcttgaagctgatcgt TCCCTCCTTG	2661
NDUFA10	42	intron9 + (17905-17936)	AAGGTGATGGT/Δ gtccaggtagttgtctagga	2662
MGST1	37	5'flanking - 1376	caaatatgttatcatgta (CA)12-18 tcttctatgaaaactctttc	2663
MGST1	38	intron1A + 147	ttataaatgtttatcaat T/G aaaccaactgtcaatctct	2664
MGST1	39	intron1B + 36	cctggagattttaaatttct G/A cgaagattttaaacaact	2665
MGST1	40	intron1C + 456	ggaggaaggagccagcatga A/G agggtagcagcagggagg	2666
MGST1	41	intron1C + 719	ccccttggagcgtttctac C/T tctgccccacttccccgtc	2667
MGST1	42	intron1C + 985	gcccgaagcattgtctgat A/G gcaccagggcctccagtgg	2668
MGST1	43	intron2 + 3083	cgatgaasatttttctaccg C/G ttgttttagagtgtgtct	2669
MGST1	44	intron2 + 3106	aaaaaatlttagatatggg T/G actccctatgttgcacagc	2670
MGST1	45	intron3 + 1703	ttccatgttgcacagctg A/G tcttgaatttctggctcaa	2671
MGST1	46	intron3 + 2557	ttctcttctaaagaagtc T/G gtgcagatctttagcacaaa	2672
MGST1	47	intron3 + 3032	tccagcatcttcccttcca T/C tttaaagtiagactttttt	2673
MGST1	48	intron3 + 3045	agagcatttgaatatatt C/A cttttaaaggttaggaataa	2674
MGST1	49	intron3 + 3289	atatattccctttaaagta G/G agataacccttcaactgaga	2675
MGST1	50	intron3 + 3885	ggtttatagtgttcccccc T/A ccccgcccccaaaagcccca	2676
MGST1	51	intron3 + 3978	gaagctgccgtccaggaag G/C agtctgtgttggagagag	2677
MGST1	52	intron3 + 4298	ggaaagctgggaactgttt G/T cctggacagagttctcaaa	2678
MGST1	53	intron3 + 4519	tgtcaactcgtaacacagg G/T gtagaagtggaactgtttt	2679
MGST1	54	3'untranslated + 603	tttaatagaasatgtatto C/T tgtcttttcttccatctc	2680
MGST1	55	3'flanking + 147	gggtaaaccattttgata T/G tagcattggcaatctctgt	2681
MGST1	56	3'flanking + 237	tatttcttctctctct C/T tgttttcttctctgaaa	2682
MGST1	57	3'flanking + 1318	cagcagtttttctatgaa C/T aagacattctccaataact	2683
MGST1	58	3'flanking + 1331	tggctctgtgtcatgaaca T/C gaacgctgcacggcacac	2684
MGST1	59	intron1C + (904-923)	atgaacatgcacgctgcac G/A gcacacacacacacacaca	2685
MGST1	60	intron1C + (3433-3434)	tccgattatcttggtaatt (A)18-20 ggcaaatcagtcgaatttg	2686
MGST1	60	intron1C + (3433-3434)	cccttcaatactagaacaa (AA) gcagacatttaatttac	2686

[illegible]94

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
UGT2A1	47	intron5 + 2505	taattgacttttataatc G/A tacaagtgtataagtcata	2745
UGT2A1	48	intron5 + 2639	tagactattacaagtgtt A/G gttagctgacastttgttca	2746
UGT2A1	49	intron5 + 4009	gaatccggctggacattt C/A tccagacacaaacaaaat	2747
UGT2A1	50	intron5 + 4311	atacagacccctgtcctttt G/A tcacaaacatacagatgt	2748
UGT2A1	51	intron5 + 4545	agctcacacagtatcaaat T/C atttttggaaaattatgct	2749
UGT2A1	52	intron5 + 4616	actttttatgtctacatt G/C atcactcgtgttaagcata	2750
UGT2A1	53	intron5 + 4717	tgcagaattatatttttc C/A acgtactatggcccttaacc	2751
UGT2A1	54	exon6 + 1524	gctatatttttggcataca A/G tctgtttgttttctgtca	2752
UGT2A1	55	3'untranslated + 1683	aagggttttaacaaaacac G/A tctccatcctgtttccaaa	2753
UGT2A1	56	3'flanking + 685	aactcgaaaataattatca T/C ttltataaatttttagtca	2754
UGT2A1	57	intron1 - (18967-18965)	ctccaaattagattgattag TAT/Δ gagtccctgggttactggt	2755
UGT2A1	58	intron1 - (18862-18803)	aatactttcttcccccttca (AC)14-17 atgcttactggcctattat	2756
UGT2A1	59	intron1 - (17463-17447)	aaacttgaacccctctctc (A)16-27 gaaagaaaatggcagagaa	2757
UGT2A1	60	intron1 - 10860	attcaatgcaactttttt T/Δ gtaatggcagaattagaaca	2758
UGT2A1	61	intron2 + (528-538)	ctgttaggaacaaatgggt (A)8-10 ctttttggttgaacatgg	2759
UGT2A1	62	intron2 + (1514-1533)	ttgtgtatgtgtatgtt (GT)9-11 tatttaaatgaattatctc	2760
UGT2A1	63	intron5 + (916-917)	gcttagtattatattat AA/Δ gctatattatgcttagt	2761
UGT2A1	64	intron5 + 1163	caattttatgtcattttt T/Δ ctcaatttactctgtttcc	2762
UGT2A1	65	intron5 + (3819-3838)	agacagacagacacacac (AC)8-12 tcaacacatgaaactctc	2763
UGT2A1	66	intron5 + 4785	tctcttcaatgaataaasa A/Δ caaaattgtctaatttctg	2764
OATP1	1	5'flanking - 916	scagagtgtgtttcaataa G/A tattttgttatctgtgaga	2765
OATP1	2	5'flanking - 843	tagtgacagcaactatgcctt G/A atgtgtgtgtgtttggatt	2766
OATP1	3	5'flanking - 526	aattgtgtcctgtatgtta T/C acatctgtacatatttcc	2767
OATP1	4	5'flanking - 172	caaaacacacactcaagtat G/A tgtgtatttaaaagttagta	2768
OATP1	5	intron1 + 206	tgtctcaggcgaagttatc C/G taatggctttggagagatt	2769
OATP1	6	intron1 + 454	caacataacaaataatttct G/A taagaataatggcattttg	2770
OATP1	7	intron1 + 999	gtttgcaaggttagatatt A/G atgtgtgtgttaagacaaa	2771
OATP1	8	intron1 + 1223	ttgctagaagcttagtagac C/T agcttttaaatccagagat	2772
OATP1	9	intron1 + 1326	aactagttaggcaaccatg T/C gtttttgggaaacagcagt	2773
OATP1	10	intron1 + 1336	gcaacccatgtgttttaggg G/A aaagcaatgaggtcatgat	2774
OATP1	11	intron1 + 1498	atagtttgccttaagaata C/T actctggaaggtttatagt	2775
OATP1	12	intron1 + 5041	ttatgtctccggggagttag C/T tctctaatgcataaggaga	2776
OATP1	13	intron1 + 9532	aaagactggagacacttccc A/G atgacaaatactagactaga	2777
OATP1	14	intron2 + 198	ttacctaatataaacctta A/C atattgccacatctctacc	2778
OATP1	15	intron2 + 961	aaaagtttatagaaatat A/G agtgcactcctttctagt	2779
OATP1	16	intron2 + 1110	gtctactagtgttcaactcc T/C ttactcttgccctgtatca	2780
OATP1	17	intron2 + 1419	aaagcctaaagagatgcag T/C gcaatagcctctgtgagaag	2781
OATP1	18	intron2 + 3339	tatgttttgcacaaactta T/C tctgtatttttttttca	2782
OATP1	19	intron3 + 66	caggaaatgaattgcaact T/C cctctcaggagcaatgctt	2783
OATP1	20	intron3 + 205	tcagttttgcattttacac A/G atgggttttggacctttt	2784
OATP1	21	intron3 + 6377	aataatagacttttgggtta C/T tgggttttttggataaat	2785
OATP1	22	intron3 + 7238	tgaatgtcacattttttaa G/A ttgtgttcttctctcata	2786
OATP1	23	intron4 + 1016	ttttatctggatcatgtt T/G gtggaattgcagtgatcca	2787
OATP1	24	intron5 + 110	tccacatgatgagtaggt A/G tcttggcacagttggccttc	2788
OATP1	25	intron6 + 496	agtgctgaattataagcca A/G ttltatagtttggagacc	2789
OATP1	26	intron7 + 1934	aaagtgaaggaaattaaa G/C tgagaacttgagcctgaatg	2790
OATP1	27	intron7 + 2140	tgaatgtaccaaatgaatc A/G gcatctctgaggtgggacc	2791
OATP1	28	intron7 + 2365	tgaatcttctttctcaact C/T gattttctccagactttac	2792
OATP1	29	intron8 + 88	gcaaacctctaagtgaagt G/C tttagatatattttgact	2793
OATP1	30	intron9 + 534	tcatattttgtatttaag G/A ttatctgggttttactgaaa	2794
OATP1	31	intron9 + 1286	tattctctgagataatca T/C tgaagggtgtgctatgtgt	2795
OATP1	32	intron11 + 215	ttcacctctattctcctcta C/T ttcttctcttattcttag	2796
OATP1	33	intron11 + 663	ttcttctcttttggagctc T/A aaagttaggttcagttaatc	2797
OATP1	34	intron11 + 999	ctcatcactgcagtagagt A/G gaattatcaacttttgtat	2798
OATP1	35	intron11 + 16727	ttcttttttttacaactt A/G ttactttttaggtgtatga	2799
OATP1	36	intron12 + 48	ctatcagaacaattatata T/G tatttttttttttacaact	2800
OATP1	37	intron12 + 686	tatgttttgataaacttgc C/A gtaaaataaagaattga	2801
OATP1	38	intron12 + 708	tacaataaagaataatgaa A/G tatttccaataaatcaagt	2802
OATP1	39	intron13 + 418	tctctgtcttccaaatcat A/G tatttctccctctttacat	2803
OATP1	40	intron13 + 436	ctatattttctccctttta C/A atttgcgtgaacacttctc	2804

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
OATP1	41	3' untranslated + 2130	gtctttaagaacclaaaaa C/A ctcttaactcaaatatata	2805
OATP1	42	3' flanking + 57	agtgaactaaagtgtttctta C/A aaacaagtgtctgaatcaa	2806
OATP1	43	3' flanking + 572	aatacactctgtgtatttat G/A tgtactataaatggaglgag	2807
OATP1	44	3' flanking + 788	atttctaaatgatcagatg C/T atcatatgaasaaagaaagc	2808
OATP1	45	3' flanking + 1356	aggtgactgacataaatggg G/A gcagaggacataatgaggtt	2809
OATP1	46	5' untranslated - (189-188)	attttcactcgtatataa (A) gcgttccaggattttttgta	2810
OATP1	47	5' untranslated - (189-188)	attttcactcgtatataa gcgttccaggattttttgta	2811
OATP1	48	intron4 + (725-726)	tgatcttttaagcggggaa AA/Δ caggcaagtcgctatagt	2812
OATP1	49	intron4 + (1082-1083)	attgagtcaggaaacaaaa GA/Δ gtttcaaaaatttgaaaaat	2813
OATP1	50	intron4 + 2301	aatgicactgtcttttttt T/Δ atgcagagtgatcaaaagga	2814
OATP1	51	intron9 + (241-246)	attgtatgtcagtgagggt TGTGTG/Δ catgattgtctttgtat	2815
OATP2	1	5' flanking - 2574	ggataaggcaacccctatgt A/G tcaactctcaggagagggga	2816
OATP2	2	5' flanking - 2366	aaacataggaaatgacagagc C/T ctgtggggattagaaagag	2817
OATP2	3	5' flanking - 2244	tgatgatccagagccttga T/G cattgtgggtatagaacca	2818
OATP2	4	5' flanking - 1723	tcttcagacttcaaaagccc A/G tgaattttcatcagagctgt	2819
OATP2	5	5' flanking - 1180	tgcttatttaacaggcataa T/G ctttgcctcctgagccaga	2820
OATP2	6	5' flanking - 811	tatgtgcataatgtgtatca G/A gtaaaagtgtgtatgtgt	2821
OATP2	7	intron1 + 7188	aatcatttgaaatttaagaa A/G aaatattgttcagagaaaa	2822
OATP2	8	intron1 + 7331	gtgaatgaggaaacaaagt T/C ccaccttttttctgaata	2823
OATP2	9	intron1 + 7391	agagagatgtgaatgtgt T/G ttcttggggagtaggggaa	2824
OATP2	10	intron1 + 7888	ttgttagtagaaagaaatc G/A aggcctaaactaaaggag	2825
OATP2	11	intron1 + 7958	ttgtatttatataattttt T/A aaaaaagatttctaataat	2826
OATP2	12	intron1 + 7959	tgtatttatataattttt A/T aaaaaagatttctaataat	2827
OATP2	13	intron1 + 8036	ggaaaaaatgggggaaatt A/T atcaaaagggcagctatttc	2828
OATP2	14	intron1 + 9164	acattatattctataaasa G/T agtcagttgaagttaaaagt	2829
OATP2	15	intron1 + 10123	tctgtcttctcactttgt T/G tccagcattgacctagcaga	2830
OATP2	16	intron2 + 193	tgttaagattttctttggc G/A aaatttttgatgcttaatag	2831
OATP2	17	intron2 + 1020	ttgagtaacatttaggcaa G/A tggcagtcataaggaaaaag	2832
OATP2	18	intron2 + 14865	agaggatttaactataagag G/T ttattttggctaaagtgcaca	2833
OATP2	19	intron2 + 14931	gttagttaataacagaaaaa A/T talcagaaatttaaaaaat	2834
OATP2	20	intron2 + 15417	ttctaaatgaatgaatc A/T tttcttatattataactata	2835
OATP2	21	intron2 + 20823	ttgtataagagatacacaac A/C aatttctactagggaata	2836
OATP2	22	intron2 + 20852	ctagggaataaaagcttca G/G taaggaggtgcttaagct	2837
OATP2	23	intron2 + 20930	atggagagaagcagcaggt A/G ccacagataaatgaagtgg	2838
OATP2	24	intron2 + 21360	ttcaaaagcgtatttttca T/C taagtcttttggtaataa	2839
OATP2	25	intron2 + 21467	tatatcacataacactgtcc A/G gaagatgtgtataagccaa	2840
OATP2	26	intron2 + 21621	tatcaactattatgaagaga A/G ctactcttcttaactaggga	2841
OATP2	27	intron2 + 22760	ttccccactctctgtgtt G/C tctctttaaacttctcttg	2842
OATP2	28	intron2 + 23199	ctactctgcacataacatta C/T aaacttaaggcaattataa	2843
OATP2	29	intron2 + 23218	acaaacttaaggcaattata A/G aaactcaatcatattatct	2844
OATP2	30	intron2 + 23330	gccttgttctgttctct G/A tacttgcctcaactacatag	2845
OATP2	31	intron2 + 23673	ctggagacgttgaatcaac T/C gaggatgaasatagacatt	2846
OATP2	32	intron3 + 89	ggtttcaactgggttaaat T/G tatctctcaaggcaatttg	2847
OATP2	33	intron3 + 224	tgtatattttctatagtc A/G caaagatgatgaactgae	2848
OATP2	34	intron4 + 97	cccttaaataggcagttac C/A tttaggaagatacccaata	2849
OATP2	35	intron4 + 568	ttcatgtaccaattgtggc A/G acgtatttccaggcaacaag	2850
OATP2	36	intron4 + 599	aggcaacaagatgaagaag A/G aaagaataagaagcaacaaa	2851
OATP2	37	intron4 + 753	aaatagacattattccag T/A taccaggttccgggttaaa	2852
OATP2	38	intron4 + 781	ttcccggttaaaaatcccaa G/C tatattactgtgaaggaa	2853
OATP2	39	intron4 + 1196	aaggaccacaactatagatca G/T catgtcttaaatatgccat	2854
OATP2	40	intron4 + 1229	tatgcataatgtgtgacac T/C ttgcacotgtatttctac	2855
OATP2	41	intron4 + 1623	catctgttgaaatggatta G/C atttatttttactacatt	2856
OATP2	42	exon5 + 388	atttcaagaacataatc A/G attcatcagaasattcaaca	2857
OATP2	43	exon5 + 452	taattcaattttatcactca A/G tagagcatcacctggatag	2858
OATP2	44	intron5 + 165	ttatatacacagttgcccc A/T ttacaacacaggttaaac	2859
OATP2	45	intron5 + 189	acaacacaggttaaacctac G/A cgttttcaacttctatgcaa	2860
OATP2	46	intron5 + 191	aaacacaggttaaacctac G/A tttaacttctatgcaaat	2861
OATP2	47	intron5 + 507	atataactttgtcttcttg C/T aaaggcaaacgttttatc	2862
OATP2	48	intron5 + 520	ttcatgtcaaaaggcaaac A/G ttatctatttaaaagattt	2863
OATP2	49	intron5 + 856	agtcattgataacctaag A/G ataaacacaaasaaagaa	2864

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
OATP2	50	intron5 + 1157	acagataattttacttgg T/C gtgttttctgtatgatg	2865
OATP2	51	intron5 + 1226	ccttgatgttaatactctcc A/C catgccaaaggtggggccag	2866
OATP2	52	intron5 + 1228	ttgattgttaatactccac A/C igccaaaggtggggccaggt	2867
OATP2	53	intron5 + 1304	actgttctctgtgtaataa G/T aagtctccaaagctctgatg	2868
OATP2	54	intron5 + 1348	ttataaagtagagttccct G/A caaaagctctctgtccctgcc	2869
OATP2	55	intron5 + 1407	ttgtctctctctctctctcc G/A ccatgattgtgagccccc	2870
OATP2	56	exon6 + 521	gtcatacatggtatata T/C gtccatgggaatattgcttc	2871
OATP2	57	exon6 + 571	gggagactcccatgaccca T/C tggggtttcttacttgat	2872
OATP2	58	exon6 + 597	ctttcttcatattgatatt C/T gctaaagaggaacttttc	2873
OATP2	59	intron7 + 33	agaaacaggtaccatgata C/T gtcttctcagccacatgc	2874
OATP2	60	intron7 + 267	caaaataaccaaatgtaaa T/A gtctcctcccaaatgact	2875
OATP2	61	intron7 + 1260	gtaactctcactttctctgc A/G tttaacttgtaaaacttt	2876
OATP2	62	intron7 + 1386	agttcctaataatagccaa G/A agcatgctttattgttaacc	2877
OATP2	63	intron7 + 1472	ctttccacatgacagatg G/A catgttttagcaataata	2878
OATP2	64	intron7 + 1697	tttcatgttcaattttag C/A atatgctttagagtgctac	2879
OATP2	65	intron7 + 2273	tttccactctctctagcc C/T gatttgacccttagttact	2880
OATP2	66	intron8 + 207	gtggaagagatagggttg T/C acttttagcagggagaac	2881
OATP2	67	intron8 + 546	tccggagaagtttcccta T/C gtaattagatattttat	2882
OATP2	68	intron8 + 565	atgtatttagatattttt A/C ttgtgttaattctatcta	2883
OATP2	69	intron8 + 668	taagtaattgaatttaggt G/T catcagctttgacagtcc	2884
OATP2	70	intron8 + 739	tggagaccattagagtgca A/G taacaaagagaatgacttg	2885
OATP2	71	intron8 + 2193	tgatcacagatccaaatgac A/G taatttctaccatgaacga	2886
OATP2	72	intron9 + 112	atttttagtaacagagata G/C tataattttctgtatctt	2887
OATP2	73	intron9 + 266	tttaggttagtattctata A/G ttgatcttataatttagt	2888
OATP2	74	intron9 + 305	tgtcaagatctgagacaaac C/G cttttgtaattataactt	2889
OATP2	75	intron9 + 888	eggttctgtattgttttaa T/C aaatgacaaagatatataa	2890
OATP2	76	intron11 + 10224	tacactgttccataaaaaa T/C tctctatatttctctagt	2891
OATP2	77	intron11 + 10359	attatagatttcaactgag G/C ttcccttaacttttagccta	2892
OATP2	78	intron11 + 10916	ctttatagaaagaaatcca G/G aaaaactttttacttttt	2893
OATP2	79	intron11 + 10997	aatatattagtgtgaacaa T/C gagacttctactaatataat	2894
OATP2	80	intron11 + 11018	gagacttctactaatataat G/A caatgtatttgagccctgt	2895
OATP2	81	intron12 + 442	aacattccaaaactttttt C/T gactcagcagctgacttta	2896
OATP2	82	intron12 + 445	atcccaaaacttttatacga C/T tcacagcatgactttataa	2897
OATP2	83	intron12 + 447	tccaaaacttttatacga C/A acagcatgactttataata	2898
OATP2	84	intron12 + 907	aagtgaagagagctggcaga T/C tgaacactatgaatagag	2899
OATP2	85	intron13 + 65	tatttatatatatatata C/T acacacacatcatetatta	2900
OATP2	86	intron13 + 870	aattctgagtctctttt G/A atgttccaactctgtggcac	2901
OATP2	87	intron13 + 1935	taaaasasasasagcttgc T/G ttacagcaattgagccag	2902
OATP2	88	intron13 + 2261	aacgaactcctccaaatttt G/C aacttttatttaacaaaat	2903
OATP2	89	intron14 + 248	tcaggataataaccaactt G/A tcaaaatcagagataatag	2904
OATP2	90	intron14 + 2463	attgtttactaatatgaa C/G cttcttcaagcctattttt	2905
OATP2	91	intron14 + 2857	tcactcatgtatttccaggac A/T cctggcaagatgctctcag	2906
OATP2	92	intron14 + 11458	atctccagaggtcctgtgt C/T tccccaagtcactgaccc	2907
OATP2	93	3'untranslated + 2243	ataataaaacaaactgtagg T/C agaaasatgagagtactca	2908
OATP2	94	3'untranslated + 2404	tcttaataaaacaaatggt A/G tcatcaggttagaggttaa	2909
OATP2	95	3'untranslated + 2515	cagagtttgaactataatc T/G aaggcctgaagcttagcttg	2910
OATP2	96	3'untranslated + 2539	gcctgaagcttagcttggat A/G tatgtacaaataatctgt	2911
OATP2	97	intron1 + 457	taattggcaaacataaaaa (A) caggtgtctcaagtcacat	2912
OATP2	98	intron1 + 457	taattggcaaacataaaaa caggtgtctcaagtcacat	2913
OATP2	99	intron1 + (7537-7538)	gatcagcattacaaccaaga (G) atggagaatgacattcagga	2914
OATP2	100	intron1 + (7537-7538)	gatcagcattacaaccaaga atggagaatgacattcagga	2915
OATP2	101	intron1 + (10032-10035)	tgtgtgattctatattactt AGT/Δ gtttcaatttctctccaca	2916
OATP2	102	intron1 + (10058-10061)	ttcaatttctctcccaaa TTA/Δ ttttctatttaattgtaat	2917
OATP2	103	intron2 + (413-423)	acttatttaaaattctttt (A)11-13 caaaacacaggttttaaaa	2918
OATP2	104	intron3 + (1595-1603)	tggcaagtaattcaagtc (T)8-10 gattttaaacaacttttca	2919
OATP2	105	intron4 + (10-23)	ttcatggagtgtaagttgtt (A)12-14 cctctgtgccactatcagta	2920
OATP2	106	intron5 + (1567-1572)	gtgastataaattacttga CTTGTA/Δ aattaaaaaataaagtag	2921
OATP2	107	intron5 + (1577-1585)	attactttgtctgttaatt (A)9-10 taagtagaataataagagt	2922
OATP2	108	intron8 + (1939-1941)	ttcttcaactcttctactc GTT/Δ atttcaagcagatgcaactg	2923
OATP2	109	intron10 + (3077-3078)	aaattctttatctactttt (CTT) ttccctctttctctgctttc	2924

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
OATP2	110	intron10 + (3077-3078)	aaattctttatctactttt tccctctttctctgttc	2925
OATP2	111	intron11 + 11011	aacaaagtggagcttcaactaa A/Δ tataatgcaatgtatttgc	2926
OATP2	112	intron12 + (1160-1169)	agcatgcatggtagaggtg (A)9-11 gcatttlaacattgttaa	2927
OATP2	113	intron12 + (1310-1312)	tccatcttaataataaaagt TGT/Δ ctactcaaaaggagaagtct	2928
OATP2	114	intron13 + (9-34)	tacgagcactggatgatg (A)24-27 tataatetatatatatata	2929
OATP2	115	intron13 + (35-64)	aaaaaaaaaaaaaaaaaaaa (TA)10-21 cacacacacacatatatt	2930
OATP2	116	intron13 + (1379-1387)	aaatttttccaccacatac (A)8-10 caaagtaagttatgaacac	2931
OATP2	117	intron13 + (1916-1928)	aattctcttaaaataagtt (A)11-13 gtctgttttacagcaattg	2932
OATP2	118	intron14 + (588-596)	caattatactttacctctt (A)8-10 ctaatticaaattcttat	2933
OATP8	1	5'flanking - 1413	aalaggggcttaataactct G/C aaacttatgatttcalat	2934
OATP8	2	5'flanking - 1945	gaatttactctacgataig A/G ccacacagaaatgacatct	2935
OATP8	3	intron1 + 38962	atgaattagttttaaata G/A caacttlaactatactctc	2936
OATP8	4	intron2 + 253	acagacttaccacaaagaa T/G tctcttcccaaatgtcta	2937
OATP8	5	intron2 + 329	actcatggtttccaaattaa C/G tttttggaactttatctc	2938
OATP8	6	intron2 + 2568	ccattctgggtctttcttc G/A tgaactattttccatcagl	2939
OATP8	7	intron2 + 2679	ctcttattgctcttttcca T/C gttttatctaaataattta	2940
OATP8	8	intron2 + 2753	caggaaactttccaaagcc C/A ctaattlaattagctccct	2941
OATP8	9	intron2 + 3132	tggttaattgtaggaggtt T/C accttccacgtlaaallaca	2942
OATP8	10	intron2 + 3183	aattgtcttggcatatttgc A/G ttcatttggggcattcagt	2943
OATP8	11	intron2 + 3207	atttgcattcatttgggca T/C tcaattctactagatacaaa	2944
OATP8	12	exon3 + 334	gaactgggaagtatttgaac T/G ctttaccacattttctcag	2945
OATP8	13	intron3 + 76	agaattttatttttactt G/A taagtgggcagttacattt	2946
OATP8	14	intron4 + 2443	tcaattttctgttctctta C/T agttatgggtttcttaaga	2947
OATP8	15	intron4 + 67	taatcagctctataaagtt C/G tgatattcttlaacaaatt	2948
OATP8	16	intron4 + 91	tatttttaacaaattgt T/A taagacacaaatgggaagac	2949
OATP8	17	intron4 + 197	ggtttgaactgcacattgtc G/A ctattatgcagctttgtcc	2950
OATP8	18	intron4 + 813	tttaacagaataaaaaaaa T/A attttgtaacgacaaagaa	2951
OATP8	19	intron4 + 974	atatgcaccttaaaaaaac C/G tggatttttaaatatgtat	2952
OATP8	20	intron4 + 1003	taaatatgtatgtacataa G/T gaattatagcatattttgt	2953
OATP8	21	intron6 + 155	catttaataacgaataaaa A/G agaaatttagtctcttcta	2954
OATP8	22	intron6 + 750	atccaactgggttttagatt T/G cctcttttgcctctctcc	2955
OATP8	23	intron6 + 780	gcctctctctcatctgcac C/T tctcttttctctcagcaaca	2956
OATP8	24	intron6 + 1248	ctatgcctgtatctcaca C/T ttcctttatttaaaattg	2957
OATP8	25	intron6 + 1500	tctgtctgttttagcalat A/G ataactcatcagggttttg	2958
OATP8	26	intron6 + 2008	ataacataatggttagaga A/G tatcaaggcaggaaattag	2959
OATP8	27	intron6 + 2087	actactctccccatcacac T/C aaactcatgtctccccag	2960
OATP8	28	intron6 + 12305	tcatctatggagactgcaa T/C cattatcatttttccaga	2961
OATP8	29	intron7 + 363	taacaantgatccagccat C/G atactattctctgtaatag	2962
OATP8	30	intron7 + 411	ccittttttttgagaacct G/A gtgatgatattaaagcgtta	2963
OATP8	31	intron7 + 428	cctgttgatgatatttga C/A gtatgatgatcatgttata	2964
OATP8	32	intron7 + 634	apaattatataatatacat A/G taattctacctaagtattca	2965
OATP8	33	intron7 + 1791	tgtttttttaggtagtga T/C gtaagtagtaagcgaattt	2966
OATP8	34	intron7 + 2000	agttggcaaatgtgtctca G/A gtgcatataagtcacttgaa	2967
OATP8	35	intron7 + 2043	gtttattgattcattttta A/G tggatcaactgttagtgag	2968
OATP8	36	intron7 + 2171	attttttttagcgaaggtc G/A cgaactctttagaagcctc	2969
OATP8	37	intron7 + 2173	tttttttagcgaaggtcgc G/A actctcttagaagcctcac	2970
OATP8	38	intron7 + 2179	teagcaaaagtcgagctct C/T ttgaagccctccaaatca	2971
OATP8	39	intron7 + 2219	atttgaectttaagtttta T/G ataacttatatttacaatt	2972
OATP8	40	intron7 + 2261	cagatattaatatatttt A/T ttattgaatatgttatttt	2973
OATP8	41	intron8 + 150	acaaattttccattttgt T/C atactctgtttctgtcat	2974
OATP8	42	intron8 + 154	aatttctccatttttata A/T catctgtttgtctgatttga	2975
OATP8	43	intron8 + 1303	ttttttttagatggagtct C/T gctctgttgcacggcctgg	2976
OATP8	44	intron8 + 1372	aagctcgcctccaggttc T/G ccacccctctcttaagaaa	2977
OATP8	45	exon9 + 1272	tccttctttttcaactctt A/G tatttccctctcatctgcga	2978
OATP8	46	intron10 + 63	tcacagatttgatttaata A/T tacttatacaattctctat	2979
OATP8	47	intron10 + 911	ctlgcccaatactctaccaa G/T gtattattaaacggccttga	2980
OATP8	48	intron10 + 872	tcctagtcttcttgagata G/A gctacaacttttagtaact	2981
OATP8	49	intron10 + 1101	tccttggttctgtgttcc A/T gtatgaaagccgtgaagag	2982
OATP8	50	intron10 + 1103	cctgtctctgtgttccag T/C agtgaagacctgaagagag	2983
OATP8	51	intron10 + 2027	ccccttttcatgagtgcta A/G gttttgtcccttttcaact	2984

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
OATP8	52	intron10 + 2028	ccatttcatgagtgctaa G/A tttgtcccggttcaccta	2985
OATP8	53	intron10 + 2148	gtatttggaaagaaatgt A/G ggtggagagaaatattta	2986
OATP8	54	intron10 + 2214	atatacagaatttcatacac T/G aatttcttaattccaaat	2987
OATP8	55	intron10 + 2316	taaatattttagtttgagac T/G tcitttaaatataatggaaig	2988
OATP8	56	intron10 + 2372	tgtatttggcaaatgtttt G/T tteatttttcaaaactatt	2989
OATP8	57	exon11 + 1557	cagaacagaaattactcagc A/G caatttgggtgaatgcccaag	2990
OATP8	58	intron11 + 147	ttcttgaattttttgat A/C ttcaataacatcataata	2991
OATP8	59	intron11 + 10339	aaaaaactgcatttttagtg G/C ttacagagaaagatttgc	2992
OATP8	60	intron11 + 10358	ggttagctagaaagatttg T/G ctcatatacaacataaatta	2993
OATP8	61	intron11 + 10538	caacagaggatcaatgtaa T/G gaactctcttaaataaaca	2994
OATP8	62	intron12 + 55	ataaatattatgtttaa C/T taagactgaatgcaatlaa	2995
OATP8	63	intron12 + 1802	taaaatgaatcggtaaaaca T/G tcatgtataaatcactgtca	2996
OATP8	64	intron12 + 2612	ataggcatataactcttt C/A ttccctctgtatataggagg	2997
OATP8	65	exon13 + 1833	aacagctgtgggcacaaagg G/A gctttaggtatataattc	2998
OATP8	66	5'flanking - (1590-1587)	atatataacatataccta TATC/Δ tatgttatgtgtctcttat	2999
OATP8	67	5'untranslated - (11-28)	agcatcagcaacaaataaa ATATTTCACT	3000
OATP8	68	5'untranslated - (4-7)	TGGTATCTG/Δ tagtttaataatggaccaac	3001
OATP8	69	intron4 + (213-214)	tattcaactgtgtctctgtag TTTA/Δ ataaggaaccaatcaaca	3002
OATP8	70	intron4 + (213-214)	cctgttcgtttatgacgc (T) ttgttccaaaccaaacagaa	3003
OATP8	71	intron4 + 505	cctgttcgtttatgacgc ttgttccaaaccaaacagaa	3004
OATP8	72	intron4 + 616	tataactttctctttataaa G/Δ atgcaaatgtttatgcatt	3005
OATP8	73	intron4 + (804-812)	aaaaataaatgaatggagg A/Δ aaaaaaatgtttcaagttt	3006
OATP8	74	intron4 + 855	acatccatgtttaacagaat (A)9-11 tattttgtaacgacaaaga	3007
OATP8	75	intron7 + (619-628)	ggatgtgtttaaacaaatta G/Δ gaactattttcaacacac	3008
OATP8	76	intron7 + (1773-1779)	tttttatetgaattaaaat (AT)4-5 catataaatcttcaactaag	3009
OATP8	77	intron7 + (1773-1779)	atttttatattatgaact (T)7-8 aaggttagtgaatgcaatag	3010
OATP8	78	intron8 + (1270-1290)	tagtggccaccctctctc (T)19-23 gagaatgagctctgctctgt	3011
OATP8	79	intron10 + 665	ttcttcttaactcaaaagg T/Δ ttttttttccatgtgacac	3012
OATP8	80	intron11 + (247-250)	aaaaatcttaaggcaccac TGAT/Δ tgacagttgccttgatgta	3013
OATP8	81	intron12 + (1622-1630)	aaataaattgttgacatca (T)8-10 atttttcaagggtcgtgt	3014
OATP8	82	3'untranslated + (2464-2465)	ggaaaagcctgatgccttt A/Δ aaaaaaatgaacactttg	3015
OAT1	1	5'untranslated - 127	gcagctcagactcagctccc G/A gagcaaccagctcagagg	3016
OAT1	2	5'untranslated - 20	gaagccacagccccagcc A/G ctgagctggcctggcccaa	3017
OAT1	3	intron3 + 150	caatgaacaaactttttc G/A ggcctatgcgccttgaccc	3018
OAT1	4	intron4 + 211	ttctctgcttcccccactc A/C gttctcagcctgctctc	3019
OAT1	5	intron5 + 33	gagacttccatgatgaact C/T ccagggttcccccacaa	3020
OAT1	6	intron8 + 168	gaaccagatgccccagcct C/T gactcagtcacagctctcac	3021
OAT1	7	intron1 + (58-71)	ggagatgggggcctttgtt (A)13-15 gtacatggagaattaaactg	3022
OAT1	8	intron3 + (1306-1319)	aataagttggagagagcag (A)12-15 tcaagagtggaggggca	3023
OAT2	1	intron4 + 842	ttgaactccaaagtgttg G/A attacaggcatggccattg	3024
OAT2	2	intron5 + 33	gtgtgtgtgagcatgat C/A tgtgtgtgtggaggtgg	3025
OAT2	3	intron5 + 183	ccacatccatcttcagagc A/C aactgtctcagctgccatg	3026
OAT2	4	intron5 + 184	caactccatcttcagagc A/C actgtctcagctgccatg	3027
OAT2	5	exon7 + 1269	actagctgtagtgctctc C/T ggtgagccagtcacatagg	3028
OAT2	6	3'untranslated + 1792	ataaatgtgtacatgaggt A/G tgaacacaaatacaaggt	3029
OAT2	7	3'flanking + 1386	tgtagcagccacatgcaca G/A ttttcaacactgagagag	3030
OAT3	1	5'flanking - 580	ctgtgtcagagacacagaca C/G ggaagctcgtgctgccccag	3031
OAT3	2	5'flanking - 463	ttcttgagaggaactcccc T/G tcccctctcaggaggtgoc	3032
OAT3	3	5'untranslated - 16	cctgccacagctctgctc G/A tcttgcacagtgccatgac	3033
OAT3	4	exon2 + 153	cctgtccacccatgtgcccc G/A ccccaaatgcctccacagg	3034
OAT3	5	intron2 + 177	gcacaaagaccccttgcctc T/C tcccactcagatccaaaga	3035
OAT3	6	intron2 + 6201	gtcatctctctgtgctct T/G tgcacacagcaggttctc	3036
OAT3	7	intron3 + 79	tcgtctccacccgtgacccc G/G caaagaggcaaaagagctgg	3037
OAT3	8	exon5 + 723	tggcgttggctgagttaac T/A gtgtccattcccttctctgt	3038
OAT3	9	intron5 + 524	tggagttacaaaggaaagt T/C aaaggaagcctgagcctgg	3039
OAT3	10	intron7 + 386	gacaaatgggttgcagact G/A aagacaaaattatgttat	3040
OAT3	11	intron7 + 754	gcccacgtcagacatgacca G/A tcaatcacagcatttctcc	3041
OAT3	12	intron9 + 81	attgtctgtctctctaccca G/A ggaagcaatcctttatgac	3042
OAT3	13	5'flanking - (661-660)	tacatttggctccacgggg (G) agcggctgacaggagagaa	3043
OAT3	14	5'flanking - (661-660)	tacatttggctccacgggg agcggctgacaggagagaa	3043

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
QAT9	15	Intron 4 (211-212)	ttcgaatgctgagcaca AA/A cagagtgatctgag	3044
ALDH1A2	1	5' flanking 716	caagatccatctctcag C/G cagacagcagcagcagc	3045
ALDH1A2	2	Intron 1-314	cagcccccctcccccag G/A cagcccccctcccccag	3046
ALDH1A2	3	Intron 1-854-8751	tttgcagctgagcagcagc (T)11-12 cagcccccctcccccag	3047
ALDH1A2	4	Intron 1-1270	tcctgctgctgagcagc A/G ttgcagcagcagcagc	3048
ALDH1A2	5	Intron 1-1287	tttcagcagcagcagc A/A ttgcagcagcagcagc	3049
ALDH1A2	6	Intron 1-1304	tcctgctgagcagcagc C/G ttgcagcagcagcagc	3050
ALDH1A2	7	Intron 1-1971-1980	agccagcagcagcagc (T)5-11 cagcccccctcccccag	3051
ALDH1A2	8	Intron 1-2105	tttcagcagcagcagc T/G ttgcagcagcagcagc	3052
ALDH1A2	9	Intron 1-2187	ttgcagcagcagcagc C/T ttgcagcagcagcagc	3053
ALDH1A2	10	Intron 1-2441	agccagcagcagcagc T/A agccagcagcagcagc	3054
ALDH1A2	11	Intron 1-3035	agccagcagcagcagc A/G agccagcagcagcagc	3055
ALDH1A2	12	Intron 1-3319	tttcagcagcagcagc T/G agccagcagcagcagc	3056
ALDH1A2	13	Intron 1-3474	tttcagcagcagcagc T/G agccagcagcagcagc	3057
ALDH1A2	14	Intron 1-4418	tttcagcagcagcagc G/G agccagcagcagcagc	3058
ALDH1A2	15	Intron 1-4727	tttcagcagcagcagc A/G agccagcagcagcagc	3059
ALDH1A2	16	Intron 1-4754	tttcagcagcagcagc T/A agccagcagcagcagc	3060
ALDH1A2	17	Intron 1-4957	tttcagcagcagcagc A/G agccagcagcagcagc	3061
ALDH1A2	18	Intron 1-5835	tttcagcagcagcagc T/G agccagcagcagcagc	3062
ALDH1A2	19	Intron 1-8206	tttcagcagcagcagc T/G agccagcagcagcagc	3063
ALDH1A2	20	Intron 1-9525	tttcagcagcagcagc C/T agccagcagcagcagc	3064
ALDH1A2	21	Intron 1-1001-1030	tttcagcagcagcagc (AAG) agccagcagcagcagc	3065
ALDH1A2	21	Intron 1-1031-1032	tttcagcagcagcagc agccagcagcagcagc	3066
ALDH1A2	22	Intron 1-1231	tttcagcagcagcagc T/A agccagcagcagcagc	3067
ALDH1A2	23	Intron 1-1342	tttcagcagcagcagc G/A agccagcagcagcagc	3068
ALDH1A2	24	Intron 1-14173-14176	tttcagcagcagcagc AAAA/A agccagcagcagcagc	3069
ALDH1A2	25	Intron 1-14580	tttcagcagcagcagc G/G agccagcagcagcagc	3070
ALDH1A2	26	Intron 1-14585	tttcagcagcagcagc A/G agccagcagcagcagc	3071
ALDH1A2	27	Intron 1-14711	tttcagcagcagcagc A/G agccagcagcagcagc	3072
ALDH1A2	28	Intron 1-15377-15377	tttcagcagcagcagc (T)2-11 agccagcagcagcagc	3073
ALDH1A2	29	Intron 1-17128	tttcagcagcagcagc A/G agccagcagcagcagc	3074
ALDH1A2	30	Intron 1-18777	tttcagcagcagcagc A/G agccagcagcagcagc	3075
ALDH1A2	31	Intron 1-18784	tttcagcagcagcagc T/A agccagcagcagcagc	3076
ALDH1A2	32	Intron 1-19081	tttcagcagcagcagc C/T agccagcagcagcagc	3077
ALDH1A2	33	Intron 1-21514	tttcagcagcagcagc T/A agccagcagcagcagc	3078
ALDH1A2	34	Intron 1-21752	tttcagcagcagcagc A/G agccagcagcagcagc	3079
ALDH1A2	35	Intron 1-21865	tttcagcagcagcagc C/T agccagcagcagcagc	3080
ALDH1A2	36	Intron 1-24782	tttcagcagcagcagc A/A agccagcagcagcagc	3081
ALDH1A2	37	Intron 1-27805	tttcagcagcagcagc T/G agccagcagcagcagc	3082
ALDH1A2	38	Intron 1-28204	tttcagcagcagcagc C/G agccagcagcagcagc	3083
ALDH1A2	39	Intron 1-28201	tttcagcagcagcagc T/G agccagcagcagcagc	3084
ALDH1A2	40	Intron 1-48476	tttcagcagcagcagc C/T agccagcagcagcagc	3085
ALDH1A2	41	Intron 1-48834	tttcagcagcagcagc C/T agccagcagcagcagc	3086
ALDH1A2	42	Intron 1-48851	tttcagcagcagcagc G/G agccagcagcagcagc	3087
ALDH1A2	43	Intron 1-51181	tttcagcagcagcagc C/T agccagcagcagcagc	3088
ALDH1A2	44	Intron 1-5854	tttcagcagcagcagc G/A agccagcagcagcagc	3089
ALDH1A2	45	Intron 1-6968	tttcagcagcagcagc C/T agccagcagcagcagc	3090
ALDH1A2	46	Intron 1-7172	tttcagcagcagcagc T/G agccagcagcagcagc	3091
ALDH1A2	47	Intron 1-1772	tttcagcagcagcagc T/A agccagcagcagcagc	3092
ALDH1A2	48	Intron 1-1743	tttcagcagcagcagc C/T agccagcagcagcagc	3093
ALDH1A2	49	Intron 1-2881	tttcagcagcagcagc A/G agccagcagcagcagc	3094
ALDH1A2	50	Intron 1-2818	tttcagcagcagcagc G/A agccagcagcagcagc	3095
ALDH1A2	51	Intron 1-290	tttcagcagcagcagc T/G agccagcagcagcagc	3096
ALDH1A2	52	Intron 1-3280	tttcagcagcagcagc T/G agccagcagcagcagc	3097
ALDH1A2	53	Intron 1-4661	tttcagcagcagcagc G/A agccagcagcagcagc	3098
ALDH1A2	54	Intron 1-506	tttcagcagcagcagc G/A agccagcagcagcagc	3099
ALDH1A2	55	Intron 1-1852	tttcagcagcagcagc C/G agccagcagcagcagc	3100
ALDH1A2	56	Intron 1-2079	tttcagcagcagcagc C/T agccagcagcagcagc	3101
ALDH1A2	57	Intron 1-2519	tttcagcagcagcagc C/G agccagcagcagcagc	3102
ALDH1A2	58	Intron 1-2840-2851	tttcagcagcagcagc (T)1-13 agccagcagcagcagc	3103

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ALDH1A2	59	intron4+7231	aalaggatcaaatcacaa A/T gtagtgattcagatcctaa	3104
ALDH1A2	60	intron4+7958	taaaatcgtttttatgtta C/T taggtatataaaatttcta	3105
ALDH1A2	61	intron4+8090	tctgtttttctactgttta C/T agattgcttagctactca	3106
ALDH1A2	62	intron4+12823	tgttagcctgtactaaatg C/T tttaaatatgtgaacgt	3107
ALDH1A2	63	intron4+12939	atgaggtccgacttttaaga T/C tttgtclacattttctcc	3108
ALDH1A2	64	intron4+14935	tettgtggagtcttttta T/G aaatggactttaccttctt	3109
ALDH1A2	65	intron4+15321	gcatttgggtgtctggaga C/T atatccagaataatgctatg	3110
ALDH1A2	66	intron4+15412	tticaagttatttctgttt T/G tttttttttttttttttt	3111
ALDH1A2	67	intron5+1888	aatccaaactctgtacttt G/T tagtgacaagattttctgc	3112
ALDH1A2	68	intron7+9166	gaasagclactttaticaaa G/A ataaagttattttaagaata	3113
ALDH1A2	69	intron7+9914	aagctggagaaactactagg C/T ttctctcaacagtatttcc	3114
ALDH1A2	70	intron7+18942	tttggaggggaactaatccc G/A tgaattctaggtttctctt	3115
ALDH1A2	71	intron7+19820	ttcaccctctatttttaggtt A/G ggggggttggttctacag	3116
ALDH1A2	72	intron7+19826	cctctatttaggttagggga G/A gtgcttgcacagtgtttg	3117
ALDH1A2	73	intron7+19913	ctgcaatcttcctgtttt A/G tttaaaatccagtttgaa	3118
ALDH1A2	74	intron7+(20110-20111)	catgttttattcttaacta (ACTA) tgcatagtcaaatgttctgc	3119
ALDH1A2	74	intron7+(20110-20111)	catgttttattcttaacta tgcatagtcaaatgttctgc	3120
ALDH1A2	75	intron7+21857	acaatgaatataagaagg A/T ggaagggaaggaagcagaga	3121
ALDH1A2	76	intron7+21929	tacaagacacagcagctctt A/G actagtttactggatctct	3122
ALDH1A2	77	intron7+23308	ggctttgacttcgaaacct G/T tgggttatccaaagtctgc	3123
ALDH1A2	78	intron7+23554	gacattgttgaaacccggg C/T tttttagggtgtcctgtcc	3124
ALDH1A2	79	intron7+(23701-23703)	catctgagatttgcctgtg GTG/Δ ttaccaggttagtggttc	3125
ALDH1A2	80	intron7+26479	gatcatgtacaatttttt T/C atctcatgatattcttcaa	3126
ALDH1A2	81	intron7+26561	taagggccacaaatgcagta T/C tgaactctcagttacatt	3127
ALDH1A2	82	intron7+26662	ttccttagtcttccatca C/T gaactaaagctgtctcca	3128
ALDH1A2	83	intron8+78	tttatctctcactttttgat G/A ggcactagcaaatgatat	3129
ALDH1A2	84	intron8+(700-711)	accatctcatttagtattc (T)11-12 cctctcactgttgccaggc	3130
ALDH1A2	85	intron8+724	ttttttccctcactgtt T/C gccagggcagagctgtcttc	3131
ALDH1A2	86	intron8+800	cagattgtgtgaatttcagc C/A ccagcttggaatttcagag	3132
ALDH1A2	87	intron8+1251	gatttctgtgaatttgaga G/A gatctggcaacclggggc	3133
ALDH1A2	88	intron8+1627	ggccctctccagcgaagc G/A gtgagaacatggctgtttcc	3134
ALDH1A2	89	exon9+141	tggagcggccaaagggc G/A tagtggaggtcccttggac	3135
ALDH1A2	90	intron9+778	aeccagctctgacagatccc T/C tgtagcttggaaagtgtg	3136
ALDH1A2	91	intron9+801	tagcttggaaagtgtaga A/G gtaagggtgctgctcacttc	3137
ALDH1A2	92	intron9+868	tctgaaggctctgttact T/C agtgggtggggggggccac	3138
ALDH1A2	93	intron9+1338	aatttttgccttttttact A/G tcaatcaaatgttctaagt	3139
ALDH1A2	94	intron10+(227-229)	ctatgtcttattgtattta TTA/Δ gccacagacaatcagaat	3140
ALDH1A2	95	intron10+316	ctaatgttgggtcactggga T/G gtaaccaggagaggaatc	3141
ALDH1A2	96	intron10+368	ctttacattctgtgcaagaga G/A ggcaagagcaaatcagcc	3142
ALDH1A2	97	intron10+660	gtaaacttgactgaattgt G/A gaaagcaggtaaaggaatg	3143
ALDH1A2	98	intron11+104	tgggaataccaaaggaac C/T aagttcacccgaagaggg	3144
ALDH1A2	99	intron11+229	aaacttctaaagaantacc A/G tccagctcagatttgtgt	3145
ALDH1A2	100	intron12+117	catcattcccaaacattt C/T gtggagcacatgctactata	3146
ALDH1A2	101	intron12+691	gatagggaagatcactgtga A/G ctggaaatctgggaacc	3147
ALDH1A2	102	intron12+1934	catcttctctagattgat T/C ttgtttgtttgtttctct	3148
ALDH1A2	103	intron12+1973	ctacttaccctcaaacatg T/A ttctctttcttaaatgacc	3149
ALDH1A2	104	intron12+2722	ccaggtgactccagatata C/A tcaatgccaggaccacag	3150
ALDH1A2	105	intron12+3855	cacttgaagcaaccataat T/C gtgggtttctgtgtctga	3151
ALDH1A2	106	intron12+4185	tigtattaaagcaaatgaac T/G atcggagcagaggaacgcc	3152
ALDH1A2	107	intron12+4991	acaggaaacacttagcatgc A/G acccactcccaacctcgtc	3153
ALDH1A2	108	intron12+(5018-5019)	cccacctcctgttgggg (G) aggaagcacactactgtcc	3154
ALDH1A2	108	intron12+(5018-5019)	cccacctcctgttgggg aggaagcacactactgtcc	3155
ALDH1A2	109	intron12+(5051-5052)	actgtcccaagaaactata (A) ctgaaccagtgctgcttgt	3156
ALDH1A2	109	intron12+(5051-5052)	actgtcccaagaaactata ctgaaccagtgctgcttgt	3157
ALDH1A2	110	intron12+(5300-5302)	ttaaagttttaaaaaactt CGT/Δ taaaactactcatgagtg	3158
ALDH1A2	111	intron12+5405	calccaggactgtctgttc G/C caggtgataactgcacctc	3159
ALDH1A2	112	intron12+5435	aactgcacctcccaagact C/A ccgtcgaactcacatgcagc	3160
ALDH1A2	113	3'flanking+449	tttggccgggaacaaattt T/C caaggttgaaagccaatt	3161
ALDH1A2	114	3'flanking+597	acctgggatattcctgaccc A/C atctgttttttttaccac	3162
ALDH1A2	115	3'flanking+669	atgagagctgaagctatca T/C gtgcagttaccgcttctga	3163

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ALDH1A2	116	3'flanking+1122	cgctccactgagctctc T/G gtcacacccattctgccc	3164
ALDH1A2	117	3'flanking+2214	tgcagctgtgaaagaaatc T/C gtaaatggtagccgtactac	3165
ALDH1A3	1	5'flanking-1425	cagtgtagccagccgatat C/T ggtcaaggctgccccgctcg	3166
ALDH1A3	2	5'flanking-1379	ccattatcccccttccccg G/T ctacgtgtgacactcagge	3167
ALDH1A3	3	5'flanking-1270	aacttaccctctatccagc T/A ctatccagaaggacaccagg	3168
ALDH1A3	4	5'flanking-(1214-1213)	acggaggccctcaaacagga (GGA) aaataaggagacccctcccc	3169
ALDH1A3	4	5'flanking-(1214-1213)	acggaggccctcaaacagga aaataaggagacccctcccc	3170
ALDH1A3	5	5'flanking-1103	gcacagctttgtcaggagt C/T cgtccctccggtctttgttc	3171
ALDH1A3	6	intron1+986	gccttaactttccccacct T/G ggttctctgtgttttgc	3172
ALDH1A3	7	intron1+1462	glacaggatttcaaaactac G/A tatatagaaaccagacagta	3173
ALDH1A3	8	intron1+1661	ccgtgtgtctgtgtgtgtc G/A caacctttgccagtlaaagg	3174
ALDH1A3	9	intron1+2360	agggatagaagtccttct A/G atttagagggcctctttctt	3175
ALDH1A3	10	intron1+2516	tgaaaacattctcttttga G/A tttagctgagtgccctgtg	3176
ALDH1A3	11	intron1+2624	cctgagacaccttacagctc C/T gtcctgttccatgtctatc	3177
ALDH1A3	12	intron1+3255	tttctctttctcaaatgg G/C cccctcttccgtgtcact	3178
ALDH1A3	13	intron1+(3643-3656)	gcttcagaggtttttgtgg (T)12-14 acattctatcaactttaa	3179
ALDH1A3	14	intron1+4265	ccaaagccctctcttttaa T/C algacattaaagaacaatt	3180
ALDH1A3	15	intron1+5187	caagatggataagacgtcac C/T taaggctcttagcatgtga	3181
ALDH1A3	16	intron2+43	ctctaagttaattcaattatg G/T atgaccnaaggtataggaa	3182
ALDH1A3	17	intron2+127	caggccctggctagctgcg T/C gaattggcatgtgttctca	3183
ALDH1A3	18	intron2+(285-300)	aggaaggtttttctttt (T)16-17 atcaattattggacctga	3184
ALDH1A3	19	intron2+778	cgtgtcagagtaggcttgg A/G ttattctgtccctgaatt	3185
ALDH1A3	20	intron2+1216	actcgttagagtcactctg A/C ctgtgtccacatccactc	3186
ALDH1A3	21	intron3+81	accatgggtatgggaaaa A/C gatcacgttccgttttgt	3187
ALDH1A3	22	intron3+236	gctcagctcttgaccagt T/G gtgtctataggcagttgag	3188
ALDH1A3	23	intron3+1467	ggccgggttgaggaggga G/T atctctttctgaccttga	3189
ALDH1A3	24	intron3+1725	ccacatgttccccggtag A/G gtatgctcctccagggtaa	3190
ALDH1A3	25	intron3+3777	gccegaagtagatgccccca A/G ttacgtgtctgaltactg	3191
ALDH1A3	26	intron3+3829	caagtcactgggcccgttagc G/C tccgtccctgcacctgaag	3192
ALDH1A3	27	intron3+4299	tcaatttccacagccacact G/A gccagcctggccggaggga	3193
ALDH1A3	28	intron4+84	agggccccctgactgttt G/G cctlaaggacacattccaac	3194
ALDH1A3	29	intron4+126	ccactccctctcaaatgtt G/G ctgcgaattcttctctaag	3195
ALDH1A3	30	intron6+(290-291)	tagagaattttcagggggg (G) tcaaccaagaggagccaaa	3196
ALDH1A3	30	intron6+(290-291)	tagagaattttcagggggg tcaaccaagaggagccaaa	3197
ALDH1A3	31	intron6+705	aacagctggtgatgagcaa T/G ttccactttctttgtga	3198
ALDH1A3	32	intron7+56	ggggcgtgtttttgaccc C/T gtgagctttctttgacag	3199
ALDH1A3	33	intron7+1107	gatgctgttaactctcttgg A/G gacagacactgcccgttga	3200
ALDH1A3	34	intron7+1610	aagagccacacagaaccacc G/G cctactggcgtttggat	3201
ALDH1A3	35	intron7+1820	cacctgaagtggagccgtt T/C agacaaaggatccagagtg	3202
ALDH1A3	36	intron8+963	gagaaaggacagggaggga C/T acaggctctcaggaaaggaa	3203
ALDH1A3	37	intron8+1824	accattttatccactaagc G/A tglccccaaagatcttatic	3204
ALDH1A3	38	intron8+2384	cgctccctgcgccctcccc C/A tccagtggacttgcagtg	3205
ALDH1A3	39	intron8+24	atccccctggtgtgtgaa A/G ccatgtgtctgtgtatggg	3206
ALDH1A3	40	intron8+91	gcctacaggtccctctccg T/C gaaggaatgctgacctgtc	3207
ALDH1A3	41	intron8+219	actgaggcatgggggggg C/G gctattccagggcagaagg	3208
ALDH1A3	42	intron9+435	ccagacggagagagcctggg G/A caggagaatgtatctcagg	3209
ALDH1A3	43	intron9+1472	ttgacttttgaggccagata C/T accgtttcttccaaaggaa	3210
ALDH1A3	44	intron9+2038	taaacaaatgttccctacgg G/A ctctccaggaggtgtggagt	3211
ALDH1A3	45	intron9+2124	caaacagggtctccagatg G/A catatgccagccagccagg	3212
ALDH1A3	46	intron9+2154	agcagccagggaggacctgc G/C gttggcgagccccctgt	3213
ALDH1A3	47	intron9+2197	ctttggccccctcagggagg G/A gaagagcagctcagcagcat	3214
ALDH1A3	48	intron9+2466	ttcttagttctcatgttct C/T ctctagaatgtttctgtg	3215
ALDH1A3	49	intron9+3655	gatttgcaagtggcatgca C/T gtttatgcccctctctctg	3216
ALDH1A3	50	intron9+3954	gggtgcgttttgacaactg C/G tccgtagcgtgttcacaaag	3217
ALDH1A3	51	exon10+88	tggatgcgggggtcagcc A/G tggaaagacaggggctcttc	3218
ALDH1A3	52	intron10+8	tgcacaagaggaggtacaag G/A gggctgtggcaggctacga	3219
ALDH1A3	53	intron10+307	ctctctgattttctaacaca A/C ccgtgccccagtcagtcac	3220
ALDH1A3	54	intron10+378	gtgggttttgccaggaaatca G/A ttcaagaacctgtgattca	3221
ALDH1A3	55	intron10+975	aatattgtctactcttcc C/G ctgtagttattatgaaac	3222
ALDH1A3	56	intron10+1088	cagtgcaggagccaggggg C/T ctctccagctgactctgag	3223

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ALDH1A3	57	intron11+105	ttgtttacattgtatattat A/G taccagccctgtctcagtg	3224
ALDH1A3	58	intron11+274	agggctccagtagcctgtgcc T/G gtggccctgtgtgtactg	3225
ALDH1A3	59	intron11+1088	cagtgccaggagccaggggg T/A ctctccagatgactctgag	3226
ALDH1A3	60	intron12+96	ctccatctgtgtacacccc G/A tccccccacacccgctc	3227
ALDH1A3	61	intron12+5642	ttgtgtctaacgtgtgtcttc T/C ctcatgccccctaggctggc	3228
ALDH1A3	62	exon13+104	ggctccttctcctcaacatc G/C gacggcgaatgtggcagct	3229
ALDH1A3	63	exon13+281	ataggtttgtctggaatcg C/T agtctgcccgtggagggag	3230
ALDH1A3	64	3'flanking+743	gtggcaggaactgtagga G/A aaggatattttccctcattt	3231
ALDH1A3	65	3'flanking+1145	gcctccagctacccccccc A/G ctccaggaggggtcattcca	3232
ALDH1A3	66	3'flanking+1185	aecctaggggtgtgagaatc T/C ggggtggattaccagcaaa	3233
ALDH1A3	67	3'flanking+1600	acaccaagccctgcaaatg T/C lgggaactgtcgtgtggca	3234
ALDH1A3	68	3'flanking+1847	caggagccctgcggctccc C/G ggttctgtgaatggcagtg	3235
ALDH1L1	1	intron1+252	cgccagccagggactggccc G/C ccgaggtctggccggccc	3236
ALDH1L1	2	intron1+544	ctcaggggctgcctggagt G/T ccagctcagccactgctct	3237
ALDH1L1	3	intron1-6596	cagattttcttaaggatga C/G tagccactgaggtattttt	3238
ALDH1L1	4	intron1-6513	caattatggttlatcttagg G/A acatgtttctagagtagta	3239
ALDH1L1	5	intron1-6478	atagttcttcttactgactt G/A cattctaaattttgttccct	3240
ALDH1L1	6	intron2+240	gtggcattagggctcggag A/G agggctctagaggaagccag	3241
ALDH1L1	7	intron2+1326	gaggagagaccggagggga G/C agccagtcagtcagggccc	3242
ALDH1L1	8	intron3+386	gtcctactctaacctccact G/A ccgtctctctggcagcaca	3243
ALDH1L1	9	intron4+271	gggccccttcagtagacag G/C aaggctaaagccaggagctg	3244
ALDH1L1	10	intron4+356	taggtattctattttctctc C/T ttcaactgttgattctcct	3245
ALDH1L1	11	intron4+608	gtctctgtagggctgtctc A/C gtccactgttctctctggg	3246
ALDH1L1	12	intron4+664	gttcacatggcctgagccgc A/G gggcggctcagtcacccggg	3247
ALDH1L1	13	intron4+785	gagggtctgtgcccctgcc C/G gaggacagggctgacaggac	3248
ALDH1L1	14	intron4+874	ccctgggagccctgtcgt T/G tgggcgcagccggaagagca	3249
ALDH1L1	15	intron4+1349	tcctcagggctctgtctcac G/A tggccacagactccttgct	3250
ALDH1L1	16	intron4+1789	ctgggtctgggaaggaggca G/A ggtctattgtctgggtag	3251
ALDH1L1	17	intron4+1815	ggcagggtctcattgtctgg G/A atagcaaccactggatctc	3252
ALDH1L1	18	intron5+272	aaagcccccagggagagag A/G gtggggttagggggcaca	3253
ALDH1L1	19	intron5+301	tgaggggcaaacagtcagcc G/A tagtgcagcagcttctcaag	3254
ALDH1L1	20	intron5+343	caagggtgagggacagtg G/A ggtctctggagcaatagcca	3255
ALDH1L1	21	intron6+926	ctgcctgggctactggctt C/T gggggtctctctcaccac	3256
ALDH1L1	22	exon7+41	aacgctgaacacttcaggcc T/C ggtgcccagggagagcgtt	3257
ALDH1L1	23	intron7+305	cctgaatcagagagaagcc G/T tcccagggagccctgggtca	3258
ALDH1L1	24	intron7+837	gtccggacaacccccatgg C/T gtgtacccccagccgtgtt	3259
ALDH1L1	25	intron7+866	cccagccgtgtgtctgtgtc C/T ggcctaccagagtgaggct	3260
ALDH1L1	26	intron7+884	tcggcctaccagagtgagg C/T gtggcagtaggggcttggc	3261
ALDH1L1	27	intron7+1118	aatgtccagaaatcatgc G/C aggcagtaaggcagagga	3262
ALDH1L1	28	intron7+1168	aaagttaaggctcaggagaa G/A tctagcctgggctgtccc	3263
ALDH1L1	29	intron7+1451	caggccaccacagcatctg T/C ccagagacctgcaagagacag	3264
ALDH1L1	30	intron7+1489	caggaaatgcaaaagagcaa T/C taagtgtcttaaggaggaagc	3265
ALDH1L1	31	intron7+1579	tcagggtgggggggagtag G/A gaggagaccagctgagcacac	3266
ALDH1L1	32	intron7+1691	ctggctgggctttgcttgc A/C gaagctccagaaactcttt	3267
ALDH1L1	33	intron8+2627	aaagaggagagccgggggtg C/T ttgtgccaggggttgggga	3268
ALDH1L1	34	intron8+2646	gcttgtagcaggggttggg G/A aactgttctgattgggct	3269
ALDH1L1	35	intron8+2925	ctgctgcccctcataggctc C/G agactgaatccttcagagga	3270
ALDH1L1	36	exon9+4	caggtctgttggcagagt G/T ttggcagcggatcclocc	3271
ALDH1L1	37	exon10+109	cagctgttagtgaggagct G/T cgaaggagctgaggggg	3272
ALDH1L1	38	intron10+(671-672)	tggcattttctctgtctga (AG) gtctcttagccaccctaa	3273
ALDH1L1	39	intron10+(671-672)	tggcattttctctgtctga gtctcttagccaccctaa	3274
ALDH1L1	39	intron11+8	caccgatggaagtgtagtg C/A agggccagcccccctctcc	3275
ALDH1L1	40	intron11+447	atgagccaaagcagccctat G/A gtatgacacccgtgaact	3276
ALDH1L1	41	intron11+601	ctcaaatgagtcatttag A/G ggaagtaatgaagactcct	3277
ALDH1L1	42	intron11+639	catctgcagagggagggga G/A ggggtaggacacagcagg	3278
ALDH1L1	43	intron12+684	tcctgggagagagaggggtg C/T gggcagatgagccgagaca	3279
ALDH1L1	44	intron12+767	cgctcaggggtgcgaagcca A/G gtatggcgtgttcccaacg	3280
ALDH1L1	45	intron12+1014	tcataggttccagctccctt C/T cgaagccctcaattctaga	3281
ALDH1L1	46	intron12+1359	ctggttctgctcagctcag C/T acagcagaggctgggtcag	3282
ALDH1L1	47	intron12+1734	gtgtgtccaggtctgtgtg G/T tcagtggggcggccggccc	3283

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ALDH1L1	48	intron12+1901	ttcagcagcctaactgaatt G/A acaatagaatagctctgca	3284
ALDH1L1	49	intron12-470	gggatggggccacctctcca T/C ctctggagatgccaggctca	3285
ALDH1L1	50	intron12-334	aagggcagcctcttgggcca T/C gaccccttgcgtctgcag	3286
ALDH1L1	51	intron12-325	ctcttggccatgacccctt T/C gctgtctgcagcaagggt	3287
ALDH1L1	52	intron12-221	gaaggagcaggggaagatc G/G aggaaggagagaggacag	3288
ALDH1L1	53	intron12-4	cccgttccctcaccctgg T/C caggttgcagatctcatg	3289
ALDH1L1	54	intron13+34	tccacccagtgtagcaca T/C gcagactggcccgccat	3290
ALDH1L1	55	intron13+58	gaactggccagccatata A/G gaactccaaggcagcacag	3291
ALDH1L1	56	intron13+125	ccacaactgggcttggaa T/G gacacctgtttatgcttg	3292
ALDH1L1	57	intron13+126	cacaactgggcttggaa G/A acacctgtttatgcttg	3293
ALDH1L1	58	intron13+281	acctgcatccagcagcttc T/G ggtgttgacaggttcagtt	3294
ALDH1L1	59	intron13+299	tccgtgttgacagcttca A/G tccgtgttgacagcttca	3295
ALDH1L1	60	intron14+121	catttatcaaacagccatcc A/G tctgtcttggagcactgc	3296
ALDH1L1	61	intron14+167	gccagcattgtgtgaaga C/T ttgaggaactgttttaa	3297
ALDH1L1	62	intron14+205	taacttccagtaacactgg A/C tcaagtggatccacgttgg	3298
ALDH1L1	63	intron14+219	cactgtatcagtcagttcca C/G ggtgggaacagagtaaac	3299
ALDH1L1	64	intron14+2275	tctctctgtgtgctatcc T/C cagacctgtgctccagct	3300
ALDH1L1	65	intron14+2431	agaatgactgagtgacaga G/G ctgagagcccccagcccg	3301
ALDH1L1	66	intron14+2660	agccagcattcttggaga C/T accaagaaacctgtctgt	3302
ALDH1L1	67	intron14+2740	aactcacctccacgttcca T/C gcagctcccccagagcttca	3303
ALDH1L1	68	intron14+2756	tccctgagctccccaggg T/C gtccagggcagaggggg	3304
ALDH1L1	69	intron14+2805	ccgcacagcaggaatggc T/C ccaaggaggagggagcgg	3305
ALDH1L1	70	intron14+(3636-3637)	tctctgggtgtgttggg (G) tgtggggcagctccctatc	3306
ALDH1L1	70	intron14+(3636-3637)	tctctgggtgtgttggg tgtggggcagctccctatc	3307
ALDH1L1	71	intron14+4347	tccagcagagaacagcagg C/T gtggctgctctcagggg	3308
ALDH1L1	72	intron15+380	atgcccttatgtgcttcc A/G agccaggaagtctgtgagag	3309
ALDH1L1	73	intron15+(1055-1056)	gcccaactcagcagctatc (C) tccagctgtctgctggct	3310
ALDH1L1	73	intron15+(1055-1056)	gcccaactcagcagctatc tccagctgtctgctggct	3311
ALDH1L1	74	intron17+15	gaaaaggttgcgttggg G/C tggagcagggggggctgc	3312
ALDH1L1	75	intron17+44	aggggggctgctgtggg C/T gctgggacatggcagtgct	3313
ALDH1L1	76	intron17+51	gctgtgtgagtgccctgg G/A acatggcagtgctgcaca	3314
ALDH1L1	77	intron17-(2224-2223)	ctgtgtcatctcccagact CT/Δ gtaactaaaccacatgga	3315
ALDH1L1	78	intron18+140	agctgtatcacaagcatagc G/A tggcaggcagcaggttagg	3316
ALDH1L1	79	intron19+(51-52)	tgttccctgggacagcgc GC/Δ ctgctggagggggttggag	3317
ALDH1L1	80	intron19+399	tcaagtacagctggccctga C/A catggacagggccctggag	3318
ALDH1L1	81	intron19+1794	gtctgtcttggggtcttca G/C ggaatcagtgacttccaca	3319
ALDH1L1	82	intron19+1969	tgatgggttgcgttggg G/T ccagagacagggcagagaga	3320
ALDH1L1	83	intron19+1972	tccgggtgggttggggc A/G caggacagggcagagagata	3321
ALDH1L1	84	intron19+2083	tgaagaagcagaggggtgt G/T ccgggtgtcagtgacacc	3322
ALDH1L1	85	intron19+2119	acacctgtgtgtattggg G/T tgaatagggtgcagagttt	3323
ALDH1L1	86	intron20+1388	ttccctcttccacactccc C/T tggactgtgattccatgag	3324
ALDH1L1	87	intron20+1564	ccaggaacccaggaacagt G/A ggaacccaccccccctg	3325
ALDH1L1	88	intron20+1873	tcaagttaaacatcatll G/A tgaatgtatgaataattg	3326
ALDH1L1	89	intron20+2427	actaggattggtgacttg G/C gatcaggtctcagctctgc	3327
ALDH1L1	90	intron20+2458	cagctctgtcaactgccac C/T ggcggccatttccctcaa	3328
ALDH1L1	91	intron20+2544	ccgggtgggagggccatctg C/T agcgtgtgacacccatcac	3329
ALDH1L1	92	intron20+2573	gacpccatcacacgggtgc C/T gtagcccggtcttatgtc	3330
ALDH1L1	93	intron20+2574	acacccatcacacgggtgc G/A tgaacccggtcttatgtc	3331
ALDH1L1	94	exon21+33	agccaactgtttcacagac G/A tggagaccacatgttata	3332
ALDH1L1	95	exon21+87	ccttgggctgtctatgac A/G tctctggttgcgtatgg	3333
ALDH1L1	96	intron21+323	ccatgcatcaacaccccc C/G acactgagtgcttgaata	3334
ALDH1L1	97	intron21+361	ataatcagagattttttta C/G tcaaggtctaggttcaatga	3335
ALDH1L1	98	intron21+478	gtcttggggaggttcttc C/A gctggcagctcgggttg	3336
ALDH1L1	99	intron21+1086	caacccaacttgcctcccg C/T gctgagcccgccacatttt	3337
ALDH1L1	100	intron22+235	gggcttggagggacactcc A/C gccaggagcactggggcc	3338
ALDH1L1	101	intron22+313	atagcagggaggggttggcc G/A tgaagaccagggcccggtg	3339
ALDH1L1	102	intron22+1214	tgggccaacttatgaactc G/C cccaggttccctcagctccc	3340
ALDH1L1	103	intron22+1226	tgaatcctccccaggttccc T/C cagctcctcctaaccctag	3341
ALDH1L1	104	intron22+1623	gggcttcccatgctccaga C/G aaggcgggtggagctgggg	3342
ALDH1L1	105	intron22+1698	attctgggagctcctggccc A/G ctatccactgccagggataa	3343

1 **Detection Using PCR**

The amplification can be performed using a polymerase chain reaction (PCR). The DNA polymerase can be LA Taq DNA polymerase (Takara), Ex Taq polymerase (Takara), AMPLITAQ Gold polymerase (Applied Biosystems), AMPLITAQ (Applied Biosystems) or Pfu DNA polymerase (Stratagene), as well as other polymerases.

An illustrative example of amplification conditions is provided below. The present invention is not limited to the conditions provided in this example. In preferred embodiments, each cycle in the transforming phase should last between 10 and 40 seconds at 85°C to 105°C and preferably 20 and 30 seconds at 94°C, each cycle in the annealing phase should last 30 seconds to 1 minute at 50°C to 72°C and preferably 20 seconds to 1 minute at 60°C, and each cycle in the elongation phase should last 1 minute to 4 minutes between 65°C and 75°C and preferably 2 minutes to 3 minutes at 72°C. There should be 30 to 40 cycles, although fewer or more cycles are contemplated. In order to completely transform the template DNA and the primer, each cycle in the transforming phase should last 1 minute to 5 minutes at 95°C before the amplifying cycle. If AMPLITAQ GOLD polymerase manufactured by Applied Biosystems is used, it should last from 8 minutes to 15 minutes and ideally from 10 minutes to 12 minutes. In order to completely elongate the amplified DNA, the elongation phase should last between 1 minute and 10 minutes at 72°C after the amplification cycle. If the amplified product is not immediately detected, it should be processed again at 4°C to make sure the amplification was not irregular. In this way, the gene encoding the drug metabolizing enzyme is amplified.

After amplification, gel electrophoresis is performed on the amplified product, the amplified product is stained using ethidium bromide or SYBR Green, and one, two or three bands are detected in the amplified product (DNA fragments) to determine the portion (DNA fragment) of the drug metabolizing enzyme containing the genetic polymorphism in the gene encoding the drug metabolizing enzyme. Polyacrylamide gel electrophoresis or capillary electrophoresis can be performed instead of aerogel electrophoresis. PCR can be performed using a primer tagged with a fluorescent dye to detect the amplified product. A detection method that does not require electrophoresis

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ABCA1	1	(5' flanking region -99)	acataaacagagggccgggaa G/C gggggcggggaggaggaggag	3361
ABCA1	2	(intron 1 159)	gcgggtgttaaatggggagac G/T atgtcctagtagcagctctg	3362
ABCA1	3	(intron 1 506)	gaattggctatatgtctccc G/C ggactggagcggcacagctcc	3363
ABCA1	4	(intron 1 5897)	gtacaaaacccttttagcttt T/G gcaaacctccttaagacct	3364
ABCA1	5	(intron 1 5929)	ttaagaccgattttaaatgc C/T tccctcctcatgaagctctt	3365
ABCA1	6	(intron 1 5962)	aagctctcttggtaccactc T/C tccccatcactaagtgtgaa	3366
ABCA1	7	(intron 1 5985)	cccatcactaagtgtgaagt A/C agatcccccttctcttactt	3367
ABCA1	8	(intron 1 11416)	ttacagtgccttttatagga G/A agaaagaagaaattgtgtct	3368
ABCA1	9	(intron 1 11935)	ttctctgtggagcaaatagag G/A gctgtctgacacttggttcc	3369
ABCA1	10	(intron 1 12281)	gaatgtttgattgttgaaaa T/A cttaataacagtagtttttt	3370
ABCA1	11	(intron 1 12924)	gtctgtgacaactcttatactc T/C aggttgaaacctccggggaag	3371
ABCA1	12	(intron 1 13002)	gagcctcaatcacagattct C/G tctagctcacatgaagttaa	3372
ABCA1	13	(intron 1 17715)	ggagcatgactttgtggaag C/T ctctcctcttccaccagag	3373
ABCA1	14	(intron 1 17848)	gagggctgactgtcacccctt T/C gataggagcccagcactaaa	3374
ABCA1	15	(intron 1 21384)	gtgggtgggaggaattggag G/C aggaagctgtgcctaagtgtg	3375
ABCA1	16	(intron 1 23063)	ggaggcacctgtgacaccca G/A cggagttagggggcggtgtg	3376
ABCA1	17	(intron 1 23131)	agtgtgcatatgtgtgtacc G/A tgggagcttgtttgtcgtgt	3377
ABCA1	18	(intron 2 2801)	aagaaaagtgtatttttca A/G gttgctgatgcttagattgt	3378
ABCA1	19	(intron 2 2830)	tgcttagattgttagattgt C/G aaagatctggctgtcatctt	3379
ABCA1	20	(intron 2 2856)	tctggcttgcatctgttaca A/G ctgacagaactggggtcag	3380
ABCA1	21	(intron 2 3187)	tgatagctgttgccctgagc A/G tacggagcttcattgcccag	3381
ABCA1	22	(intron 2 3190)	tagctgttgctgagcagata C/T ggagcttcattgcccagttc	3382
ABCA1	23	(intron 2 3194)	tgttgctgcagcatcagga C/T gttcattgcccagttcctgt	3383
ABCA1	24	(intron 2 3204)	agcatcaggagcttcattgc G/A cagttcctgtctctcagat	3384
ABCA1	25	(intron 2 3401)	acataaagcctgtgtgtgc T/C gccaggaagactagaaacgc	3385
ABCA1	26	(intron 2 13927)	gtcaccacatcctggcact A/G tgctaaggctgggaatgcag	3386
ABCA1	27	(intron 3 4163)	ccagcccacttcatcttacc G/A tagttacctccttagagtat	3387
ABCA1	28	(intron 3 4262)	tgtaaaagaggaaactaagga T/C gccaggagctttctgcttag	3388
ABCA1	29	(intron 3 4306)	ccctctcatcacttctccaa C/T gctggtatcatgaacccat	3389
ABCA1	30	(intron 5 490)	gatgggcatgtgaactgtgt G/A tctttaaaagtgaatctt	3390
ABCA1	31	(intron 5 583)	tatctggggagtgggcattt T/G ctgactgaggcattggctgc	3391
ABCA1	32	(intron 5 1051)	ggctacaaaactgtgtcttc C/T ttgggagctaaaagagcaa	3392
ABCA1	33	(intron 5 3051)	tagagaacaagtctaatctc G/A ttttcttgaaatagtcgaa	3393
ABCA1	34	(intron 5 3127)	aagtcctgatttttttaggc A/G aaatggcctccttctctct	3394
ABCA1	35	(intron 5 5924)	ctttctttcacaaaattgcc C/T cccagagctttctggaagg	3395
ABCA1	36	(intron 5 6831)	ccagtcctcagccttgcca T/C tgcttatgctgtgttgaaa	3396
ABCA1	37	(intron 5 12678)	gtcaccgctctgtctcacc G/C accctctggccatctctct	3397
ABCA1	38	(intron 5 14214)	cagcttggtgccagaggcct G/A gacctgggtgccagaggtcc	3398
ABCA1	39	(intron 5 14257)	gctgggttcccggtgtgttc C/T cagaggcctggatgtgtgc	3399
ABCA1	40	(intron 5 18078)	cctaccacacatgacagtg C/T acagccaagggttgtgtgact	3400
ABCA1	41	(intron 5 18795)	ctgggctcttctggacctg G/A ccagctaaaaggaaatctcc	3401
ABCA1	42	(intron 5 18948)	gcattgggtgactaagaac G/A catattccctatcctatagg	3402
ABCA1	43	(intron 5 19053)	ctcccccaacattaaaagt T/C aagggtatgttattcaaatg	3403
ABCA1	44	(intron 5 19148)	ggcccaagaactgcatttt C/A gcattgtcctcaaatgaagc	3404
ABCA1	45	(intron 5 19229)	atgtcaacagtgtagatca C/T atgtgatgggaagcatcagg	3405
ABCA1	46	(intron 5 19405)	cttgctcaatttattctgtc T/C atataactcaattattactga	3406
ABCA1	47	(intron 5 19534)	catgtgacctcttagctcc G/A cggattaaactcctgtcctca	3407
ABCA1	48	(coding region 474 (Leu 158 Leu))	gaaacctctctggttctc G/A tatcacacctctctctccc	3408
ABCA1	49	(intron 6 210)	gcaacctggcgtcatgggcc A/C gctggttaaaataaaattga	3409
ABCA1	50	(intron 6 334)	acagttctgaggcaataacc G/A tggttaagggttattgatct	3410
ABCA1	51	(intron 6 2288)	cttctttcaagcttgggt C/T cactggaccacgtatgaagt	3411
ABCA1	52	(intron 6 2322)	atgaagttagaatttttagg T/C ccagaaaggcaattaagtaa	3412
ABCA1	53	(intron 6 2820)	gtgcttggatatactctgag T/G ttcagttaaagagacctgatg	3413
ABCA1	54	(intron 7 416)	catcataaagatgacattgt G/A ggctgtcacagttggaaggc	3414
ABCA1	55	(intron 7 471)	agaccacactatttagctta C/T ttagtaataacattgcaag	3415
ABCA1	56	(intron 7 504)	ttgcaaaagaaaaattccgac G/A aagtttttccagcctaggaa	3416
ABCA1	57	(intron 7 679)	gctctggtgaaattcctctc G/C ctaccccaaacatcatcatt	3417
ABCA1	58	(intron 7 1740)	acaaatgctcaccctttcag C/T tggaaatgattgaaattttgg	3418
ABCA1	59	(intron 7 2122)	tgattaaagggtgctactacc A/G ggtgctttctgcatatctcg	3419
ABCA1	60	(intron 7 7753)	taggaattccaagctgtgaa T/C tttttactgaagctctttgg	3420
ABCA1	61	(intron 7 8973)	atggaaattgttttatattg A/T ctacagattgccaatattat	3421
ABCA1	62	(intron 7 8976)	gaaattgtttatattgact A/G cagattgccaatattattag	3422
ABCA1	63	(intron 7 11327)	ctaaacaattctatttccatt G/C agtccttataaaagaagtgg	3423
ABCA1	64	(intron 7 11738)	ctgacgtttaaggagagccg C/T gtaggctcccttgaggactg	3424
ABCA1	65	(intron 7 12295)	agtcgtgaaattattgttct T/A ttttttcttttagcttatgt	3425
ABCA1	66	(intron 8 387)	tagcaaggccaatcatttta C/G caacacacatgctgtcaac	3426
ABCA1	67	(intron 8 697)	ggaactgtctggtgtccccc A/T gcatagggaagctgagccagg	3427
ABCA1	68	(intron 8 3036)	ctttatgtgggaagaaattt T/G tttttttgattggggagtgg	3428
ABCA1	69	(intron 8 3176)	aaatggcctggttctctgtc C/A cctttctgtctgtatgctc	3429

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ABCA1	70	(intron 8 3364)	ggcagaaggcaaaagcttagg A/T cctagagagtgtggaccac	3430
ABCA1	71	(intron 8 3373)	caaagcttaggacctagaga G/A tgctggaccacgccactcac	3431
ABCA1	72	(intron 8 3561)	cagggatttattaatgattt C/A ttgtgaaatgtttggaata	3432
ABCA1	73	(intron 8 3654)	agtgcggaatacatttgca T/C gtaagacagaacgctgctcg	3433
ABCA1	74	(intron 8 4715)	ggcagagggtctcagaatc C/T gcatttccacaatgtctcc	3434
ABCA1	75	(coding region 936 (Pro 312 Pro))	cgtattgtctgcgggcatcc C/T gagggaggggggtgaagat	3435
ABCA1	76	(intron 9 2309)	ccctcaagagtcagtttaa A/G tgttggtcatgttagttgtc	3436
ABCA1	77	(intron 9 2392)	atgggagggtctgtgcttca T/C gaaaacatttttccagatca	3437
ABCA1	78	(intron 10 228)	tggggatggggaggactggc A/G cagggctgtgtgatgggt	3438
ABCA1	79	(intron 10 319)	ttctgcgttcctggctccc C/T acctgactccaggtgaacaa	3439
ABCA1	80	(intron 11 377)	gaaagaagtgtgggagcaaa A/C gcattgtgttacatgtagac	3440
ABCA1	81	(intron 11 521)	agtgtcttagagacaattgg G/A ttcaaatgtggagcaggctg	3441
ABCA1	82	(intron 11 2850)	ctctatacaatcattatgct G/C ccattgaaataataatata	3442
ABCA1	83	(intron 11 2976)	ctccaattcggtagaaccag A/G gcttcctctctctgtcgaa	3443
ABCA1	84	(intron 11 3056)	gtttgcagctgtgtgttttc C/T ggcagcacatctgtgcaggc	3444
ABCA1	85	(intron 12 340)	ggcattattgtgaaactta T/C ctataaatgaattcgggtcc	3445
ABCA1	86	(intron 12 381)	aattaaatttttgaaatttt A/G tattaaaaattatattagta	3446
ABCA1	87	(intron 14 1728)	caggctcagaggccttgccc C/T atcacccctggctcacgtgtg	3447
ABCA1	88	(coding region 2040 (Ile 680 Ile))	atgggacctggacaacagcat C/A ctctggtttagctggttcat	3448
ABCA1	89	(intron 15 1382)	cttttagacagaaaagttac G/A tgggatattatctcccacag	3449
ABCA1	90	(intron 15 1453)	tatataaggagaaaccagtt G/A aaattacctattgaagaac	3450
ABCA1	91	(intron 15 1567)	ttctgcgttagttttgggtaa G/A tcatttatcttcttttaggt	3451
ABCA1	92	(intron 15 1617)	cagttgcctcatcagaaaga T/A gaacagcattacgcctctgc	3452
ABCA1	93	(intron 16 95)	agttgagaacagaagatgat T/A gtcttttccaatgggacatg	3453
ABCA1	94	(intron 16 452)	tggtgttttctgttagtaat G/A ttttctgaactaagcacac	3454
ABCA1	95	(intron 16 657)	ctgttgctcagctgtgggt T/C cataggcatcagcagccca	3455
ABCA1	96	(intron 18 1730)	tgaagtccaagcgagtg C/G ctgtgtccttacactccact	3456
ABCA1	97	(intron 19 426)	aggaccttacagtggttagt A/G tcaggagggtcaggggtg	3457
ABCA1	98	(intron 19 468)	aaagcaccagcggttagcctc A/G gtggcttcacagcagattcc	3458
ABCA1	99	(intron 20 876)	ccctcctcatctaaagtga C/T acatgggggtcatgtgcagg	3459
ABCA1	100	(intron 22 118)	catgggatactcttctgtta T/G cacagaagagataaaggga	3460
ABCA1	101	(intron 22 560)	aaagctttgccattctaggg G/A tcattagccatacagggtgaa	3461
ABCA1	102	(intron 23 102)	accctctttgccattgtgaa A/G ccaccatctccctgctctgt	3462
ABCA1	103	(intron 23 287)	gtcaagaagaaagagactgt C/T aagaggttaagagccttggt	3463
ABCA1	104	(intron 23 1063)	acctttcacctcaggaagc G/A aggtgtttcacacggcacac	3464
ABCA1	105	(intron 25 321)	ctctttacttaagtacagtg T/G gaggaacagcggcatcaga	3465
ABCA1	106	(intron 25 376)	gttagaaattcagcaacttg G/C gccagctcagacctactga	3466
ABCA1	107	(intron 25 478)	catacataggaaatgacaaa C/T gtttatggatggatagtcta	3467
ABCA1	108	(intron 25 579)	tcatttaattctcaaaaaaa G/T atgaaaaatgaacactcag	3468
ABCA1	109	(intron 27 153)	aatggttaaaagccacttggt C/T ttgtcagcactgtgcattgtg	3469
ABCA1	110	(intron 28 1058)	actatcatgggagataatga C/T tatgggtgtccatgattgga	3470
ABCA1	111	(intron 28 1317)	caggaccagtggtttctgagt C/T acctgaatgtgagcactat	3471
ABCA1	112	(intron 30 372)	tatatgtatttttaggttttg T/C ttatcagcttctctgctttt	3472
ABCA1	113	(intron 30 506)	cccttttaaaagtaagcagt A/G gataataaattcagtgaaag	3473
ABCA1	114	(intron 30 1033)	ctggatttcatgggtgcctt G/C attttccacatgaaggttgt	3474
ABCA1	115	(coding region 4281 (Thr 1427 Thr))	tcttccctttgcagagacac G/A ccttgccaggcaggggagga	3475
ABCA1	116	(intron 33 626)	ggctccttgttactgatttc C/T gtcttttctctctgctttt	3476
ABCA1	117	(intron 33 719)	taatagccctcatgctagaa G/A ggagccggagcctgtgtata	3477
ABCA1	118	(intron 33 726)	cctcatgctagaaggagcc G/A gagcctgtgtataaggccag	3478
ABCA1	119	(intron 33 889)	ctttcctcaatgtctcagct A/G tctaactgtgtgtgtaatca	3479
ABCA1	120	(intron 33 1097)	ctgtgcacccactgtctgg G/C ttttaattgcaggctgttct	3480
ABCA1	121	(intron 35 234)	aacctatctaaacctcagtt T/C cctcatctgtgaaatggaga	3481
ABCA1	122	(intron 37 411)	aactctgtacattttatcag C/T agcttatccatccattgcaa	3482
ABCA1	123	(intron 37 1224)	caggcatagtgattcagag A/G tgaagggtcaagtcctgaa	3483
ABCA1	124	(intron 37 1720)	aaattaaaattactctgact G/T ggaatccatcggttcagtaag	3484
ABCA1	125	(intron 40 251)	tgaaggtaaggaaaatagtg T/G tatttgcttggtatccactgg	3485
ABCA1	126	(intron 40 252)	gaaggtaaggaaaatagtg T/C atttgcttggtatccactggc	3486
ABCA1	127	(intron 40 319)	agcactggaaaagtcacac A/G taactttgagaattaggtga	3487
ABCA1	128	(intron 40 957)	ctgttactcttttttctctt G/C tcattgggtgatagccatttg	3488
ABCA1	129	(intron 41 146)	tgatgtgggcatcccgcagc C/T ccctccctgcccatcctgga	3489
ABCA1	130	(intron 42 239)	cattgggttttatagcttac A/C tttatgtgttagttattaaa	3490
ABCA1	131	(intron 42 321)	aataaatggttgattttgag T/A ttgagtttcatagtcacaaa	3491
ABCA1	132	(intron 42 322)	ataaatggttgattttgagt T/C tgagtttcatagtcacaaa	3492
ABCA1	133	(intron 42 533)	agatgaaaaattatgtatag G/A ataataatgatcacggttct	3493
ABCA1	134	(intron 42 546)	tgtagatgataatgaatgat A/G cggttctaaaaagacaggtt	3494
ABCA1	135	(intron 43 739)	tacagccacacttaaaatgg T/A ccattatgaaatacatatt	3495
ABCA1	136	(intron 44 18)	taggtgagaaaagaagtggc T/C tgtattttgctgcaaaagact	3496

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ABCA1	137	(intron 44 264)	acaatataattgtctgttt T/C ttaagagtataatttagtga	3497
ABCA1	138	(intron 44 279)	tgttttttaagagtataatt T/C agtgatttttggttaaattga	3498
ABCA1	139	(intron 44 508)	tttacattgtctacataaaat C/T cccctatgtacatgtaccta	3499
ABCA1	140	(intron 44 1477)	gatctcctctcctgtctctt A/T cttttttgcagtagcaatgt	3500
ABCA1	141	(intron 44 1665)	tggttgtaagaactgatttg G/A ttggtatagctgtgagggcc	3501
ABCA1	142	(intron 44 1956)	gtgttgctcacactcaaaaat T/G tctgggctctctcatttggt	3502
ABCA1	143	(intron 45 68)	aatatataccttatggcttt T/C ccacacgcattgacttcagg	3503
ABCA1	144	(intron 46 608)	ttatactgacttcaatagag G/C ttccagacaaaaagttgttt	3504
ABCA1	145	(intron 47 336)	ttcacaaattgtaaacaccac T/C acactgaacagcatcatccc	3505
ABCA1	146	(3' untranslated region 7479)	aacaaaaatgtgggtgtctc C/T aggcacgggaaacttggttc	3506
ABCA1	147	(3' untranslated region 8226)	aggagcccactgtacaata C/T tgggcagccttttttttttt	3507
ABCA1	148	(3' untranslated region 8697)	ttccagaatttgaatattaa C/T gctaaaggtgtaagacttca	3508
ABCA1	149	(3' untranslated region 9097)	aactattttgaagaaaacac A/G acatttttaatacagattgaa	3509
ABCA1	150	(5' flanking region (-1033)-(-1032))	tgacttaaatatttagacat (AT) ggtgtgtaggcctgcattcc	3510
ABCA1	150	(5' flanking region (-1033)-(-1032))	tgacttaaatatttagacat ggtgtgtaggcctgcattcc	3511
ABCA1	151	(intron 5 6368)	ttctgtatgggtgtgtgtctg C/Δ tgagaatcatgactgggtgg	3512
ABCA1	152	(intron 5 9709)	cattttctgtctgaaccccc T/Δ caccattcaggcagctgct	3513
ABCA1	153	(intron 5 13816)	tcctactctctcttttttt T/Δ catttgctctctccaccac	3514
ABCA1	154	(intron 10 270-271)	cttttcagggaggagccaaa (G) cgctcattgtctgtgcttct	3515
ABCA1	154	(intron 10 270-271)	cttttcagggaggagccaaa cgctcattgtctgtgcttct	3516
ABCA1	155	(intron 20 611-612)	tttagccatcctctcccc (C) gccaccctccttattgagc	3517
ABCA1	155	(intron 20 611-612)	tttagccatcctctcccc gccaccctccttattgagc	3518
ABCA1	156	(intron 32 391-392)	gagtgccttgggtactctct (T) gatgggggactccatgataa	3519
ABCA1	156	(intron 32 391-392)	gagtgccttgggtactctct gatgggggactccatgataa	3520
ABCA1	157	(intron 37 847)	gctgtatattgtgaatgtcc C/Δ gttttcaaaagcaagccaa	3521
ABCA4	1	(5' flanking region -1005)	tgccatcataagcagaaact A/C tctctctcttcttggagct	3522
ABCA4	2	(5' flanking region -819)	gtctagagtctttcaaagag A/T acacattctgagatttgagg	3523
ABCA4	3	(5' flanking region -680)	agcaccacccattgcaggg C/A tggaatgacagtaatgggccc	3524
ABCA4	4	(intron 1 208)	tgcccttcccaggagatgt G/A tttctctgtcctcagccaca	3525
ABCA4	5	(intron 1 234)	ctgtctcagccacatgaaa A/G tcttttgctaccgtgctg	3526
ABCA4	6	(intron 1 510)	agctcagcatcaagtcacag T/C ttaactggacacattatatt	3527
ABCA4	7	(intron 1 1527)	gcttaacaaccagcataaaa G/A agagcagcatgggacacgct	3528
ABCA4	8	(intron 1 2077)	caggactgtagctgtggcc T/C aaaaatgagccattcctgtg	3529
ABCA4	9	(intron 1 2174)	ccctctcaatctggcccttc G/C ctggcatgggtgggagactc	3530
ABCA4	10	(intron 1 2246)	gctcccaggagatggagcc A/G ctcgggctgagggccttggc	3531
ABCA4	11	(intron 1 2364)	ttctgtctggcagcctccc G/A atggctcccacactgctacc	3532
ABCA4	12	(intron 1 4243)	ctccctggggatgcctgta C/G gcagttaagcgtcaaggaca	3533
ABCA4	13	(intron 1 4287)	atgccgctctggggagggga A/C gctgagcatgattttggaag	3534
ABCA4	14	(intron 1 4309)	ctgagcatgattttggaagc C/T ggcagaagaggctattgtga	3535
ABCA4	15	(intron 1 4416)	tgacagcaacgccccgcc C/T ccgcaaaaaacacacact	3536
ABCA4	16	(intron 1 4996)	tttaccctgggaacaggcag G/A ccaagctggc t/c ggtccctc	3537
ABCA4	17	(intron 1 5007)	aacaggcag g/a ccaagctggc T/C ggtccctcctctgatacaca	3538
ABCA4	18	(intron 1 5080)	gtgtgtggctgtttcttag C/G aagcacoatggttccaagtt	3539
ABCA4	19	(intron 1 5152)	gggagatgaacgttaagtga G/A ggcaggcctacaaggttgca	3540
ABCA4	20	(intron 1 7110)	ccactggatctgcttttga A/G tcaagagtccttaagctcca	3541
ABCA4	21	(intron 1 7290)	gattttgttggttttgcga T/A ggatcagatgctcttattca	3542
ABCA4	22	(intron 1 7483)	tctgagcctctttccttaac T/C gcagagtgtgtgg c/t tacaga	3543
ABCA4	23	(intron 1 7497)	cttaac t/c gcagagtgtgtgg C/T tacagagaaatctttactac	3544
ABCA4	24	(intron 2 1067)	tcaagcagcagcgaactg C/A gtggagtctctttgaaactaa	3545
ABCA4	25	(intron 2 1243)	caccagcacagggaactggc A/T cacatgagatgctctgttt	3546
ABCA4	26	(intron 3 26)	tggtgagatccctaccatgc A/G ggggaggaagtgcacacc	3547
ABCA4	27	(intron 3 101)	agcatggagcactgagtgtt C/T ttgtggctttgctgagcccc	3548
ABCA4	28	(intron 3 330)	tgcttgggtggagtgaatca T/C tgtaggagaaaaactcagtt	3549
ABCA4	29	(intron 3 470)	tgaagtgcaggtttacaaagt C/G aagtttacttcttgggagaa	3550
ABCA4	30	(intron 3 634)	tgaaaaccaatgacctctt T/C ccaagaaaaatggccacata	3551
ABCA4	31	(intron 3 1016)	ccttggggagctcagtagt A/G ttcttccaggagaagcctgc	3552
ABCA4	32	(intron 3 1554)	gaaagtgtgggtttcatgttt T/C gcactcacattatgagttaa	3553
ABCA4	33	(intron 3 1686)	ctagacattctcacagagcc A/G agggcagcaaggcggggctc	3554
ABCA4	34	(intron 3 1823)	ttcacctctctccatggacc A/G gtctcccctgctctcaatg	3555
ABCA4	35	(intron 3 1938)	caaattcctgggaacaaatc G/A ggttgaccacgc t/g ttattct	3556
ABCA4	36	(intron 3 1951)	acaaatc g/a ggttgaccacgc T/G ttattctccctgtcccatca	3557

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ABCA4	37	(intron 3 2063)	ggctgtcagagcctacctgc G/T tgaatgggtggaagg g/a cagg	3558
ABCA4	38	(intron 3 2079)	ctgc t/g tgaatgggtggaagg G/A caggtctcagagaattgggt	3559
ABCA4	39	(intron 3 2186)	agacacacagagcatggggac C/T gagaggcgagcagaccctgc	3560
ABCA4	40	(intron 3 2214)	gagcagaccctgccaaaact G/A ggagactgaatagatcgctc	3561
ABCA4	41	(intron 4 3182)	ccccagagccacagcagcc C/G tgtctcctgggtggtcttgt	3562
ABCA4	42	(intron 4 3515)	agtataataaaagcaggagc C/T atagcccccactctcaaga	3563
ABCA4	43	(intron 4 3952)	agagaagccactgtgccact G/C tgtggtcgaacttcaagacc	3564
ABCA4	44	(intron 4 4637)	aatcacttgccccaaggtca C/T cttaactgttaggtgttctt	3565
ABCA4	45	(intron 4 5319)	acctctagggggtccacagag A/G ccccaagaacagaaaccttc	3566
ABCA4	46	(intron 6 2266)	cacccttgacagcctcagac G/A ggtcctgggggcttgccttc	3567
ABCA4	47	(intron 6 2857)	ccagaggagaaagctctgcc G/A tag t/c cggcctcagttaacca	3568
ABCA4	48	(intron 6 2861)	aggagaaagctctgcc g/a tag T/C cggcctcagttaaccacgga	3569
ABCA4	49	(intron 6 3078)	gcaggcattaaaaatgggact T/G tgcctttattgtcctctgggc	3570
ABCA4	50	(intron 6 3375)	ttaaatgccaaatgagttct C/G attacaagaagaaggaggaa	3571
ABCA4	51	(intron 6 3412)	ggaaaatctcagtaaacac C/T gtgacggcattctaccactt	3572
ABCA4	52	(intron 6 4635)	cttctgggtggatattgcta C/T gtcaagtgtctgggaaagcc	3573
ABCA4	53	(intron 6 -264)	aaacagcaattagaatcact T/C tgaatatgtgatagtattta	3574
ABCA4	54	(intron 7 828)	gatgtgggaaggttagagaa G/C agcccatgttactaatgtct	3575
ABCA4	55	(intron 7 1019)	aggctctctgactgtctaga T/C agcaagtctaactattgtgt	3576
ABCA4	56	(intron 8 374)	gtaaacacggctgtgggatg C/A ttttacaacacataatcgt	3577
ABCA4	57	(intron 8 874)	tgtatgagctgttattgggt G/A ggtacagcctatttaatttag	3578
ABCA4	58	(intron 9 605)	tctgtctctctgtcttctat C/T tgtctggttttagggcaact	3579
ABCA4	59	(coding region 1268 (Arg 423 His or His 423 His))	aacttttgaagaactggaac G/A c/t gttaggaagtgtgtcaaag	3580
ABCA4	60	(coding region 1269 (Arg 423 Arg or His 423 His))	acttttgaagaactggaac g/a C/T gttaggaagtgtgtcaaagc	3581
ABCA4	61	(intron 11 5687)	atcatgtaatgtacttttaga C/G tcagatatataaatatttgt	3582
ABCA4	62	(intron 11 7136)	gacttcccaacttacccttag T/C ggagctgtagtccacatagaa	3583
ABCA4	63	(intron 11 7180)	acgctcataaatgtctctct G/A ggctgtaaaaggtgaatttt	3584
ABCA4	64	(intron 11 7701)	gttagacgcaggcattacct C/T gtggctttgccccagtgtga	3585
ABCA4	65	(intron 11 8073)	gggatgtttgcccacatcca T/C tggcattttcctcaaaaggaac	3586
ABCA4	66	(intron 11 8586)	cagctgcctgcgctggagag G/A gctcaaacctcttccgccag	3587
ABCA4	67	(intron 11 11234)	cccaataattttgttttttc G/A ttttaggaattaaatttcag	3588
ABCA4	68	(intron 11 11641)	aagaacaacaactttattga C/G aacttttggtgtgtgacctg	3589
ABCA4	69	(intron 11 11808)	tggattttcttaagaaata C/T caattccatttcccttttaac	3590
ABCA4	70	(intron 11 11923)	aagatcattattaatatctc A/G tcagcgtggtgtcacttaag	3591
ABCA4	71	(intron 12 305)	tcaccctgtgtgcgggaggt G/A tgagtgtgactatccaagccc	3592
ABCA4	72	(intron 13 1461)	ttgggtttcagtgctcagcat G/A tagctgtctactcagatccc	3593
ABCA4	73	(intron 14 1268)	ggagctgtgagcccttctct T/C atctaggtttcccttgttct	3594
ABCA4	74	(intron 17 23)	gagtccttttaaacacacaaat C/G ttaatgtttgaaatcaactc	3595
ABCA4	75	(intron 17 715)	gggactcccctagagctgaa G/A tactctcccactctgtttgtt	3596
ABCA4	76	(intron 18 1282)	ggaagatgaagaacctaaag C/T gcttcagaaattcatgagg	3597
ABCA4	77	(intron 20 -195)	acagattatttccattgtatg C/A atgaactatgttaagccatcc	3598
ABCA4	78	(intron 23 755)	ctggctgcccgtgggttttc C/T tatgtccatccacggggagg	3599
ABCA4	79	(intron 26 702)	tatcaatacaactcagacg T/G cagtctcctggcccttttga	3600
ABCA4	80	(intron 27 156)	cctgctttccaaacccttat C/T ttgattotttgtaacatgaa	3601
ABCA4	81	(intron 27 385)	tttaagaacagtgagtcac G/A tgacttgcctttgaaatgc	3602
ABCA4	82	(intron 28 299)	gacatgccatcagaccactg C/T gagtgttcaggcagcctacc	3603
ABCA4	83	(intron 29 168)	ctccttccacacttggtgtc A/G gggacattcactacctccta	3604
ABCA4	84	(intron 29 497)	gctgtcaataaggaccacaaa C/T agactaatttcaaatctctc	3605
ABCA4	85	(intron 29 567)	agctgtctaggaataaaaagg G/A agacaaaaa g/a atccacaagc	3606
ABCA4	86	(intron 29 577)	aataaaaagg g/a agacaaaac G/A atccacaagctagagatggt	3607
ABCA4	87	(intron 30 -2494)	aatcacagctcatctgtctc A/G tcatagggatcccaaaagaa	3608
ABCA4	88	(intron 30 -2169)	aatgtaacagccaaagtctc A/G gaaaaaggcaagccagttcc	3609
ABCA4	89	(intron 31 535)	ctaactgtgaattatcatct T/G tgatcactgcccctttgagat	3610
ABCA4	90	(intron 35 209)	ctcctccacatttatgtgg C/A aagtaagtttacatttggtt	3611
ABCA4	91	(intron 37 525)	ttaatttgatgagtaattc A/G tccatctcggcctcagtttc	3612
ABCA4	92	(intron 37 766)	tgttgaggctgggagaacc T/G cctatgaattgtacagggtc	3613
ABCA4	93	(intron 37 856)	aaaaccccatgaagtggta A/G ggcaggcatcattatctcca	3614
ABCA4	94	(intron 38 62)	tagtagagtatgtgtgttc G/A agcagagccaggggcaagca	3615
ABCA4	95	(intron 38 761)	tccttgggcaagttaattct G/A atgaagagactgggtgttct	3616
ABCA4	96	(intron 38 1315)	cagagtcagactctggaag G/T c/a ggggggataagaacacagc	3617
ABCA4	97	(intron 38 1316)	agagtcagactctggaag g/t C/A ggggggataagaacacagcc	3618
ABCA4	98	(intron 38 1561)	gtattttcatgtaaattatc C/A g/a atacacagctgctatggaa	3619
ABCA4	99	(intron 38 1562)	tattttcatgtaaattatc c/a G/A atacacagctgctatggaaa	3620
ABCA4	100	(intron 38 2874)	ctagacaaaagggg a/c agctcc C/T gccactagaaacttcagg	3621
ABCA4	101	(intron 40 1904)	gacactgtacagccagccca A/C tcttgaccccttttcttcat	3622

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ABCA4	102	(coding region 5814 (Leu 1938 Leu))	ggaaataaaaactgacatctt A/G aggcctacatgaactaacaa	3623
ABCA4	103	(intron 41 122)	atttggttcccagttttatg T/G aggggtcatcatccctgtgtt	3624
ABCA4	104	(intron 41 411)	cctcttcccctcctgtctct C/A accctgtctcagttctcagt	3625
ABCA4	105	(intron 41 443)	gttctcagtcgggtttcttc G/A tatcttgagatttatcc a/g g	3626
ABCA4	106	(coding region 5844 (Pro 1948 Pro))	c g/a tatcttgagatttatcc A/G ggcacctccagcccagcagt	3627
ABCA4	107	(intron 43 328)	ttttagcctattcctataa A/G aatgcaccattgcttc c/g cat	3628
ABCA4	108	(intron 43 345)	taa a/g aatgcaccattgcttc C/G cattacctccctccacacat	3629
ABCA4	109	(intron 43 370)	acctccctccacacattttt A/G caaaa c/t gtttcaggaggattt	3630
ABCA4	110	(intron 43 376)	ctccacacattttt a/g caaaa C/T gtttcaggaggatttactgag	3631
ABCA4	111	(intron 43 670)	ttaaacagactggttcccta T/C gggcaggacagagaggatga	3632
ABCA4	112	(intron 43 822)	gttaggtgctgctgacatct G/A tccagcatctgcttgactgg	3633
ABCA4	113	(intron 43 915)	ggcaggacgagtcctgagca C/T gcttcactggctcagacagg	3634
ABCA4	114	(intron 43 1242)	actgagctggagcctagaaa G/T aaactataggcttaagacac	3635
ABCA4	115	(intron 43 1671)	tagagaagtttacttccatc G/A ggacacatgcattctttcta	3636
ABCA4	116	(intron 43 2036)	ttgaaggatactcagtaatt G/A ctttttttctgagcattttt	3637
ABCA4	117	(intron 45 176)	gtgtttggttcacacagctc C/T ggagaaaaacaagtca c/t ggc	3638
ABCA4	118	(intron 45 193)	ctc c/t ggagaaaaacaagtca C/T ggcacagccttgactggga	3639
ABCA4	119	(intron 47 238)	cccaagtctctggtggggc A/G tctgacagagatgcagtcag	3640
ABCA4	120	(intron 47 269)	atgcatgacagcctggctg G/A gatgagggagggtgcttacc	3641
ABCA4	121	(intron 47 326)	accacttatctcaacagatc C/G gggacctgtggccttttac	3642
ABCA4	122	(intron 47 715)	aagtcactaagctggttggg G/A ggaggaacagcacataac c/t c	3643
ABCA4	123	(intron 47 734)	t g/a ggaggaacagcacataac C/T cacttatctatgctgaggt	3644
ABCA4	124	(intron 47 931)	ggacactgcatagatatcta T/C agaaatagcagcatgtcagg	3645
ABCA4	125	(intron 47 1260)	acactctctggtggaccatc A/C ctcatccaagagagggtaac	3646
ABCA4	126	(intron 48 1663)	tctcgtctcttcttaccctc T/C aggtgtttgttaatttttct	3647
ABCA4	127	(intron 49 127)	agagagccccacccacacca C/T ggtccctaccaagtcaccac	3648
ABCA4	128	(5' flanking region (-1441)~(-1400))	gtaaatctcagttgaatcag (TCA)14-16 atttttctcgtctgttctc	3649
ABCA4	129	(intron 1 4712-4720)	gaggggccccgactatagcc (A)8-10 cagcctaattcaaggatgag	3650
ABCA4	130	(intron 1 7295-7304)	ttgtttggctttgcaa t/a ggaat CACAGTCAT/Δ ttattcactcatt	3651
ABCA4	131	(intron 2 951-952)	cctgtccatcagactctctt TT/Δ acctctccccgaggagccca	3652
ABCA4	132	(intron 3 2642-2653)	cctgggtgacagagcgagat (A)10-12 tagcatgagatatttact	3653
ABCA4	133	(intron 4 5202)	cacaaagcatctgacacccc C/Δ atccagccctggcttaacttt	3654
ABCA4	134	(intron 6 3029-3044)	cactaaaaacaaaaatttac (A)16-18 cctgaagaattgcaggca	3655
ABCA4	135	(intron 6 5138-5139)	ttcatgacagatcagatgtt (G) cttttatggatttacaaga	3656
ABCA4	135	(intron 6 5138-5139)	ttcatgacagatcagatgtt cttttatggatttacaaga	3657
ABCA4	136	(intron 6 5985)	tttctcttctcaaacccccc C/Δ agactaggagaaggctctgc	3658
ABCA4	137	(intron 6 6094)	gggacggacagaaaaagacc T/Δ agtttctgttgagcccaaga	3659
ABCA4	138	(intron 6 -161)	tattttttcaattaaataaa A/Δ gagttttttgtttcttaaaag	3660
ABCA4	139	(intron 7 809-810)	ggcccgagtagtcacactga (TG) tgtgggaagttagagaa g/c a	3661
ABCA4	139	(intron 7 809-810)	ggcccgagtagtcacactga tgtgggaagttagagaa g/	3662
ABCA4	140	(intron 8 472-484)	atcttccccacctttcacta (T)10-13 ggtcttctatggggtaaaag	3663
ABCA4	141	(intron 9 48-71)	gtaccctggacccctccagaa (GT)11-13 gagagagatgtgcttctc	3664
ABCA4	142	(intron 9 554)	ataggggacagaaaagacaca A/Δ ccaaaagtctctctcactt	3665
ABCA4	143	(intron 10 11)	catgatcagagtaagggggg G/Δ ttggaggatggggaggggag	3666
ABCA4	144	(intron 11 4242)	ggagaggaatgatgttagt G/Δ cctcctgttaaataggccag	3667
ABCA4	145	(intron 11 13743-13753)	tgctcttttgggttaatgg (T)9-11 cctcttcaggagaagaaaa	3668
ABCA4	146	(intron 13 636-637)	cggggtggagggttgggagg (G) ctcatctgtcattatagatg	3669
ABCA4	146	(intron 13 636-637)	cggggtggagggttgggagg ctcatctgtcattatagatg	3670
ABCA4	147	(intron 18 569-570)	tgctgccctcatcttctctc TT/Δ aaactagtctctgtatttctc	3671
ABCA4	148	(intron 20 (-304)~(-297))	tataacctgacttttttttc (A)7-9 ggattgcttttttaacata	3672
ABCA4	149	(intron 22 1236-1246)	gctgaattagttcccttggg (T)9-11 agttaactcctgatttttgc	3673
ABCA4	150	(intron 26 4626-4635)	gataaatcaatgctgtaaggg (A)9-10 tggcattagagatccagacc	3674
ABCA4	151	(intron 33 115-116)	taaaaccgtctgtttgttt GT/Δ ttacatgggttttttagggccc	3675
ABCA4	152	(intron 36 1078)	taagcagctatcaacttaaca A/Δ taaaaaacagagattatca	3676
ABCA4	153	(intron 37 290-291)	ccttgaccaaaagcctggggg (T) cagccattcccca a/g cccctc	3677
ABCA4	153	(intron 37 290-291)	ccttgaccaaaagcctggggg cagccattcccca a/g cccctc	3678
ABCA4	154	(intron 38 896)	ataaaaagaggggaaaaaa A/Δ gaaggcagctcgtgcagggc	3679
ABCA4	155	(intron 38 1209-1210)	gtggaccctcgagactgact CT/Δ ttccagatctttaggggtt	3680
ABCA4	156	(intron 38 1322)	agactctggaag g/t c/a ggggg G/Δ ataagaacacagccccag	3681
ABCA4	157	(intron 38 3107)	gggccccacctgctgaagag A/Δ ggggggggtggggtttgcccc	3682
ABCA4	158	(intron 40 152)	tttttccaataatacaagt A/Δ gaggatcgggttaaaatagg	3683
ABCA4	159	(intron 43 330)	tgtagcctattcctataa a/g a A/Δ tgcaccattgcttc c/g ca	3684
ABCA4	160	(intron 43 1354)	tttaattggcccagccatgc C/Δ ttgtgtggtttttgtcattg	3685
ABCA4	161	(intron 47 1305-1308)	catcctgctgaaggagaaag AAAG/Δ caccatggcccaagcccta	3686
ABCA7	1	(5' flanking region -1596)	agaatgttgccccctcccc C/T t c/t ctgcattcctctgcagaag	3687
ABCA7	2	(5' flanking region -1594)	aatgttgccccctcccc c/t t C/T ctgcattcctctgcagaagcc	3688
ABCA7	3	(5' flanking region -1180)	ggccagtgagtgacgggcag G/A tcgccaatagcagcgtgc	3689

[illegible]111

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ABCA7	57	(coding region 6133 (Ala 2045 Ser))	tggcgccgaggtccctctggg G/T cggagctgcgcgaggcacat	3743
ABCA7	58	(coding region 6159 (Gly 2053 Gly))	ctgcgcgaggcacatggagg C/T cgctgcgcttccagctgcc	3744
ABCA7	59	(intron 45 27)	acggcgccggggctgggctg G/C gggaggcaggctgggggcca	3745
ABCA7	60	(3' flanking region 108)	caagctgagtggtgcacatag G/A ggccaagtggcattcatag	3746
ABCA7	61	(3' flanking region 376)	ettacaggagccgggtgcc C/T ggagcacaggccaggccgg	3747
ABCA7	62	(3' flanking region 687)	cagcaggagagcttggggag G/A g/a gggagagagttcacactgc	3748
ABCA7	63	(3' flanking region 688)	agcaggagagacttggggag g/a G/A gggagagagttcacactgcg	3749
ABCA7	64	(3' flanking region 1169)	cctcgacctgaccttca C/T ggggctgcaggcggggtgat	3750
ABCA7	65	(intron 9 398-422)	cgtgaactaccagctctgc (T) 22-26 aagagatggagttcactct	3751
ABCA7	66	(intron 12 175-184)	ggggactctgagggtctggt (G) 8-10 actctgagggtctggggcc	3752
ABCA7	67	(intron 30 81-87)	ccccctgggagctctcccg (C) 6-7 ggccctcagctccccctccc	3753
ABCA7	68	(intron 34 349-361)	agaaagagaaagagagaaag (A) 12-14 cagaaatgtgctttgggtga	3754
ABCA8	1	(intron 1 204)	ctggttaattatattagata A/G ataaaaacatttgattagaa	3755
ABCA8	2	(intron 1 266)	aacattatgtgttttaaac A/G taactgagtgtagaaataag	3756
ABCA8	3	(intron 1 733)	ttgccatagtataataaag T/A attcatgtttttgctagcct	3757
ABCA8	4	(intron 1 861)	agactggagtttgcagtgta C/T ctaagactgtagctgattcc	3758
ABCA8	5	(intron 1 907)	gaggagatcatctctctggc C/T aatgtctattaacttcgcca	3759
ABCA8	6	(intron 1 1262)	cagaaacttttgcctctct G/A taggctagctcactgtgaaa	3760
ABCA8	7	(intron 1 1537)	agctctctttaaagatcca T/C gctgaattttctgcacctta	3761
ABCA8	8	(intron 1 7622)	tcgttaacagcaatgataat T/C tagcccatcttattcc c/t a	3762
ABCA8	9	(intron 1 7639)	t t/c tagcccatcttattcc C/T agaaacaacaggctcataag	3763
ABCA8	10	(intron 1 7720)	tcattgtgttcaaaactgcc C/T tggagaacagaaaaagagaa	3764
ABCA8	11	(intron 1 9397)	cataatatatatacatatgc G/A cacacacacacatacacaca	3765
ABCA8	12	(intron 1 9519)	agtagtctcatgttggaacaa T/C atgcttgagaaatgcagaaa	3766
ABCA8	13	(intron 1 12973)	ttgataaacaggcacaggga T/C cacaataaatgatggaaca	3767
ABCA8	14	(intron 1 13100)	cattggagttattaggctacg T/C tttttgtgttttcaggat	3768
ABCA8	15	(intron 1 13128)	ttgtttgcaggatatttctt T/C ttcttaagaacttcatatta	3769
ABCA8	16	(intron 2 420)	caattagttttcttcaaaaa A/G gtagaaaagtggaaattgta	3770
ABCA8	17	(intron 2 505)	catataaaaaatcttgatta A/T actttggtatatttttaaaaa	3771
ABCA8	18	(intron 2 819)	gcaatgccttggaactatct C/T ttaaacacatttgactttca	3772
ABCA8	19	(intron 3 915)	ttgtgttcgatagatcagta G/A ggtgactagttaacaatgat	3773
ABCA8	20	(intron 3 1539)	aaagggaaatctgtgtgat C/T gccctgtcatttcattcatag	3774
ABCA8	21	(intron 3 2341)	ttccttctcttgcaacttc C/T gtccaaattccactcaagct	3775
ABCA8	22	(intron 3 2882)	tattctataattctgtactct A/G ttaattattctataataataa	3776
ABCA8	23	(intron 3 3314)	atttaaatatctatctctct A/G tatttaccattttcaaattta	3777
ABCA8	24	(intron 4 89)	gagggttagtatgccaaatta G/A agcatcactatctgtcataa	3778
ABCA8	25	(intron 4 3264)	ttccattggcctattatgcc C/T gtgttatatccagtggttaga	3779
ABCA8	26	(intron 4 3403)	aagagaccaaaaaattctt C/G atcagcagaaaaagcacagga	3780
ABCA8	27	(intron 5 389)	gcttactgaatatataaatt G/C agaaaagccatgccagcaaa	3781
ABCA8	28	(intron 5 479)	tgagagtggtgagtaactca A/G aatgcctggactcc g/a aggtc	3782
ABCA8	29	(intron 5 494)	actca a/g aatgcctggactcc G/A aggtccagcagggtcaatga	3783
ABCA8	30	(coding region 792 (Ala 264 Ala))	atgggtctctcgggattcagc G/A ttctggtgagtcaaacgcag	3784
ABCA8	31	(intron 6 200)	cctcccaagtagctgggact G/A caggtgccc a/g ccaccatgcc	3785
ABCA8	32	(intron 6 210)	agctgggact g/a caggtgccc A/G ccaccatgcctggataattt	3786
ABCA8	33	(intron 6 1751)	gtgagttattattgtgttg C/T ttgagctgttttgttttt	3787
ABCA8	34	(intron 6 1808)	atttcattatagttttcaaa G/T aatattgttaaaacaaagaa	3788
ABCA8	35	(intron 6 2412)	tattcctaattctaaagaat T/C ctgcccaaaacttttacctt	3789
ABCA8	36	(intron 6 2506)	tgatgaataaagtgaatgaa G/A agttatcttaga a/g tccattt	3790
ABCA8	37	(intron 6 2519)	gaatgaa g/a agttatcttaga A/G tccatttcagggtcttcttt	3791
ABCA8	38	(intron 7 28)	agtgaattaaatatctttcc A/G tccacctatagcctaaaaat	3792
ABCA8	39	(coding region 991 (Gly 331 Ser))	taaaagaaatctttctctcacc G/A gccctggtgtgtctctctc	3793
ABCA8	40	(intron 8 74)	tggaatccataggctgtaat C/T atttacaacctcagcattgt	3794
ABCA8	41	(intron 9 1417)	acacatacttaaatatattt T/C ctctgttctacttttgtttt	3795
ABCA8	42	(intron 9 2504)	agagggaaattatggtttgg G/A aatgaaataaagcagaaata	3796
ABCA8	43	(intron 10 2013)	tgcccaagatctttccaac C/T tgtgccagtggttcacagga	3797
ABCA8	44	(intron 10 2378)	ctgaagaaattgtcacttt G/A aagtatcttttctttttttc	3798
ABCA8	45	(intron 11 -697)	aaaaaaaaaaaaaagagag A/G gagaagaaaaattttgtta	3799
ABCA8	46	(intron 11 -528)	tataaaagttagaaaaaat G/T a a/g tatgttttagaaatagat	3800
ABCA8	47	(intron 11 -526)	taaaagttagaaaaaat g/t a A/G tatgttttagaaatagatgt	3801
ABCA8	48	(intron 11 -342)	ctcaaaggagttttagccat G/A taataacttactattaatct	3802
ABCA8	49	(coding region 1632 (Asn 544 Asn))	ggttcagtcaccatctataa C/T aataagctttcagaaatggc	3803
ABCA8	50	(intron 14 252)	cttattgcaaaaagtga G/A ttgagtttctaaagatcaa	3804
ABCA8	51	(intron 15 130)	ttttgtttttgagacggagt A/C tcgatcatctcgggtcactg	3805
ABCA8	52	(intron 16 534)	acatatcatttcattcaat A/G cacattttatggtgacaaca	3806
ABCA8	53	(intron 16 588)	gaatcatcaggaaagtgtta C/T gcaattctgattagtactt	3807

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ABCA8	54	(intron 16 645)	atttaagaaaaattttaga C/T gttttaggtggaatgaagaa	3808
ABCA8	55	(intron 17 431)	tgctcagggtttttcttttttt T/A ttctttatgttagaaattgg	3809
ABCA8	56	(intron 17 1390)	gctgtaaaactcgtttttaga C/A tttagtaccatgatttcta	3810
ABCA8	57	(intron 17 2452)	cacgtttacacctatagtaac G/A cggaaga g/c tctaatacatgag	3811
ABCA8	58	(intron 17 2460)	acotatagtaac g/a oggaaga G/C tctaatacatgagat g/c ctt	3812
ABCA8	59	(intron 17 2475)	gaaga g/c tctaatacatgagat G/C cttagcagagccaatctcta	3813
ABCA8	60	(intron 18 152)	gaagaagcacaggagagagg C/T agaactctgacatccaaagg	3814
ABCA8	61	(intron 19 7477)	aaaatctatittgaaagaca C/T ttggaaactaaaaaatcttt	3815
ABCA8	62	(intron 21 196)	ttgttttaaagtaaaaa T/C g/c aacaaaacatttttcaaag	3816
ABCA8	63	(intron 21 197)	tgtttaaagtaaaaa t/c G/C aacaaaacatttttcaaaga	3817
ABCA8	64	(intron 21 287)	actgtggtgggtgggggga G/T gggggagggtatgacattggg	3818
ABCA8	65	(intron 21 403)	cctgcacaatgtgcacatgt A/G ccctaaaacctaaagtataa	3819
ABCA8	66	(intron 21 1207)	cccagcc g/a gagtgcagtgcc A/G ggatcatagctcactgtaac	3820
ABCA8	67	(intron 24 692)	ctcctagatatagacaaaa A/C caaggtgcacaatggccatg	3821
ABCA8	68	(intron 25 212)	cctgattataataggggaag G/A aagggttaaggggtagtgagg	3822
ABCA8	69	(intron 26 67)	aataattttcagttctgtac A/G cactgtgaaactcttttat	3823
ABCA8	70	(intron 27 515)	gtgtctcccaaccacatca G/T ttctatcttttgcattaca	3824
ABCA8	71	(intron 27 661)	cctggatattatcagactta G/A aatggagagaaagtcact	3825
ABCA8	72	(intron 30 1967)	caaaaattagatataaagg G/C tgaattgacttttaattgta	3826
ABCA8	73	(intron 31 112)	ctctaaatgctgacccaggt C/G acactgggtagatttacaac	3827
ABCA8	74	(intron 33 401)	cttctcactaggttgtaga C/T gctgttgtaaaattttatgt	3828
ABCA8	75	(intron 35 484)	taacagcatcatcctg a/t tgt A/G ttattttcatagacagaaa	3829
ABCA8	76	(intron 36 258)	tttgcattgtatgttgtaaa A/G cctaagtcacaaactcagtta	3830
ABCA8	77	(intron 36 375)	atattttttactgtcttag C/G ctgtatataaagaaactgac	3831
ABCA8	78	(3' flanking region 674)	cggttgacatagaaagccc G/A gaagcttctgtatgtgtta	3832
ABCA8	79	(intron 1 56-57)	ttttgctttgtgtgtgagt TT/Δ gtttcagaggtttttgtcttt	3833
ABCA8	80	(intron 1 1180-1191)	taaagtataataaaaaacg (A)9-11 gaaattctctctgtacagag	3834
ABCA8	81	(intron 1 9877-9885)	ctctcgaaataggtatgac (A)8-12 tcaactgagtacaaaaagct	3835
ABCA8	82	(intron 1 12588)	gtactagagtgcactccttt T/Δ gcaacaggacggccaaagga	3836
ABCA8	83	(intron 6 78)	tcaatgcactcttttttttt T/Δ gaaatggagctctgctctgt	3837
ABCA8	84	(intron 9 265)	gtatatgggtattttttttt T/Δ agacctcttagaaagctagt	3838
ABCA8	85	(intron 9 2666)	attttttttaagggtatcca A/Δ tagtcaattctcaatttcttc	3839
ABCA8	86	(intron 11 -447)	ggatattctgggttttttt T/Δ ctacaaactcaagttttttg	3840
ABCA8	87	(intron 15 8407)	gtggaataatttttgactta T/Δ gcatttgggtcaataaaatt	3841
ABCA8	88	(intron 15 9458-9470)	tatgtcgagtaacatagtc (T)11-15 ctgaatgccaggttcagtt	3842
ABCA8	89	(intron 16 54-56)	tgaataatagtcacatcat CAT/Δ aattattatcattacaacta	3843
ABCA8	90	(intron 17 433)	tcagggtttttcttttttt t/a t T/Δ ctttatgttagaaaattggac	3844
ABCA8	91	(intron 24 1462)	actccatctcaaaaaaaa A/Δ gagagaaaaaaattctgcac	3845
ABCA8	92	(intron 33 155)	caatactttgcaaaaaaaa A/Δ gatctttccctgatgatatt	3846
ABCA8	93	(intron 34 184)	atactgaatgggttttttt T/Δ ctectttctcatatgacctc	3847
ABCA8	94	(3' flanking region 1240)	atccttggaacaaaaaaa A/Δ ctttatctgtgctttgcgtg	3848
ABCB1	1	5' flanking - 196	gttttgagccatagtcacg T/C actcaaaattttattttatct	3849
ABCB1	2	5' flanking - 16	tactctttacctgtgaagag T/C agaactgaagaaatctact	3850
ABCB1	3	intron 1 + 71660	cttgctggagggaaggtgct A/C gaaatataccaatccaag	3851
ABCB1	4	intron 1 + 80091	gaaataaattatcaagttctg A/C aataatcatgacacatag	3852
ABCB1	5	intron 1 + 103126	gatatgaatcagaattcatc T/C gtgtctcaagaaaaggtcat	3853
ABCB1	6	intron 1 + 103148	tgctctcaagaaaaggtcatg C/T gataaattaaagttctgtag	3854
ABCB1	7	intron 1 + 108428	aattaatattatcatcatcg A/G tcaccatttcacacaactca	3855
ABCB1	8	intron 1 + 112042	cataagttgaaatgtcccca A/G tgattcagctgtagcgcgtt	3856
ABCB1	9	intron 2 + 491	gctctctggcttcgacgggg G/Δ actagaggttagtctcacct	3857
ABCB1	10	intron 4 + 36	attaactattcaaaatactt C/T ggaaatttgacatctcctta	3858
ABCB1	11	intron 5 + 1596	ttagctctcttactgcttca T/C agtgggaatcaaaatactt	3859
ABCB1	12	intron 8 + 1789	aaacactctgaaatattaac C/T gctcctggaaccacagctca	3860
ABCB1	13	intron 14 + 24	agttgtccttgccctttggc T/C ttctagaggtgcacaaaata	3861
ABCB1	14	intron 14 + 81	tgagggaagttaggaaacta C/T tataaatcggaagaaggaa	3862
ABCB1	15	intron 15 + 38	caaacacacctgatttataa A/G cataagaacattctactact	3863
ABCB1	16	intron 17 + 73	gtttggtgggctagggctac A/G gtaggagtggaacaaagaga	3864
ABCB1	17	intron 18 + 564	caacagtaaaagttacaatct G/A aaaggaatgctctctgttta	3865
ABCB1	18	intron 18 + 2062	tttccctgaggaatggttat C/T ctctgtgttccttgagttca	3866
ABCB1	19	intron 18 + 2293	ccacatcaggtttttccccc A/G caccttgggacagtttgaag	3867
ABCB1	20	intron 20 + 557	aaaaccctaaccattgacac G/A tgtgaatgttttccctgggga	3868
ABCB1	21	intron 21 + 24	cgtgctctcttctactggt G/A ttgtcttaattggccattt	3869
ABCB1	22	intron 21 + 2725	ctgacctgtttttggctgac A/G ggttttagttctctccctca	3870
ABCB1	23	intron 21 + 4725	tcttgggtattaaaagatcca A/G agagataggaatatgttaatt	3871
ABCB1	24	intron 22 + 8507	tgcaacttaggaaaaaacaa T/C atggaaatgtgtaaaatata	3872
ABCB1	25	intron 22 + 8537	tgtaaaatatacttttttt T/A aaaaaaaaggacacatttat	3873
ABCB1	26	intron 22 + 8565	aggacacattttatcagcat T/C atgatcagactattacattt	3874
ABCB1	27	intron 22 + 8952	caccttgggtttcatggtttg G/A caaagtactggcctgtacca	3875
ABCB1	28	intron 22 + 9520	caccaacaaatcttttttc A/G cagttgggtgggcatctggt	3876
ABCB1	29	intron 22 + 9836	agactctgacttagacatga C/T ggcaggggaagagagactt	3877

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ABCB1	30	intron 24 + 377	taaaatcacagatgtgttga C/A taagttctgcaagccttgg	3878
ABCB1	31	intron 24 + 1493	ggggagggtgtccaggcacga A/Δ catggagagctggacttgat	3879
ABCB1	32	intron 24 + 1495	ggagggtgtccaggcacgaac A/T tggagagctggacttgatac	3880
ABCB1	33	intron 25 + 342	tcagaccttgatcttctggg C/T tcaagcgatcctcctgcctc	3881
ABCB1	34	intron 26 + 134	cttgataaaagtctgagagc C/G taaatatggcttccaagtgg	3882
ABCB1	35	intron 26 + 1272	gtccttcaattttgtggtga A/G cttaaaaaacaggactctaaa	3883
ABCB1	36	intron 26 + 1394	tattaaagtggtgtgtttaaag A/G ttgtgctataatgaattgta	3884
ABCB1	37	intron 26 + (1987-1988)	aagggtgtggaagagtgaag (AAG) gaggctatttgctcccagac	3885
ABCB1	37	intron 26 + (1987-1988)	aagggtgtggaagagtgaag gaggctatttgctcccagac	3886
ABCB1	38	intron 27 + 59	gcagcctctctggcctatag G/T ttgatttataagggctgggt	3887
ABCB1	39	intron 27 + 80	ttgatttataagggctgggt T/C tcccagaagtgaagagaaat	3888
ABCB4	1	exon 3 + 3	aacaccccttattttatagat C/T caatgactgagtcaagaatt	3889
ABCB4	2	intron 3 + 45	cagcatctctacttatacca T/C gctctgcttttaaggttctct	3890
ABCB4	3	intron 3 + 498	actcaaatagtggttaggag C/T agagacaattcaatacacagac	3891
ABCB4	4	intron 3 + 515	gagcagagacaattcaatac A/G gacagaagtcttagatgaga	3892
ABCB4	5	intron 6 + 1030	tagttttgccatgtagaatt G/C aaaaagtgtagatggtgtt	3893
ABCB4	6	intron 6 + 1437	gttaagcctgcttcaatcaa G/A ttagttatattcttgttcta	3894
ABCB4	7	intron 6 + 2449	ttgacttagcagactgtta G/A catacttatcttctctgtgt	3895
ABCB4	8	intron 7 + 451	ccttgctgcacctgtgctgt A/C taagtttggcttattatagt	3896
ABCB4	9	intron 7 + 530	agtagagacaggctggcgat C/G acaccggacagagctaactg	3897
ABCB4	10	intron 7 - 152	aacagaatcatgaattaaag T/C tgttaagtatttgaaggcct	3898
ABCB4	11	exon 8 + 40	aggataaattgtttatgtcg C/T ctgggtaccatcatggccat	3899
ABCB4	12	intron 8 + 130	ctgggtgactccagatatca T/C agaaggagtgttaaaattct	3900
ABCB4	13	intron 8 + 248	aatacacagggaagctcttaa A/G taaagtaagggaagctactct	3901
ABCB4	14	intron 8 + 531	ctaaagagtgaattgattca A/G tacgtcccttggaaactcacc	3902
ABCB4	15	intron 8 + 4240	ctgaggttccagcttatctc T/A tagagatgtttacttagtct	3903
ABCB4	16	intron 8 + 4343	tgttagaagaaaaaagggt C/T atattacaaggaggtctgac	3904
ABCB4	17	intron 8 + 4677	cccaagatatcttataact G/C tccatagtgcctagggtgcc	3905
ABCB4	18	intron 9 + 113	tttaccagagattcacctatt A/G ttatcatttttgcctccaaa	3906
ABCB4	19	intron 9 + 982	tgctctatacagtttttgtt T/A taagtttagtaaatgtatta	3907
ABCB4	20	intron 11 + 241	gcacttgggaggccaaggt A/G cataaatcacttgaggtcag	3908
ABCB4	21	intron 11 + 457	tccagcttgggtgacagagt A/G agacttcatctcaaaaaaaa	3909
ABCB4	22	intron 11 + 1337	tactcttggggagcctatca C/G cagggtgggtcagatatagc	3910
ABCB4	23	exon 12 + 3	tgtttttttctgtccagat A/T ctctcgccatttagtgacaa	3911
ABCB4	24	intron 12 + 1288	cagaccacactaacctcag T/C tggacctcaggatgtcagtg	3912
ABCB4	25	intron 13 + 206	tgtggataagaaaaatagcat G/A tggttagaccatttltgaaa	3913
ABCB4	26	intron 13 + 988	cagtcgggttgggaagcttgc T/C accctttcttctacttctca	3914
ABCB4	27	intron 13 + (1413-1414)	tttatcttcaacttatgtttt (T) ctacagtttaagttatgcta	3915
ABCB4	27	intron 13 + (1413-1414)	tttatcttcaacttatgtttt ctacagtttaagttatgcta	3916
ABCB4	28	intron 13 + 1931	cttgcaaatgttgcctctcc A/G caaaaaaaaaggaaaggat	3917
ABCB4	29	intron 22 + 767	acagttgggtctgacataga A/Δ cctgtagcaatccaccagca	3918
ABCB4	30	intron 23 + 784	agtatctctctaaactcttgc T/C atgcaggaaaaattatttta	3919
ABCB4	31	intron 25 + 158	gaaatattttactgtattaa T/C gtctagaacttaaatataag	3920
ABCB4	32	intron 25 + 2920	ctgagttctctatatactct T/A ttccattctcctggatgctgt	3921
ABCB4	33	intron 29 + 411	cttctcttaccttgaaattct A/C ggctctcgaaactttgacttt	3922
ABCB4	34	3' flanking + 458	agaaaatgaaattgccctac T/C gagctaactctgaaagcaca	3923
ABCB7	1	intron 1 + 220	acggggcaggaggttctctggg C/A agaggacacctggagcgctg	3924
ABCB7	2	intron 1 + 480	agtttaactcccttgcgtgaca G/A gcgtgctcttctgataggcca	3925
ABCB7	3	intron 1 + (512-513)	gataggccaaaaccgttaact AT/Δ ctttccaaaacatagaccgc	3926
ABCB7	4	intron 1 + 1690	agttctccaataaggcagat G/A aagtttaagataaaatttgta	3927
ABCB7	5	intron 1 + 5309	aatttaatatcatttattgct G/A tattgttgcagtggttatct	3928
ABCB7	6	intron 1 - 11274	tgcttcttttcaagccagcc A/G gctttaaaaaaagttagct	3929
ABCB7	7	intron 1 - 11085	cagggttttcagggtctatgt A/G gacctgaagaaaaatgagag	3930
ABCB7	8	intron 1 - 10037	attctacttttctcaacttct T/C ttattacattatctcatcat	3931
ABCB7	9	intron 1 - 21	ccactctgaaacttccccct G/A cttttttctcttgcagcag	3932
ABCB7	10	intron 3 + (135-136)	ttctctaataagaaaaaaa (A) catattaattgaccatagtt	3933
ABCB7	10	intron 3 + (135-136)	ttctctaataagaaaaaaa catattaattgaccatagtt	3934
ABCB7	11	intron 3 + 333	aaaacaatttgtgtgtgtgc G/A tgtgcttcaaggtttaatgtt	3935
ABCB7	12	intron 12 + 524	taaccactctgcctcagta C/T gaaacacagtgccgaaccca	3936
ABCB7	13	intron 13 + 1543	atcctgtgaggtggggaagc G/A tatggctagcataaataaa	3937
ABCB7	14	intron 13 + 2400	tgttaccttactgcctcatt C/G tcattcttccaccctgctat	3938
ABCB7	15	intron 15 + 2201	ctccttcttaaccttagcaa G/C agtctggagatttacttate	3939
ABCB8	1	5' flanking - 2272	ggcttaggcctaagggtgga T/C gttggggccagtaccctga	3940
ABCB8	2	5' flanking - 2070	agctatgaaaaacagacct G/A tccttctagaggtagcaaaa	3941
ABCB8	3	intron 1 + 25	aaacggaaaaacctactcag A/C gcggggccattgaccgccgg	3942
ABCB8	4	exon 2 + 308	tgctggtcctgggggtagcc G/A tctgtggtgaggttttcccca	3943
ABCB8	5	intron 2 + 334	ccccacttaaaacatttgt C/G ccctctgtctccccattcca	3944
ABCB8	6	intron 4 + 12	cctgctcgggtactgcagc C/T gcagggtgcagagttggggt	3945
ABCB8	7	intron 5 + 547	agttcatagcattctcgtc G/A gccctcctcaggcctgctgct	3946
ABCB8	8	exon 7 + 57	ggcaatgtgcggactgtgag A/T gccttcggcatggagcaacg	3947

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ABCB8	9	intron 9 + 1231	tttccgcagctgcatggaca C/T cctcgcgtgccccgtttctg	3948
ABCB8	10	intron 9 + 2164	cctcttggaggtccttctag C/T gctgcctatgtggagattct	3949
ABCB8	11	intron 9 + 2645	ttcctgctgtgtgctctccc C/Δ ggtcgtcttagcaagtgtct	3950
ABCB8	12	intron 9 + 2646	tcctgctgtgtgctctccc G/A gctgccttagcaagtgtctg	3951
ABCB8	13	intron 9 + 3229	cagggccgagcaggaggtcc G/A tgggtcagctgggtccctt	3952
ABCB8	14	intron 12 + (113-114)	tcctccactgccacaagggg (GG) cctctttctctgggacaatc	3953
ABCB8	14	intron 12 + (113-114)	tcctccactgccacaagggg cctctttctctgggacaatc	3954
ABCB8	15	intron 13 + 128	tgctctcgggagaccctggc C/T gtcttcacatgtctcagct	3955
ABCB8	16	intron 13 + 305	atccaggtctagagaagcct A/G tagtggaggtgctgagctgc	3956
ABCB8	17	intron 14 + 135	acagttgtgtcaggggaagac C/G agaaccacagccaaagggga	3957
ABCB8	18	intron 14 + 159	accacagccaaaggggacag A/T gtcgttgtgtggggacaggg	3958
ABCB8	19	intron15+747	gttggagccttgggtctgt A/G agggggacagaggaatcat	3959
ABCB8	20	3'flanking + 333	cctatcccttggtcaccctc G/A ggaccacagtcctcatctt	3960
ABCB8	21	3'flanking + 1168	ccctctttcaggggtgtgat G/A cagtgcatgtatggagcagc	3961
ABCB8	22	3'flanking + (1719-1721)	tagaccgcaggaccctggcc GTC/Δ ttcctaacctcgccctggcc	3962
ABCB9	1	intron 1 + 69	aggggtgccaggccagggcag G/C gttggggggcgtctgggcac	3963
ABCB9	2	intron 1 + 8873	tggggcccagcagctggggcc T/C ggaactacctcaaggcttc	3964
ABCB9	3	intron 1 + 8940	accagctcagcctgccaccg G/A tgcacacggcaccagctgg	3965
ABCB9	4	intron 1 + 11410	agatccaagggatccagagg T/C tggaaatgtgacctccgtgc	3966
ABCB9	5	intron 1 + 12863	gggaagccagatgcccaaa G/A gctctgtgacttcaacttcca	3967
ABCB9	6	intron 1 + 19731	gccaaagtgtcaagatcgagc G/A agggggagggcctgacaggg	3968
ABCB9	7	intron 1 + 29649	cagaatccagatgcccgtaa T/C gttgttaagaagcctgcaca	3969
ABCB9	8	intron 1 + 31793	ggccaggcggggaggggtac C/T ggccagaccggtgggcaaaa	3970
ABCB9	9	intron 1 + 37537	agagtcaacaggggtgggggt C/A ccccggaaggtggcatcta	3971
ABCB9	10	intron 1 + 38293	taccagccctgtgctttcag G/A gacctgtgacctgtcaact	3972
ABCB9	11	intron 1 + 44661	cccagagtgctgtgcttcac A/G gcaggattgccctcctgcag	3973
ABCB9	12	intron 1 + 49576	aaagtggcccggtgcttgt C/T ccctgaagccctaagaccac	3974
ABCB9	13	intron 1 + 64669	ccacagacaagccggtagc C/A cactctgcagctcaaacacac	3975
ABCB9	14	exon 2 + 448	cctggttttgggcccctgttc G/A tgtggacgtacatttcaactc	3976
ABCB9	15	intron 7 + 3364	ggtaccaggagtcgggtatc A/G gtgggacaggaacgcgtgtc	3977
ABCB9	16	intron 11 + 113	gggcccagagagctctccca G/T actatcagcctcctgggctg	3978
ABCB9	17	exon 12 + 370	cccagggcctgcagcactgaa A/G gacgacctgccatgtcccat	3979
ABCB10	1	5'flanking - 424	tcgcgtctgcgcgctccgcc C/T ggtctgcggcggtgagaaag	3980
ABCB10	2	exon 1 + 491	acaagggggcggttgccgcc G/T cagcggccgactcccggag	3981
ABCB10	3	intron 1 + 37	ccacttccctcccgccggcc T/G ctcccttctccacacgcgggg	3982
ABCB10	4	intron 1 + 217	actcgtttgcagattttaca C/T ttgttttctgtttgacacac	3983
ABCB10	5	intron 1 + 405	gcgtttatacttttttttt T/Δ aacaaaaaacacattatttg	3984
ABCB10	6	exon 3 + 185	agggccggggggccagggcttc C/T gtaggcatcagtatgatgtt	3985
ABCB10	7	intron 6 + 1269	caaatccacaactgtgcctt C/G cacagaatgggttggaaaaac	3986
ABCB10	8	intron 9 + 632	cccactccacttgggtgag G/A gcaggtggatgggtgatgggt	3987
ABCB10	9	intron 10 + 2373	tacctcagggcactcagaca G/C cctcaccatcagaggtctca	3988
ABCB10	10	intron 11 + 108	tccttttctgtttttttgt T/G ttttttttttcttggagtgg	3989
ABCB10	11	intron 11 + 2379	cattgggttttagtgtatct T/A gtgttgtgcatccatcatca	3990
ABCB11	1	5'flanking - (2596-2595)	tgtggttttagagctttctct (TT) gagacatttttgcctaaggtt	3991
ABCB11	1	5'flanking - (2596-2595)	tgtggttttagagctttctct gagacatttttgcctaaggtt	3992
ABCB11	2	5'flanking - 1746	agctgaagtgaattaaagcac G/A atcaactcagtaactcacact	3993
ABCB11	3	5'flanking - (326-314)	aggggggaaagttttaaggtta (T)9-12 gtcttgttatgtttttaaagt	3994
ABCB11	4	5'flanking - 135	agagggtttcccaagcacac T/C ctgtgtttgggttattgtct	3995
ABCB11	5	intron 1 + 511	aaatatagatgcataaaaaaa A/Δ tgagctgtggatgcattgtt	3996
ABCB11	6	intron 1 + 581	aatttcagtttttaggtcac C/T caagccagtgaggatcacat	3997
ABCB11	7	intron 1 + (1938-1951)	aaagacgtttttaagggtttt (A)10-13 gaaagaaaaaactgtag	3998
ABCB11	8	intron 1 + 4517	gggtttcccaacatctcatct G/A ataaaaaaaataatttgcca	3999
ABCB11	9	intron 1 + 5651	aaagagaataggttagtgga T/C tagtattcctgtgcttaatg	4000
ABCB11	10	intron 1 + (12200-12201)	aagagatggtctctagcccc CT/Δ gtttgatttggggcacttac	4001
ABCB11	11	intron 1 + 13023	gtttggctactttgattaaa G/A aagaagaagagataataat	4002
ABCB11	12	intron 2 + 739	cctgcactctattctgacct C/T actggggaaaaacagtatgtg	4003
ABCB11	13	intron 2 + (921-922)	tattttgtagttcaaaaagt (CAGATCTTCTTACGCTAATTAGAAATGT) tgctgtccatttgatattca	4004
ABCB11	13	intron 2 + (921-922)	tattttgtagttcaaaaagt tgctgtccatttgatattca	4005
ABCB11	14	intron 3 + 644	agccacacgtttcttattgc G/A tgggaagtttaaaaaatggg	4006
ABCB11	15	intron 3 + 2231	agtgaacctgagattgagct A/G tactgaaatctctagaagag	4007
ABCB11	16	intron 3 + 2406	aaaggggtgttctttaaattcc T/C tatgtttttctcatcaggtt	4008
ABCB11	17	exon 4 + 10	tttctcatcaggttacaaga T/C gagaagaaggtgatggcgt	4009
ABCB11	18	intron 4 + 434	acaatttatagttatttctca A/G tgccccacacagtttatcta	4010
ABCB11	19	intron 4 + 518	gtagatgagtagctaaaaac G/T aaagtcagctcctgaaataa	4011
ABCB11	20	exon 5 + 120	ggcacaatgacagatgtttt T/C attgactacagcttgagtt	4012
ABCB11	21	intron 5 + 320	gggaaggtgacccatgaattt T/C acttgagtatcatctccaag	4013
ABCB11	22	intron 5 + 16076	agaagaggttaacagtaagcc T/G cctgatttacagcacatc	4014

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ABCB11	23	intron 6 + 303	atttgcagggtgtgttttag G/C gggcagttgagtagcttgaa	4015
ABCB11	24	intron 7 + 1141	aaaggattcagcaggcatga A/G gaaagaaaagctttgcaaga	4016
ABCB11	25	intron 8 + 2463	ccattggcctaataagcaatga A/C ctatgacatggtcttaactta	4017
ABCB11	26	intron 8 + 2677	tcaatgatgtttacagtgaga A/C tctaataattgtattaaaccc	4018
ABCB11	27	intron 8 + 2699	ctaataattgtattaaaccca T/A gccacatgttaaatgaatct	4019
ABCB11	28	exon 9 + 24	gtgtcccaagtttacggacta T/C gagctgaagcgctatgccaa	4020
ABCB11	29	intron 9 + 108	caccttggtctgtggcctcc A/G gaggaagtacttgttcaaga	4021
ABCB11	30	intron 10 + 2475	taatcattccaaaccacgga C/A ttattttcattagaacatg	4022
ABCB11	31	intron 10 + 2478	tcattccaaaccacggactt T/A atttcattagaacatgata	4023
ABCB11	32	intron 10 + 2711	tttacagattggaaaagcca C/T tgaagtattgcaggtccaga	4024
ABCB11	33	intron 10 + 3539	agtgaactgttaattagtatca C/G ttgtgcacagagaaaaatg	4025
ABCB11	34	intron 10 + 3623	tgcagaaggttgtttcttca T/C gaccttctgtagtttcagaa	4026
ABCB11	35	intron 10 + 3661	gaattcattataaaaaataa A/T cacataatggagcgtgacat	4027
ABCB11	36	intron 10 + 5100	ggggcactcttggctgtggc A/G atagactgtggcccaatgaaa	4028
ABCB11	37	intron 10 + 5292	gctatttggtaggaacatct G/A ggcatgatcaggtagccttc	4029
ABCB11	38	intron 10 + 5912	gagtaaatattcagtaaaaaa A/Δ taaagtgttattttaaatca	4030
ABCB11	39	intron 12 + 116	tgtttccagtaaatagggaaat G/A gaggtgtctttctctgaaag	4031
ABCB11	40	intron 12 + 326	gataaatgacaaggcaatga G/C aacaatcagggaagcacaggt	4032
ABCB11	41	intron 12 + 335	caaggcaattacaacaatca A/G gaagcacaggttcttcccaa	4033
ABCB11	42	intron 12 + 2572	cctcatccttgccaatgttt C/T cttttactggtttttgatgg	4034
ABCB11	43	exon 13 + 23	tctaataatgacctcaacatgg T/C cattaaaccaggggaatga	4035
ABCB11	44	intron 13 + 70	atggcagtatattgatcaaa C/T agaaaggtgtagcatacatt	4036
ABCB11	45	intron 13 + (1578-1579)	ttattggcctctattttttc (C) tgcccattggtcaagtatga	4037
ABCB11	45	intron 13 + (1578-1579)	ttattggcctctattttttc tgcccattggtcaagtatga	4038
ABCB11	46	intron 14 + 32	catacattcctgggagaaac C/T aagaggtcatagaaggaaaa	4039
ABCB11	47	intron 14 + 80	cacaattatacacatttctt C/T tcgtatgattcccaagtcat	4040
ABCB11	48	intron 14 + 439	tattgtgtcaaaaacaattc A/G ttgtatatctccattctaa	4041
ABCB11	49	intron 14 + (1262-1263)	cagcctttgcatatatttt (T) gctgtgtgtcttaacaggag	4042
ABCB11	49	intron 14 + (1262-1263)	cagcctttgcatatatttt gctgtgtgtcttaacaggag	4043
ABCB11	50	intron 14 + 1283	gctgtgtgtcttaacaggag A/C aaagagacacggatttgctc	4044
ABCB11	51	intron 14 + 1339	tgagatagatatattaggacc G/A tgaccaatttttattttggt	4045
ABCB11	52	intron 14 + 1359	gtgaccaatttttatttttg T/C tgaataattcttatttgaagt	4046
ABCB11	53	intron 14 + 1480	tattgattagacaataaccc G/A tctggggaagggaattttct	4047
ABCB11	54	intron 15 + 370	ccttttctaagtctgcaca G/A cctatttaagaattttccca	4048
ABCB11	55	intron 16 + (550-559)	aaagttttagtgtttctatca (T)9-12 gctactcttgatggacttct	4049
ABCB11	56	intron 17 + 188	tttctctcccaattctatgg T/G tttttggttagcttctctc	4050
ABCB11	57	intron 17 + 194	tcoccaattcatgggttttt T/G gttagcttctcatctctctg	4051
ABCB11	58	intron 17 + (197-198)	caattcatgggttttttggt (T) agcttctcatcttcttgggg	4052
ABCB11	58	intron 17 + (197-198)	caattcatgggttttttggt agcttctcatcttcttgggg	4053
ABCB11	59	intron 17 + (289-296)	ggggactcttttaaaaaaa G/A(A)4 tctgtgttttagtcttctct	4054
ABCB11	60	intron 17 + 1070	tcagacttgggttttctat C/T tttcttcttgagaaacaagt	4055
ABCB11	61	intron 17 + 1651	tgttaaaatatctcattgtga T/C atgctgacgggatttttcttg	4056
ABCB11	62	intron 17 + 2226	ccttaagtctctctctatca T/A gcaccttgttctcaccagct	4057
ABCB11	63	intron 17 + 2979	ctctctcttctctctcagc T/Δ ctactatttcaactgttggt	4058
ABCB11	64	intron 17 + 3288	aatcccatatctcactctta T/G ccactctcctcatgaatctt	4059
ABCB11	65	intron 17 + 3289	atcccatatctcactcttag C/T catctcatcctgaatcttg	4060
ABCB11	66	intron 18 + 97	aatatgagttttctaggtat A/G tatctagcagtggtttcaagt	4061
ABCB11	67	intron 18 + 98	atatgagttttctaggtata T/C atctagcagtggtttcaagtc	4062
ABCB11	68	intron 18 + 892	ctctgaaagttagtgtatca C/T cttatttgtgtttgaatcaa	4063
ABCB11	69	intron 18 + 2681	atgtatgagatcaagtcagg A/G tcaaatattagacaccata	4064
ABCB11	70	intron 18 + 3780	ggaccatcctgtggggcaat C/G gttccagaaaatgctggtat	4065
ABCB11	71	intron 18 + 5741	ctcaccgggtataataacaac C/T gtacgcaagggttttctttt	4066
ABCB11	72	intron 18 + (5882-5883)	tgcgtattccctcagttcag (C) tttttattcaagccacagca	4067
ABCB11	72	intron 18 + (5882-5883)	tgcgtattccctcagttcag tttttattcaagccacagca	4068
ABCB11	73	intron 19 + 10022	tggctaagttaaaaaaaa A/Δ gagattcaactataatttgct	4069
ABCB11	74	intron 21 + 322	caagattcaactactgcccc C/Δ agggggtgggtgaacagggc	4070
ABCB11	75	intron 22 + 257	ctgttcaatttctctctgca T/C agtgattcattccacattcc	4071
ABCB11	76	intron 22 + 552	taattaatatcttctcttg G/C ggggtaaatgagggatggta	4072
ABCB11	77	intron 22 + 569	ttggggggtaaatgagggat G/A gtacataaacacttctcaa	4073
ABCB11	78	3' flanking + 243	aaacaccacagaatgacata G/A aactaaaggcggcaggaatc	4074
ABCC1	1	5' flanking - 1661	cattcacccttgggggaccc A/G ggccaataaaaaaatcacag	4075
ABCC1	2	intron 2 + 635	gatgtgcccctacctgacctt T/C ggctcggggcagacttgggg	4076
ABCC1	3	intron 2 + 4769	gggcaggagtggaactcagg G/Δ ttcttggtccaaatgggttc	4077
ABCC1	4	intron 2 + 10069	tatggagggttttcttctct T/C tctgtgagttttctctctga	4078
ABCC1	5	intron 2 + (11965-11984)	taaaagccaatcaaatcaac (T)18-20 aaacaagccacgcatgtgc	4079
ABCC1	6	intron 4 + 4302	cactgttaatccagcacct T/G gggaggccaaggcaagtggga	4080
ABCC1	7	intron 4 + 4394	gtctttactaaaaatacaaa A/C attagctaggtatggtggc	4081
ABCC1	8	intron 4 + 4524	ccactgcctccagcctggg T/C gacaagagtgaacactctgtc	4082
ABCC1	9	intron 6 + 9045	aggtccttaaaactaccctgc G/A ctccaagaatcagtgcttg	4083
ABCC1	10	intron 7 + (3059-3071)	agctctttgtatgcaccact (A)11-13 gccatttttctgcatgacc	4084

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ABCC1	11	intron 8 + (886-889)	ttctatgtaacagtaagaaa GAAA/Δ agcagctgccaatataacaa	4085
ABCC1	12	intron 11 + 198	tgaattgtcaggttgatgtt C/A tccttggtggcagtgccgttt	4086
ABCC1	13	intron 11 + 784	tgtggattgatccaggagat C/G aagcaatgttgctagctac	4087
ABCC1	14	intron 12 + 122	agccttgctgccagttgga C/G tcaactggggagccttaaca	4088
ABCC1	15	intron 12 + (3138-3148)	accccatctctattgaaaag (A)10-12 tcaatataaaaaacatttac	4089
ABCC1	16	intron 12 + 3227	tggatgattgtgagtgatggg C/T tgatcccagggtgcgccag	4090
ABCC1	17	intron 13 + 2060	tgtctattacaactattctct T/C ctgtgtcaggttgggcaatt	4091
ABCC1	18	intron 13 + (2061-2062)	ctcattacaactattctctc (C) ttggtcaggttgggcaatta	4092
ABCC1	18	intron 13 + (2061-2062)	ctcattacaactattctctc ttggtcaggttgggcaatta	4093
ABCC1	19	intron 13 + 11776	gccacctggggaggggcccaa G/A cgcgtctccagggtctgtca	4094
ABCC1	20	intron 14 + 179	aaagaagaacacacatttg A/T ctctctgacagagaactcgc	4095
ABCC1	21	intron 16 + 219	ctagcacagaggggtccctg G/T gattgttaagttacagcagcc	4096
ABCC1	22	intron 16 + 310	ggaagtcttactttcaggtg C/T ggtgtgatccagggtactctg	4097
ABCC1	23	intron 16 + 890	ctctccagagaaaaacatct G/T tagaaggcctgcatgaaaa	4098
ABCC1	24	intron 17 + 1171	aaacccaggttcaaaagac G/A tgggaaataatgcatactcc	4099
ABCC1	25	intron 17 + 1332	caactctttagtgtctgtgc A/G actgcacatttgtctcttgg	4100
ABCC1	26	exon 18 + 53	gattcagaatgattctctcc G/A agaaaaacactcttttggat	4101
ABCC1	27	intron 19 + (3373-3379)	ccaagctaggcagttctaca CA/Δ tgtgcaactcagtggtcg	4102
ABCC1	28	intron 20 + 2730	gcgtgaggtctgtctctcta C/T ccttcggtccaggtgacaa	4103
ABCC1	29	intron 20 + 2789	cttggtccagataggttcc G/C caaccccgctttcttctcc	4104
ABCC1	30	intron 20 + 2919	gatgcaaatgcccgcaccca C/T cctggcactcgtggttca	4105
ABCC1	31	intron 20 + 3024	cttaccataaactggggcac C/T cccctctctaccaccacc	4106
ABCC1	32	intron 20 + 9718	gtggctgcgtcagtgacga A/C caggagaagtgaaggctgag	4107
ABCC1	33	intron 20 + 9733	gacgaacaggagaagtgaag G/C ctgagggttataggaggtg	4108
ABCC1	34	intron 20 + (9895-9896)	gctgggtccagtgctcacac AT/Δ gtgtgtgaggacaggtgca	4109
ABCC1	35	intron 20 + 9952	ggtatcattcttctctctg G/A gtgtgtggtctattgtgtt	4110
ABCC1	36	intron 20 + 11120	gcggagtggtgggagtgatc A/G tcatcatcactgagttattg	4111
ABCC1	37	intron 20 + 11147	tcactgagttattgtgaacc G/A ggaagagatgatgtctgtg	4112
ABCC1	38	intron 20 + (11629-11631)	tattttgaatatcacttctt CTT/Δ tcaatgcttgggaatcacgg	4113
ABCC1	39	intron 20 + 11864	gagctccagataaccactgc C/T ccacaaccagacagcctgtt	4114
ABCC1	40	intron 21 + 3860	tggagagtgacatggtgggg G/Δ tgtggtgcatatattcatat	4115
ABCC1	41	intron 22 + 878	ttaaagatcgtctattttgg G/A caagtgttaataattctcca	4116
ABCC1	42	intron 22 + (4445-4446)	gtggggctggggctggggct (GGGGCT) ggggtcgtgcatgtgctaag	4117
ABCC1	42	intron 22 + (4445-4446)	gtggggctggggctggggct ggggtcgtgcatgtgctaag	4118
ABCC1	43	intron 23 + 62	gttgtggtcttgttctaatta T/C agaaatggatccttagatc	4119
ABCC1	44	intron 24 + 3171	aaccatgagggtcaccatat C/T tcaaacacagctgcacagct	4120
ABCC1	45	intron 24 + (3349-3368)	ctcttgaattggtgccagc (T)19-22 ccttgcatttaccataatg	4121
ABCC1	46	intron 24 + 3369	tttttttttttttttttttt T/C ccttgcatttaccataatg	4122
ABCC1	47	intron 24 + 3584	ccaaggattttttattttca A/G caacaaaggaaatgatttta	4123
ABCC1	48	exon 25 + 60	gagtcgggtcagcgcgtccccc G/A gtctattcccatttcaacga	4124
ABCC1	49	intron 27 + 4539	tcttttttactcactgcagt G/A tgaggaaacaaatcacattta	4125
ABCC1	50	intron 30 + (1708-1714)	gaccacaacactatctcctgg (T)6-7 ctccgggtcaaggtgcgggc	4126
ABCC1	51	exon 32 + 652	tggagaaaaatcattttctcc C/T ctgtggcagtggtccaggcc	4127
ABCC1	52	3' flanking + 158	ctgatgtctctccaggacac G/A aaaagaacccatctttgaat	4128
ABCC1	53	3' flanking + (187-199)	ccatctttgaatatcaatga (T)11-13 aagtactgttccggggagaa	4129
ABCC1	54	3' flanking + 2227	cattagaataggtagtatca G/A ccagccgggcatgtgtgctc	4130
ABCC2	1	exon1+77	catattaatagaagagtctt C/T gttccagacgcagtcagga	4131
ABCC2	2	intron1+413	gataagttctagaactggca A/C ctaatgatatggactagaag	4132
ABCC2	3	intron2+192	atcaaatggcctttgatttt T/G gcataagaatgggtactctt	4133
ABCC2	4	intron2+1020	agtgtgcgattacaagcct G/C agccacctgcacagcctctg	4134
ABCC2	5	intron2+3639	gtcatatccccacccccaaat C/A gacccaataggtacaatgaa	4135
ABCC2	6	intron2+3930	aaaactggcaggagaatttc A/G ctggagctgcatgcaggact	4136
ABCC2	7	intron2+3989	agttatgaaacgatttttc C/T gggactgggtgttctagtct	4137
ABCC2	8	intron2+4078	aggtttccagatgtgttccc T/C aggcattcctggtgttagga	4138
ABCC2	9	intron2+4171	cttattctttgttcagttgg C/T tttctaccacctcttagctt	4139
ABCC2	10	intron2+4257	gggtattggaagtctctgc G/A gctgctggaggctgctgtgt	4140
ABCC2	11	intron2+4436	ggactagtggagaattaga C/G ctttctgtaataaataagac	4141
ABCC2	12	intron2+5227	taccataatttatgtgtct A/G tatgacatgaatttcattgg	4142
ABCC2	13	intron2+5373	gttaaggatagtgaactca A/G gtgtgtctataggataaatt	4143
ABCC2	14	intron2+5538	ttaatgaggttaagcacatg G/T tcatatgtttaaaagccttt	4144
ABCC2	15	intron3+772	ggtataaggcaagatttttt A/T aaaaaatttaattgtcttaac	4145
ABCC2	16	intron3+1145	acatccttctccccctcagtc C/T tcggttagtggtcagttatt	4146
ABCC2	17	intron7+1658	ggactcttaccagcttagtt G/T cctggttttctaatctaaaa	4147
ABCC2	18	exon10+40	tggccaggaaggagtaacac G/A ttggagaacagtgaaacctg	4148
ABCC2	19	intron11+1672	aaacttttaagtcttaagac T/A ggaaggcctgtgtccttaggc	4149
ABCC2	20	intron12+148	ccctctcaccgccccatgcc A/G cttttctctcctttgtaccat	4150
ABCC2	21	intron13+180	catgagttttctgagcccca G/C tttatctaaactataaataga	4151
ABCC2	22	intron13+1497	gtgcagggtcccccctgatgc T/C atagccagtttctctttaga	4152
ABCC2	23	intron15+169	atgagctgaaagcaaggtt T/C tcagcccttccccctgataa	4153
ABCC2	24	intron15+949	ttccaggtgacacatttagt A/G cctaatttgggaaatgttaa	4154

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ABCC2	25	intron15+984	tgttaactctagtcacatccc A/C ttagtaagaagagggggtc	4155
ABCC2	26	intron16+4059	catcctgatgcacagttatt C/T aaatttaagctccattgtt	4156
ABCC2	27	intron19+10899	atgtatggagtatttatgga G/A taaagtattccatgctgtat	4157
ABCC2	28	exon22+51	caagcaataggattgttttc G/A atattcttcacatccttgc	4158
ABCC2	29	intron23+56	tatactgaggatctttctga C/T agggaggaattattatgtcc	4159
ABCC2	30	intron23+432	tggcagtagagcaggggtgag G/A aggtattattctgcagaggaa	4160
ABCC2	31	intron23+734	tgagccaactactgtactag G/A cactggggcactcaatgaat	4161
ABCC2	32	intron23+801	atggggcagaccacactcac T/G gatttttttagtgtatctgag	4162
ABCC2	33	intron26+154	ctggctccatcttttaccac T/C ggacgtattccttactcttc	4163
ABCC2	34	intron27+124	gggtccctaaagtttccctt C/G ctctaactcaaggacctaa	4164
ABCC2	35	exon28+52	cagattggcccgacaaaggc A/C agatccagtttaacaactac	4165
ABCC2	36	exon28+84	aacaactaccaagtgcggtg C/T cgacctgagctggatctggt	4166
ABCC2	37	exon28+129	agagggatcactgtgacat C/T ggtagcatggagaaggtagg	4167
ABCC2	38	intron29+154	ttccctaggatggacacgtc A/G ttccagaaactttgaaatgt	4168
ABCC2	39	intron30+91	gtgttagtgatgcctggca T/C agaattttcatccaggtctg	4169
ABCC2	40	intron31+170	gccaaaattttacatcacgc A/G aatgaaaacgaaccaaggtta	4170
ABCC2	41	3'flanking+371	gtgaattttttattataagct C/T gttctccttaaaactttatc	4171
ABCC3	1	5'flanking - 1064	tccttctgagcccaacaag C/T ggtgctgagttggcgtctgg	4172
ABCC3	2	5'flanking - (827-820)	ctggggcttcacctgtcctt (C) 7-8 aacctgatcaggtggaagc	4173
ABCC3	3	intron 1 + 1226	tatttgtacatatatgcctt T/G tgtgtgtgtacgcacacacg	4174
ABCC3	4	intron 1 + (1389-1399)	aaacttggggcgaatggaggt (A) 10-12 ctgtaaaaagggcatatttg	4175
ABCC3	5	intron 1 + 2070	gcgcacttctccttgatgt C/T gtgagctatcacacactcct	4176
ABCC3	6	intron 1 + 4477	gcctgtagtccccagacagg G/A aaatggctctgaaacactgg	4177
ABCC3	7	intron 1 + 6189	agtgaccatgaagtctgccca T/C gagggggcctctgccacgtg	4178
ABCC3	8	intron 2 + 268	ttgtatttttagtagagatg G/ggttttgccattttggcagg	4179
ABCC3	9	intron 2 + 376	tgtgcccagccagcattctg G/C ttttaatgaggccctctccc	4180
ABCC3	10	intron 2 + 446	ctcacctgacctgcttgggg C/T catgggaatctgacaactga	4181
ABCC3	11	intron 8 + 2323	gaggctgggtgtagagcgt C/G atcgatagggcgtgcagcag	4182
ABCC3	12	intron 12 + 85	ctcattggactctaccctga C/A accactctccacgtgctcag	4183
ABCC3	13	intron 19 + 1581	ttcttgttgccctttcaatc C/T cctctattttattttcatgc	4184
ABCC3	14	exon 22 + 180	aacacttccctgaggctggg C/T gtctatgctgcttttaggaat	4185
ABCC3	15	intron 30 + 1979	cctctgtctgttccatcctt C/G tctaccctcaccctccact	4186
ABCC3	16	intron 30 + 2340	atgcaccagccaggcctgaa A/C gaatgagtaagagttggagg	4187
ABCC3	17	3'flanking + (555-558)	ttttcttgagcaagccaaca AAGA/A gtttctttctgcaggtcag	4188
ABCC3	18	3'flanking + 1455	aacccccctatgattagaact G/A tagtgctgttttaggaagcca	4189
ABCC3	19	3'flanking + (1650-1659)	aattcacagtttaacaaagct (A) 9-11 tccttgtttataaattacaca	4190
ABCC4	1	5'flanking - 644	attcatctgggtcactactct C/T gagttaccggctttcttga	4191
ABCC4	2	exon 1 + 67	ggagcggagcccgcgccac C/T gccgcctgatcagcgagacc	4192
ABCC4	3	intron 1 + (864-865)	ctttgaccagctctcttccc C/T gtttcaatactttcacttc	4193
ABCC4	4	intron 1 + 21255	ggatggaaatgggtgagcaca A/G accttggcatttaaggaccg	4194
ABCC4	5	intron 1 + 21503	ctgttttctacccactgggg T/C cagcaaatcagccctttta	4195
ABCC4	6	intron 1 + 21900	tgatgctcaaagcaatacaa C/G tagaaaatataggaggtgg	4196
ABCC4	7	intron 1 + 22005	aagggggagtcatactccag C/T gtgcatttttagtttgctt	4197
ABCC4	8	intron 1 + (22256-22264)	tttgtgtgtgtattttgcgtc (T) 8-9 cctggaaggaagtgattggc	4198
ABCC4	9	intron 1 + 27784	ccagggaaactggtggcacac C/G ctgagctctgtaggtggct	4199
ABCC4	10	intron 1 + 27821	ggctaaagactcacaacctg A/T gggaaagggccaggaagaa	4200
ABCC4	11	intron 1 + 27837	cctgaggggaagggccagga A/G agaaaggaagccatggccta	4201
ABCC4	12	intron 1 + 27880	gggtgtttatttgggaccca C/T gccatccagggccagagag	4202
ABCC4	13	intron 1 + 40310	accaagcaggggaggtgaga A/T ttgtgcagactggggatatt	4203
ABCC4	14	intron 1 + 40372	ttgcttgaataaaaggatgc G/A agtcaactgtattgtgaagt	4204
ABCC4	15	intron 1 + 40413	ttctttcaaatccaattcct G/A actgatttcttgccttcca	4205
ABCC4	16	intron 1 + 40958	gaagtttaccgaaaaacaaa A/G caagaaactccccagtaaaa	4206
ABCC4	17	intron 1 + 50060	tgtggctatggggaacatga G/A gctcatagaactgaagact	4207
ABCC4	18	intron 2 + 181	gcctgggggaaactcctgtt G/T cctgtgctcctgtagaggtc	4208
ABCC4	19	intron 2 + 254	gaggctctgctccttagtg G/A aagtgttggtggaggag	4209
ABCC4	20	intron 2 + 290	aggaggttgctgctgttacc T/C gtgctactgatgggcttca	4210
ABCC4	21	intron 2 + 543	ttacgaagctttttctctat T/C gtagggtctgggataaagaa	4211
ABCC4	22	intron 3 + 557	ggccttgacactgggctggc G/A gtgggtccccagaggctgga	4212
ABCC4	23	intron 3 + 718	gtgtgtcttctctgtgtctg G/A agtggatgtgctggttgaag	4213
ABCC4	24	intron 3 + 801	acattccatgaaaaatcaaa G/A acagccagaagggcaataac	4214
ABCC4	25	intron 3 + 1022	aggggtggatgtgtgtgtt T/C tacaaaaggggtggctttaa	4215
ABCC4	26	intron 3 + 1471	tgtctgggtgtgtccagcgat A/G gtgtttccacatggccccga	4216
ABCC4	27	intron 3 + 1490	tagtgtttccacatggcccc G/A atcagtttcagtggaaaga	4217
ABCC4	28	intron 3 + (1833-1834)	ggggtgccagccacttgggg (G) tggggtctctaacccacaga	4218
ABCC4	28	intron 3 + (1833-1834)	ggggtgccagccacttgggg tggggtctctaacccacaga	4219
ABCC4	29	intron 3 + 1870	cagatgggtgactggactaca G/A tgagatttgggtgaagctttt	4220
ABCC4	30	intron 3 + 1927	gaagtagaggtctagaagc G/A tgaatttctctgagactttg	4221
ABCC4	31	intron 3 + 1970	gacagggcccaactctggtgc A/T agggcatggttaactttac	4222
ABCC4	32	intron 3 + 2039	gatcgaggggagctttaata T/C ggttacagttggtggagagc	4223
ABCC4	33	intron 3 + (2067-2068)	ttggtggagagctggtcttt (CTT) tagcggggtggttattgggc	4224

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ABCC4	33	intron 3 + (2067-2068)	ttggtggagagctggtcttt tagcggggtggttattgggc	4225
ABCC4	34	intron 3 + 3563	cattgactgatggtctgggc G/A gatgtcaagttccctggttt	4226
ABCC4	35	intron 3 + 3696	tgcttggcaaggatgaagac C/G ccagatgagtcactagtag	4227
ABCC4	36	intron 3 + 4093	aagtaatccttggatttttt T/C ttttcttttctcttagcag	4228
ABCC4	37	intron 3 + 4097	aatccttggatttttttttt T/Δ ctttctcttagcagtgaa	4229
ABCC4	38	intron 3 + 9724	aaaaaccagcattactcacc A/G atgagcccatttgcctgact	4230
ABCC4	39	intron 3 + 9988	aaaggcaaaagcactgagc G/A tctgctgatagcccagggtg	4231
ABCC4	40	intron 3 + 10952	gttaaaattgcattccctac A/G tcttgttcagaaggtaagcc	4232
ABCC4	41	intron 3 + 11125	gctcaatttctgtgtgttt A/G atttttgactccacactacc	4233
ABCC4	42	intron 3 + 11244	ccaagagcctggaatcctcc C/Δ aagctgtgttttttcccca	4234
ABCC4	43	intron 3 + 11916	gtcttgacaaaaa A/Δ ttttagctctacatgatggtg	4235
ABCC4	44	intron 3 + 12047	actatactccagcatgggtg A/G cagagcaaatatctctgaa	4236
ABCC4	45	exon 4 + 205	tgaggttacgagtagccatg T/G gccatattgattatcggaag	4237
ABCC4	46	intron 4 + (412-414)	ttatggaaatttttgtgtgt GT/Δ cattaaaaacctcacttaca	4238
ABCC4	47	intron 4 - (9757-9756)	tgacatctgtcatttttttt (T) cctgctgcacaaatctcttc	4239
ABCC4	47	intron 4 - (9757-9756)	tgacatctgtcatttttttt cctgctgcacaaatctcttc	4240
ABCC4	48	intron 4 - 6373	atgtttttgtctagatagta C/G agttttctgttaattctcaaa	4241
ABCC4	49	intron 4 - 6267	acttccaccattcacagtag T/C gttcttaaatggcatgggat	4242
ABCC4	50	intron 4 - 6096	agatccttccatttcttaggg T/C gtacaaatttcaaggctttt	4243
ABCC4	51	intron 4 - 6057	ttgctatgctagattgattt C/T ctccccaagattgtttaatt	4244
ABCC4	52	intron 4 - 5295	agttgtctggcttaccagtag A/G tgcttactaaatggtagctt	4245
ABCC4	53	intron 4 - 803	agcttcacctgtttcagccc C/T gcttccatgagcttccactg	4246
ABCC4	54	intron 4 - 736	attcagcagcctccacatcc C/T ccttctcctgacttctgtcc	4247
ABCC4	55	intron 4 - 728	gcctccacatctctctctc C/T gtacttctgctctagctagg	4248
ABCC4	56	intron 4 - 624	ccaccagtgctccctcagtt A/C gaactgtcccccagttctctg	4249
ABCC4	57	intron 4 - 470	ttgatactccatatttgtca C/T ttcccatgaacacattgaa	4250
ABCC4	58	intron 4 - 411	ggtagagagactaaggcccc G/A tbtgtttaaatattgttcac	4251
ABCC4	59	intron 4 - 323	tgttctctgacagcctctc C/T gttcttccctaatttggctc	4252
ABCC4	60	intron 4 - 246	gtccttttgtacttgggggc A/G tgtccaaattcattaaatga	4253
ABCC4	61	intron 4 - 199	agatttttcttctctctacc C/T ctgcttctgctctctgaca	4254
ABCC4	62	intron 5 + 73	ctttttattctttctggagg C/T aggggtcctactctgttcaca	4255
ABCC4	63	intron 5 + 403	aagggatcacgcctgtgtgc G/A caggctgtctcagaattct	4256
ABCC4	64	intron 5 + 937	ccagaatgggttcaactgtg G/C tgggtgtgtgtgtttctgct	4257
ABCC4	65	intron 6 + 150	ggctcagccaaagggggcctc C/T gtccttatgtcgaaggcaaa	4258
ABCC4	66	intron 6 + (380-381)	tgtgttagagctgttttccac (AT) gtgtatatatgtgtgttatt	4259
ABCC4	66	intron 6 + (380-381)	tgtgttagagctgttttccac gtgtatatatgtgtgttatt	4260
ABCC4	67	intron 7 + 894	tttgttgtgttggccaggga A/T ggtctcaaaactcctgggttc	4261
ABCC4	68	intron 8 + 82	tatttagcatcactatgttc C/G agtgtaatgacatttaactc	4262
ABCC4	69	intron 8 + 100	tcacagtgaatgacatttaa C/T tctctcataaccaaactgtg	4263
ABCC4	70	intron 8 + 5212	tcagggaattgtgttccaat A/T tgcagctagggaagaatcc	4264
ABCC4	71	intron 8 + 5444	gaaaccttaatttccctcca T/G gtacatagtttctgtggga	4265
ABCC4	72	intron 8 + 8969	tcaccctcctgagtgactag A/G gaaagttccagctagccctc	4266
ABCC4	73	intron 8 + 9106	ccagtgctcaataggtttac T/C gtgtgcatagttttttattt	4267
ABCC4	74	intron 8 + 9412	tgtttgttaagtgcaggatgg G/A ggacacatctctgccctgta	4268
ABCC4	75	intron 9 + 116	tggttgccttatttactgaa A/G ctatgttacaagatttctca	4269
ABCC4	76	intron 9 + 1384	cacggcaggaagctgcaccc T/C ggggctggagatgatgtctg	4270
ABCC4	77	intron 9 + 1459	agatttgggagcagaggggc A/G gggctctctctgagggtact	4271
ABCC4	78	intron 9 + 1632	agcagcactcctgccagcc C/A cactgctcctgctcctccct	4272
ABCC4	79	intron 9 + 3630	gtaaaatttttcattttgaag G/Δ ttatcttgcctcttattcc	4273
ABCC4	80	intron 9 + 3830	gggtgttccacccttcaggga C/T gccagattcattttgaagaa	4274
ABCC4	81	intron 9 + 3940	gagcatttaccaaagtgtgt C/T gtgcagaagaatagccactt	4275
ABCC4	82	intron 10 + 1504	gggcaaggctgcattgcagt G/A gcttattctgtctcagatg	4276
ABCC4	83	intron 11 + 1817	ttttaggaggttgagaacaa G/C atggcaaaatttgcctagttt	4277
ABCC4	84	intron 11 + 3342	actggaattattctggcttg T/C aggtacagagattgcctgtg	4278
ABCC4	85	intron 11 + 3377	catgtgtaatcaaacctgc T/C ggacagaaatggctcctgagc	4279
ABCC4	86	intron 11 + (3610-3625)	tectggccaccctccccgc (A)15-17 gtccatagaggaaaaatagg	4280
ABCC4	87	intron 11 + 3737	ataagttcatcgagctaaaa A/G tatatttgagataaaataat	4281
ABCC4	88	intron 11 + 6953	agagttagacaaagaaatg C/A caccttgatctgtaagagg	4282
ABCC4	89	intron 13 + 442	ctatgacaggttagaagtga G/C gtccttgggaccaacatagg	4283
ABCC4	90	intron 13 + 459	tgacgtccttgggaccaaca T/C agggctttcttgggaaggct	4284
ABCC4	91	intron 13 + 633	tgaacacttaaaaccacag G/A catgtaggcctggcttgctc	4285
ABCC4	92	intron 13 + 645	accacagggcatgtaggcct G/T gcttgcccttgaactagtt	4286
ABCC4	93	intron 13 + 3306	aatgttctcaacgagttaga A/C aattggattgaacaatatgc	4287
ABCC4	94	intron 14 + 252	taatttagaactttttgtt A/G cctcttccatgacttaattc	4288
ABCC4	95	intron 15 + 124	tggttctgtgtgtttcaggg C/T tctattccatgatattgta	4289
ABCC4	96	intron 15 + 1552	tttgacttctgctgttttc C/T ccacagctttgtcaacagag	4290
ABCC4	97	intron 16 + 157	cctactgggtttccatgtcc G/A ttacaaagacctgcgaaaaa	4291
ABCC4	98	intron 17 + 329	cccaattgtgtgttcatctt T/C aaaaaatgtatttatctaa	4292
ABCC4	99	exon 18 + 56	atggagagggaatgtaac G/A agaagctagatcttaactgg	4293
ABCC4	100	intron 19 + 7202	aattaaaaataatgtttttt T/Δ cacataacaatggttatatg	4294

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ABCC4	101	intron 19 + 7445	ttttggcataatttttaac T/C actagaatgttctgattcat	4295
ABCC4	102	intron 19 + 9018	tacgtgatggcctgaagaga A/G aaaccgtacattggttcttt	4296
ABCC4	103	intron 19 + 11388	aagagttcagagattttggg A/G gttggaggaaaaaatagcat	4297
ABCC4	104	intron 19 + 11646	cattatttttaatttttttt T/Δ cctcctgttgggtgcagaat	4298
ABCC4	105	intron 19 + 13517	gagaaacttacattattttt A/T aaaaatgctataactagtcc	4299
ABCC4	106	intron 19 + 21033	tgggagtgccctgggctagc G/A ctgaaacttcagggttttcag	4300
ABCC4	107	intron 19 + 21095	agacttttggaagaagcaga A/T ctgaaggtaagactgagtaa	4301
ABCC4	108	intron 19 + 21634	gtgctatttctgagcactca C/T ggccccattgggcatgggct	4302
ABCC4	109	intron 19 + 21715	tgttttgctcacccttaca C/T agcttgcctcactgctctc	4303
ABCC4	110	intron 19 + 23090	agcaacagacttgagactt G/A agcttctaaaagtttcatta	4304
ABCC4	111	intron 19 + 24297	cgaatgtgatgaatgtggga A/G cctttttgagatagcagcac	4305
ABCC4	112	intron 19 + 25947	gagttctaaattaatatgag C/A aaaactagaaacatttaaa	4306
ABCC4	113	intron 19 + 30193	acagatttgcaagagttctac A/C aaagtataatattctgtca	4307
ABCC4	114	intron 19 + 36938	aagccgagtcactctcttgg C/G tatcttctgtggactacttt	4308
ABCC4	115	intron 19 + 37322	gttccctagagggtgagccc C/T gcctcaccctggttaaccgc	4309
ABCC4	116	intron 19 + (38361-38362)	cgggggttagcttccctagct (T) gcggagggtttctgagaaaa	4310
ABCC4	116	intron 19 + (38361-38362)	cgggggttagcttccctagct gcggagggtttctgagaaaa	4311
ABCC4	117	intron 19 + 38746	taaaacatgtcgtgtaatta T/C gtaaaataaagataagtaaa	4312
ABCC4	118	intron 19 + 42343	tgttaaggcagaatcagcag C/T aacgattggatgttcccgga	4313
ABCC4	119	intron 19 + 44733	agcaggctgggggaaaaaaa A/Δ tacagagggttatcattatgt	4314
ABCC4	120	intron 20 + (405-419)	aaagggcaaaacttaggcac (T)13-15 ggaagaaccagggtggtt	4315
ABCC4	121	intron 20 + (637-648)	ctaagctcttaagctgtcttt (A)12-13 ccaacaatcctacagaaata	4316
ABCC4	122	intron 20 + 842	caagctggggcacttttttt T/Δ tcccaagtgtttatttttga	4317
ABCC4	123	intron 20 + 843	aagctggggcacttttttt T/C cccaagtgtttatttttga	4318
ABCC4	124	intron 20 + 1347	ggacctcgtatttttttt T/Δ cttttgcaaacatttttaaa	4319
ABCC4	125	intron 20 + (14553-14567)	tccctacacaccctcatct (A)13-15 tcagcagcttgactgagctt	4320
ABCC4	126	intron 20 + 15487	ggttttttccagtgtgatag C/T acatgtagaagcagtagctg	4321
ABCC4	127	intron 20 + 16161	gcgttgagtcagtgaagccga T/C agtgccgcttggtgcacgca	4322
ABCC4	128	intron 20 + 30891	acgtcccccactgttctatc C/T ttctcaagaagcaagcgttg	4323
ABCC4	129	intron 20 + 31180	ccttgacagtgctcctacat G/A tcatttgctattgttatcat	4324
ABCC4	130	intron 20 + 31283	gtgttaagctaaaaaaa A/Δ cctgttagacatttttgact	4325
ABCC4	131	intron 21 + 4204	ttgacctcctcctgaaaccc A/T gttggagataaaacagtggc	4326
ABCC4	132	intron 22 + 1026	gtgcccactcctcagtaaaa A/C tcttctgtagctcaactgag	4327
ABCC4	133	intron 23 + 377	gcctgggtgcatgaggttgag A/G aaaattctcagcaggagagt	4328
ABCC4	134	intron 25 + 4122	cccttttgattaaaattgca C/G/T tgggacaagaaccaccccca	4329
ABCC4	135	intron 25 + 6418	ttgcaactgaggaatggctg C/A agaaattaaagtggggtat	4330
ABCC4	136	intron 25 + (8765-8775)	tgcactcctgtgattttttt (T)5-11 aatcctgcgcctggatctc	4331
ABCC4	137	intron 26 + 67	tatgttttaattgtcttttact G/C ttattgtcttttttaattgg	4332
ABCC4	138	intron 26 + (101-109)	taattggatgaaggattgt (T)8-9 caccacatagacatgtttt	4333
ABCC4	139	intron 28 + 391	tagatatgatcttttttttt T/Δ aaatctctattgtgaagtag	4334
ABCC4	140	intron 29 + 2569	atcctcttttttctataacg C/T accactatctccacattaaa	4335
ABCC4	141	intron 29 + 7820	gaaaaacacacctgtgtcctg C/T ttggagggttcagcatattct	4336
ABCC4	142	intron 30 + 6269	tagatgttcttttgggcattg A/G aaagatgggttatctgttt	4337
ABCC4	143	intron 30 + 6320	gtttaataagggttaattag C/T tctactttgttaattacatt	4338
ABCC4	144	intron 30 + 6474	ccttgatgctatgtgttttca A/G tccacagatgttcataactt	4339
ABCC4	145	intron 30 + 6519	ttccactatgaattataatt C/T ctgccattttaacacacctt	4340
ABCC4	146	intron 30 + 6574	aatgggttttggctcctaaac C/T acactgggttcaaaactagac	4341
ABCC4	147	intron 30 + 6680	aggtgtgtctcctgtatatg A/G cgtgggttaggttttactctg	4342
ABCC4	148	intron 30 - 704	acgtttatcagaaaacctgt A/C tctcttctagtctagctaga	4343
ABCC4	149	intron 30 - 228	atctatgaatcagagtgtac A/G gaactaaaatggatctacag	4344
ABCC4	150	intron 30 - (14-5)	acattctttttatgcttacc (T)9-10 ctaggataacttcaaaagaa	4345
ABCC4	151	exon 31 + 146	agtcctgttccgaaggcattt G/T ccactagtttttggactatg	4346
ABCC4	152	3'flanking + 173	attttttaaggagtaggaca A/G agttgtcacagggtttttgtt	4347
ABCC4	153	3'flanking + (430-440)	tgtaccccttactccctatc (A)10-11 tggatacatgggttaaggat	4348
ABCC4	154	3'flanking + 556	aaaggtgcttggataactgaa G/A gacacaaatgtgaccgtcca	4349
ABCC4	155	3'flanking + 1144	cctccctgaaattgcataata T/C gtatatagacatgcacacgt	4350
ABCC4	156	3'flanking + 1426	tttaggtgactgaaattgca A/T cagtgtatcataatgaggttt	4351
ABCC5	1	intron 1 + 628	ttctgccacacagagcccg G/C gtggctttgtgtttatcaca	4352
ABCC5	2	intron 1 + 1834	tgagttccagtgacctctc C/T gtttcaaaactgctcaccgcc	4353
ABCC5	3	intron 1 + 3055	agaaagctctttaaaaaaaa A/Δ ccaacctttctattgtatcac	4354
ABCC5	4	intron 2 - 20280	gaatgcactgctactaagta T/C ttttgaagttcagacacca	4355
ABCC5	5	intron 2 - 20260	tttttgaagttcagacacc A/T tctagaatctgcttgaccgt	4356
ABCC5	6	intron 2 - 19204	tgaataaaagcattgcacac C/T ctaccacctttcttcgggac	4357
ABCC5	7	intron 2 - 19043	ttggctggcattaggctggc G/A ttacttcagctaataatgaag	4358
ABCC5	8	intron 2 - 18824	ttgaacactcttcaagatgc A/G tgcacagcactgaaccaggt	4359
ABCC5	9	intron 2 - 18807	tgcacgtcacagcactgaacc G/A agtggctggtgcagataaa	4360
ABCC5	10	intron 2 - (18735-18734)	atagaagcttaaaactcaca (A) cagctactctacatagatga	4361
ABCC5	10	intron 2 - (18735-18734)	atagaagcttaaaactcaca cagctactctacatagatga	4362
ABCC5	11	intron 2 - 15903	taccaagcctgctcatgga G/A gtagaagcaagactgacat	4363
ABCC5	12	intron 2 - 15901	ccaaagcctgctcatggagg C/T agaaagcaagactgacatgt	4364

Parameter	Value	Unit
Initial concentration of H_2O_2	0.01	M
Initial concentration of Fe^{2+}	0.001	M
Initial concentration of H^+	0.1	M
Temperature	25	$^{\circ}\text{C}$
Time interval	0.1	s
Time of sampling	0.1	s
Concentration of H_2O_2 at $t=0$	0.01	M
Concentration of Fe^{2+} at $t=0$	0.001	M
Concentration of H^+ at $t=0$	0.1	M
Concentration of H_2O_2 at $t=0.1$	0.009	M
Concentration of Fe^{2+} at $t=0.1$	0.0009	M
Concentration of H^+ at $t=0.1$	0.1	M
Concentration of H_2O_2 at $t=0.2$	0.008	M
Concentration of Fe^{2+} at $t=0.2$	0.0008	M
Concentration of H^+ at $t=0.2$	0.1	M
Concentration of H_2O_2 at $t=0.3$	0.007	M
Concentration of Fe^{2+} at $t=0.3$	0.0007	M
Concentration of H^+ at $t=0.3$	0.1	M
Concentration of H_2O_2 at $t=0.4$	0.006	M
Concentration of Fe^{2+} at $t=0.4$	0.0006	M
Concentration of H^+ at $t=0.4$	0.1	M
Concentration of H_2O_2 at $t=0.5$	0.005	M
Concentration of Fe^{2+} at $t=0.5$	0.0005	M
Concentration of H^+ at $t=0.5$	0.1	M
Concentration of H_2O_2 at $t=0.6$	0.004	M
Concentration of Fe^{2+} at $t=0.6$	0.0004	M
Concentration of H^+ at $t=0.6$	0.1	M
Concentration of H_2O_2 at $t=0.7$	0.003	M
Concentration of Fe^{2+} at $t=0.7$	0.0003	M
Concentration of H^+ at $t=0.7$	0.1	M
Concentration of H_2O_2 at $t=0.8$	0.002	M
Concentration of Fe^{2+} at $t=0.8$	0.0002	M
Concentration of H^+ at $t=0.8$	0.1	M
Concentration of H_2O_2 at $t=0.9$	0.001	M
Concentration of Fe^{2+} at $t=0.9$	0.0001	M
Concentration of H^+ at $t=0.9$	0.1	M
Concentration of H_2O_2 at $t=1.0$	0.000	M
Concentration of Fe^{2+} at $t=1.0$	0.0000	M
Concentration of H^+ at $t=1.0$	0.1	M
Concentration of H_2O_2 at $t=1.1$	0.000	M
Concentration of Fe^{2+} at $t=1.1$	0.0000	M
Concentration of H^+ at $t=1.1$	0.1	M
Concentration of H_2O_2 at $t=1.2$	0.000	M
Concentration of Fe^{2+} at $t=1.2$	0.0000	M
Concentration of H^+ at $t=1.2$	0.1	M
Concentration of H_2O_2 at $t=1.3$	0.000	M
Concentration of Fe^{2+} at $t=1.3$	0.0000	M
Concentration of H^+ at $t=1.3$	0.1	M
Concentration of H_2O_2 at $t=1.4$	0.000	M
Concentration of Fe^{2+} at $t=1.4$	0.0000	M
Concentration of H^+ at $t=1.4$	0.1	M
Concentration of H_2O_2 at $t=1.5$	0.000	M
Concentration of Fe^{2+} at $t=1.5$	0.0000	M
Concentration of H^+ at $t=1.5$	0.1	M
Concentration of H_2O_2 at $t=1.6$	0.000	M
Concentration of Fe^{2+} at $t=1.6$	0.0000	M
Concentration of H^+ at $t=1.6$	0.1	M
Concentration of H_2O_2 at $t=1.7$	0.000	M
Concentration of Fe^{2+} at $t=1.7$	0.0000	M
Concentration of H^+ at $t=1.7$	0.1	M
Concentration of H_2O_2 at $t=1.8$	0.000	M
Concentration of Fe^{2+} at $t=1.8$	0.0000	M
Concentration of H^+ at $t=1.8$	0.1	M
Concentration of H_2O_2 at $t=1.9$	0.000	M
Concentration of Fe^{2+} at $t=1.9$	0.0000	M
Concentration of H^+ at $t=1.9$	0.1	M
Concentration of H_2O_2 at $t=2.0$	0.000	M
Concentration of Fe^{2+} at $t=2.0$	0.0000	M
Concentration of H^+ at $t=2.0$	0.1	M
Concentration of H_2O_2 at $t=2.1$	0.000	M
Concentration of Fe^{2+} at $t=2.1$	0.0000	M
Concentration of H^+ at $t=2.1$	0.1	M
Concentration of H_2O_2 at $t=2.2$	0.000	M
Concentration of Fe^{2+} at $t=2.2$	0.0000	

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Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ABCC7	16	intron 3 + 13704	tttttccaaataaaaaaaaa A/Δ tcagggtgatctgtataatg	4433
ABCC7	17	intron 3 + 13758	tattaaagaacatgatgctt A/G aaacagattagggaaaacta	4434
ABCC7	18	intron 4 + 240	ctctgtttagtattttttt T/Δ ctccatcatgttatcatt	4435
ABCC7	19	intron 4 + 376	ttatgttcagcaagaagagt A/G taatatatgattgttaatga	4436
ABCC7	20	intron 4 + 586	tgccagacaaagagaccaa T/C tgccgagcatcatttaggt	4437
ABCC7	21	intron 4 + 1089	tttcaatctgaacattttac G/A taagtgaagactttgttaga	4438
ABCC7	22	intron 4 + 1615	aaagttaggttggtattgtat C/T tgtcttctcttctcaatgtt	4439
ABCC7	23	intron 4 + 1946	aatacaaaacaaacttgagct T/C tgccataacttttcaagaat	4440
ABCC7	24	intron 6 + 783	tatctaaagttttggagctaa A/G tagcactttgtttgaatccc	4441
ABCC7	25	intron 6 + (1104-1131)	gattgattgattgattgatt (GATT) 6-7 tacagagatcagagagctgc	4442
ABCC7	26	intron 7 + (731-732)	gtagcaatgagaccattttt (T) cttcagttgagctccatgtt	4443
ABCC7	26	intron 7 + (731-732)	gtagcaatgagaccattttt cttcagttgagctccatgtt	4444
ABCC7	27	intron 7 + 1434	gaatgtttggttgtaacctg T/C ataactctgcatgaaattgt	4445
ABCC7	28	intron 8 + 752	catgctctctctcagctcc A/G ttcttctattatcaccta	4446
ABCC7	29	intron 8 + 1109	tatggccaagacttcagtat G/A cgtgagctaatctctctt	4447
ABCC7	30	intron 8 + 1312	atgaagacattcattttttt T/Δ ctccgtccaatgttggttaga	4448
ABCC7	31	intron 9 + (6521-6522)	gtgtgtgtgtgtgtgtgtgt (GT) ttttttaacagggttttggg	4449
ABCC7	31	intron 9 + (6521-6522)	gtgtgtgtgtgtgtgtgtgt ttttttaacagggttttggg	4450
ABCC7	32	intron 10 + 2119	gaacactttatagttttttt T/G ggacaaaagactctagctaaa	4451
ABCC7	33	intron 11 + 3867	tttttcttcaagaatttaga A/Δ gaggggagaaattgttttaa	4452
ABCC7	34	intron 11 + 11844	tgaatcaaaatcatctaaaa A/Δ gctttcagaacacagacttt	4453
ABCC7	35	intron 11 + 12144	atattaaacagagttacata T/C acttacaactctacacat	4454
ABCC7	36	intron 11 + 20975	gtgtgtagtagtaaatgccag G/A gtaaatcacatagcatctaa	4455
ABCC7	37	intron 11 + 27057	atggaagagaaagtttagta G/A aggggaggaaggaggaggtg	4456
ABCC7	38	intron 11 + 27131	gagagagactttttttttt T/Δ aaggcgagagtttactacct	4457
ABCC7	39	intron 13 + 152	gtattaaactcaaatctgac T/A gccctactggggccaggattc	4458
ABCC7	40	intron 13 + 287	tttgtagtactcattgacctg T/C gatataattacttttaatta	4459
ABCC7	41	intron 15 + (85-86)	atacatatatatgcacacac AT/Δ aaatatgtatatatacacat	4460
ABCC7	42	intron 15 + 106	taaatatgtatatatacac T/A gtatacatgtataagtatgc	4461
ABCC7	43	intron 15 + 3341	ggaagtataaaatttgaat A/C actgagaccacaaacttaca	4462
ABCC7	44	intron 15 + 5556	tgctattgactaatagtaat A/T attttaggcgagctttatga	4463
ABCC7	45	intron 15 + 5919	tggttagttctatgtgggaac C/A gtgagggaataattttatat	4464
ABCC7	46	intron 17 + 2479	caaaaagggtatggaagtac A/C ggagaaggagaccctatgt	4465
ABCC7	47	intron 18 - 81	aagtatgcaaaaaaa A/Δ gaaataaacactgcacacac	4466
ABCC7	48	intron 19 + 751	cattaataaaaataacaaatc A/G tatctattcaagaatggca	4467
ABCC7	49	intron 19 + 820	tgacatttgtgatattgatta T/C tctaatttagtctttttcag	4468
ABCC7	50	intron 21 + 1532	ttacctttaactttttttt T/Δ agtttgatcagctctcttta	4469
ABCC7	51	intron 21 + 1607	atgcttttggagttgggtct C/T ataatgtatagaaatgttt	4470
ABCC7	52	intron 21 + 12160	atgtggaacaatcatgacta T/C atgccttttactttctctat	4471
ABCC7	53	intron 22 + (130-131)	agaatcaatattaaacacac AT/Δ gttttattatattggagtcac	4472
ABCC7	54	intron 23 + 1837	ctgtctcaagttttaaag A/Δ aaaaaaaaggaagaggaa	4473
ABCC7	55	intron 24 + (7100-7112)	cccttacaacactcttagaca (T) 12-14 agtttaacatgtttacaaaac	4474
ABCC7	56	intron 25 + 237	actcttcccccttgtcaaca C/T atgatgaagcttttaatac	4475
ABCC7	57	exon 27 + 115	gggtgaagctctttcccccac C/T ggaactcaagcaagtgcag	4476
ABCC7	58	exon 27 + 334	ggatgaattaaagttttttt T/Δ aaaaaagaaacatttggtaa	4477
ABCC8	1	5'flanking - 1099	aaaggggctgaaggggtctt T/C cttttgtgttccctgactg	4478
ABCC8	2	5'flanking - (424-422)	caccccaccaccaccaccac CAC/Δ aaggtaacgtttctgccccac	4479
ABCC8	3	intron 1 + 1212	agcctgggcaacatagtgag A/G cccccccgcccctttctaca	4480
ABCC8	4	intron 2 + 1003	aggaggactgtgaatcccag C/A ctgcatgtttgggtcgatt	4481
ABCC8	5	intron 2 + 1253	catctcactaaggaagaatc C/T agtaaccagcaaggatgaga	4482
ABCC8	6	intron 2 + 1382	cccagactgcactcctgcag T/C gctgcctggctcctgtagtt	4483
ABCC8	7	intron 2 + 2371	tttcagagctgtctggaaat T/A tagggggcaggtgggagggg	4484
ABCC8	8	intron 3 + 1957	ccctaccctagcccagggg C/T ccccatatgagtatgaatgg	4485
ABCC8	9	intron 3 + (2088-2089)	agagaacccttcattaacca (CCA) gggcgtggctgaccagtgtc	4486
ABCC8	9	intron 3 + (2088-2089)	agagaacccttcattaacca gggcgtggctgaccagtgtc	4487
ABCC8	10	intron 3 + 2204	taaagcacaagttatcacc C/G tggatggattgtcttttc	4488
ABCC8	11	intron 3 + 2286	ttatctccccctgaaaggac A/G ctccacagagccagaaatc	4489
ABCC8	12	intron 3 + 2312	cagagccagaaattctagaa C/G agggaaaagtggaggggag	4490
ABCC8	13	intron 3 + 2356	ctgtgaactgcaggagacaga A/G ggaatgggtattggagaa	4491
ABCC8	14	intron 3 + 2359	tgaactgcaggacagaaagg A/C aatgggtattgggagaatgg	4492
ABCC8	15	intron 3 + 2370	gacagaaggaaatgggtatt G/A ggagaatggccagccctcca	4493
ABCC8	16	intron 3 + 2382	tgggtattgggagaatggcc A/G gccctccaaggggctgatgt	4494
ABCC8	17	intron 3 + 4910	ggggacagccttcagctgtg G/A aattctccagctcctagaga	4495
ABCC8	18	intron 3 + 4969	cattattccagctcctgaggg A/G tgagagcagaaaggccagtc	4496
ABCC8	19	intron 3 + 5003	cagatgtcttctgcccctcat C/G ctaagtctcctcctgagga	4497
ABCC8	20	intron 3 + 5019	ccatcctaatgtcctcctgc A/C gggacccaaggtggatggca	4498
ABCC8	21	intron 4 + 14	gggtgagggtaagcaggccac C/T tgggccaaggtggggtggga	4499
ABCC8	22	intron 4 + 187	agacactgcacttgcgccac G/A tgtgctctacccaggggtcc	4500
ABCC8	23	intron 4 + 204	cacgtgtgtcttaccacagg G/C tcccagaggagaggggggt	4501
ABCC8	24	intron 4 + 254	gttcgctgaggttggcggat G/A actttccgtagaaaggggaag	4502

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ABCC8	25	intron 4 + 357	tgtattcatatcgtcacgct G/C gtaaatgaatgagtaagtgt	4503
ABCC8	26	intron 5 + 92	ggcattaggtcaaaatcctg G/A tgggacaaaaggggaaactg	4504
ABCC8	27	intron 6 + 4205	tctgtagaagatcacatgggg G/A catgaagatcattggcttga	4505
ABCC8	28	intron 6 + 5519	gattccccgggaatgtttaa A/C aggaccgggtcttccctaaac	4506
ABCC8	29	intron 6 + 5575	tctgaccagtagcagccag G/C ggggcaagtttccatcccc	4507
ABCC8	30	intron 6 + 6587	gttgccatctgagatcttgc C/T ggaagtacacaagagaccct	4508
ABCC8	31	intron 6 + 6747	ttccactggcctttttctgct C/T agtaattgctacattacagg	4509
ABCC8	32	intron 9 + 191	gaggaagctgcctcccggtg A/G ggacaggaagcgggcatggc	4510
ABCC8	33	intron 10 + 1963	cccaggatcccaacctccct T/G tgtccagctagaccatgggt	4511
ABCC8	34	intron 10 + 2724	cctgggacatgttttcttat A/G taaacagcatcaaaagatgt	4512
ABCC8	35	intron 10 + 2938	gcccgccaggaactcctcac G/C tgtccaagtccataggag	4513
ABCC8	36	intron 10 + 3094	tcggagtagtgtttttttt T/Δ cctccggttagtcagcagt	4514
ABCC8	37	intron 10 + 3368	tctgtctcatatgcggcacc A/G tcagacttctggcgaggcaa	4515
ABCC8	38	intron 10 + 8897	ggtattgattaaaagcctca C/T gggcagagaaattcgccatc	4516
ABCC8	39	intron 11 + 308	tgtgtattgtagaagtgtg G/A gaaatccagaacagaaagct	4517
ABCC8	40	intron 11 + 1171	gccctctcatttcccttcca G/A tgctgagcgtttccagtgtg	4518
ABCC8	41	exon 12 + 7	gcctctgtccacagacttcc G/A tgggccacgtcagcttcttc	4519
ABCC8	42	intron 12 + 356	accaagaatgagggccatccc G/T tccccacgtggctgccccat	4520
ABCC8	43	intron 12 + 934	tggttccaagatggaaatgg G/T gcataactcagcaaaattat	4521
ABCC8	44	intron 12 + 1370	gggagggaggctggacaggg C/G atgaaggcagagcctgggtg	4522
ABCC8	45	intron 15 + 412	ggaggtgggacccaggtagg C/T gtttcttgggaccacaagga	4523
ABCC8	46	intron 15 + 688	actccccgggcccactcac A/G tctgccaccttccctccctg	4524
ABCC8	47	intron 16 + 4464	actcatccaagtattgtatc G/A agaagagaggttaggtactgg	4525
ABCC8	48	intron 16 + 4574	ttgaagactcttaagtgttt T/C tgggtcactcatttcgcaaa	4526
ABCC8	49	intron 16 + 5011	agctaaaagcaaaacagcct C/T tgacctggcaagcattccca	4527
ABCC8	50	intron 16 + 7608	tgtcctacttttcttttgac C/G cttataacttctcgtacttcg	4528
ABCC8	51	intron 16 + 7730	ccagctcctagtgggctgga G/A ggaaggacatcggttgggg	4529
ABCC8	52	intron 16 + 8369	ttgcaaaactgagttagggcc T/C ggagagccttactgtgtgctg	4530
ABCC8	53	intron 16 + 9708	tgcaacttgcgcctacttat T/G ccagaccctaagtattgggtc	4531
ABCC8	54	intron 17 + 651	tatagattaatgagggtctg A/G gtcctcctcaaaaccttccctc	4532
ABCC8	55	intron 17 + 692	cccttacctctccaaaaaac A/G cttgagataaccttagagggtg	4533
ABCC8	56	intron 17 + 1541	ctcaggatcttctcggagga C/T atgtgtcactcccatgagag	4534
ABCC8	57	intron 18 + 580	actaagcagatttctaccaa C/T tgcacctccccatccccctg	4535
ABCC8	58	intron 18 + 658	gaacaagccctcagagaatgc C/T ttccgcacccccactcccg	4536
ABCC8	59	intron 18 + 660	acaagccctcagagaatgcct T/C ccgcacccccactccccccg	4537
ABCC8	60	intron 19 + 93	gcccttccatcgatcaccca T/C acccagccatctcactcccc	4538
ABCC8	61	intron 19 + 123	tctcactccccagggtgetta T/C ctgcactccagcctctccat	4539
ABCC8	62	intron 19 + 219	cataggggagagggcaggaa C/T ggaggggaaggagagagccc	4540
ABCC8	63	intron 19 + 845	tagtatttaacctgcccaaa C/T gctgtgtgaagtgtgctgact	4541
ABCC8	64	intron 20 + 338	ttccctccacaagcttagac A/G aacaggattctcctgtgact	4542
ABCC8	65	exon 21 + 10	tttgggtgacagggcatcaac C/T tgtctggttggtcaacgccag	4543
ABCC8	66	intron 21 + 192	caaggatagcacaaatgacc C/Δ attgcagacttcagatggag	4544
ABCC8	67	intron 23 + 17	gaagggtgggtatatccaggg A/G tggccaagcagccaccctcg	4545
ABCC8	68	intron 23 + 67	gttctgtcagaacctgaact C/T ataaaggcttctcctgctcctt	4546
ABCC8	69	intron 26 + 268	gtgagcgtctgcacatccaa G/C taaagattgttttctctccc	4547
ABCC8	70	intron 26 + 308	cgataagtgggtgtaatttg C/T ccatccccaccatgagttc	4548
ABCC8	71	intron 26 + 348	cagctcctgcctccccctc A/G ctctctctcctcagccagc	4549
ABCC8	72	intron 26 + 807	gacagctgctgagtcaggcc G/A agccggcagctgagaaagcc	4550
ABCC8	73	intron 26 + 834	cagctgagaaagcgccgagc G/C gtcagatgggcttgagaaac	4551
ABCC8	74	intron 28 + (118-121)	cctccaaaaataaaaaaa AAAA/Δ cagaatgaaggaaatagaa	4552
ABCC8	75	intron 28 + 1348	tggggtaagcggaagacggg G/A ttgaacgctttgagtttgggt	4553
ABCC8	76	intron 29 + 1253	ctcttagggatcttctctaa G/T taaagaagagcagagcaaaag	4554
ABCC8	77	intron 29 + 1589	cagatcccagcttctcgttaa A/G cagcctcagatcaggccaaa	4555
ABCC8	78	intron 29 + 2322	gcgcctcacactcctataac G/A cgcacatgcctgatgcaca	4556
ABCC8	79	intron 29 + 2348	atgcctctgatgcacacat T/C ttcaacacgcacttactcta	4557
ABCC8	80	intron 29 + 2418	agacacgtcacctccacaca C/T gtctccacctgggggtgtg	4558
ABCC8	81	intron 29 + 2494	tcagtcctccctcagacacatg C/A cctctctccacgcagagaca	4559
ABCC8	82	intron 29 + 2735	gcggccaaggagagtgtatga C/T ggcagccaggttgatcaga	4560
ABCC8	83	intron 30 + 386	gtccttggggctccagcctt C/T gcagccttgtgtgtgtctg	4561
ABCC8	84	intron 33 + 93	ggcttcgcagtcacctctgtg G/T cctccagggccgaggcctc	4562
ABCC8	85	intron 33 + 358	agggacctgggggacagac C/T gaggccaccttgtatttag	4563
ABCC8	86	intron 38 + 54	cccagggacaggaactggcct G/C ttgtggcgtcatcagtga	4564
ABCC8	87	intron 38 + 466	aggacattctggccacatgc C/Δ tcactctcctctccaagcc	4565
ABCC8	88	intron 38 + 529	tggcccccccggggtgggt A/G ttccccactcctgacccgc	4566
ABCC9	1	intron 3 + 38	tgtgtttctccttaagag C/A tatttgtttttcccccaaa	4567
ABCC9	2	intron 3 + 305	gctggccttctggttgcag T/A agttgtattttaagaatcag	4568
ABCC9	3	intron 3 + 320	tgcagaagttgtattttaag A/G atcagagctcttgtgaggag	4569
ABCC9	4	intron 3 + 631	ttctgtggaaatcagaggct G/C tctaaaattctctaaattt	4570
ABCC9	5	intron 3 + 8644	tggacgcactcaacatttcc A/G agttattactcctcaactc	4571
ABCC9	6	intron 4 + 757	aggatatcatgaacaactga A/C tcttagtaaaaaactatctt	4572

One example of information generated using SEQ ID Nos. 1-3360 and 3361-7669 and information in publicly available databases is provided in Figure 143. The first column in this figure shows that 3360 entries are made, corresponding to the first 3360 entries found in Table 1. The second column, entitled "GENE" provides a gene name abbreviation, while the next column provides a long gene name. The next columns show the chromosome (CHROM), a reference mRNA accession number (REF. MRNA), a locus link database accession number (L-LINK), an OMIM database accession number (OMIM_ID) which allows disease association information to be readily obtained, the exon count for the gene (EXONS), and the number of polymorphisms in the gene (NO GENE).

Creating an Oligonucleotide Probe or Oligonucleotide Primer

In some embodiments, an oligonucleotide used as a primer and/or probe in the detection method of the present invention serves as the template of the base sequences (Sequence No. 1 through 3360 and 3361 through 7669) shown in Table 1 if, for example, a SNP is to be detected. The primer/probe can be designed so it is synthesized as the base sequence itself or as a portion of the base sequence. In preferred embodiments, the SNP is included in the base sequence of the primer/probe (and denoted in capital letters in the base sequence column of Table 1). The primers/probes may also be complementary to the non-mutant sequence.

The SNP in the following example is designed so it is on the 3' or 5' end of the base sequence. It is designed to be within four bases of the 3' or 5' end, and ideally within two bases of the end. The SNP can also be in the center of the oligonucleotide base sequence. Here, "center" means the number of the bases from the SNP base to the 5' end is substantially equal to the number of bases from the SNP base to the 3' end. If there is an odd number of bases in the oligonucleotide, the central region should be essentially five bases in length, preferably three bases in length, and ideally one base in length. In a base sequence with 41 bases, for example, the central region should be bases 19 through 23, preferably bases 20 through 22, and ideally base 21. If there is an even number of bases, the central region should be four bases and ideally two bases. In a base sequence

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ABCD3	16	(intron 9 1493)	tcacctcttccataggctt A/G ggtgtggagaggagatagaa	4643
ABCD3	17	(intron 13 1534)	tctgttgagttggggatcct A/G tggaaacctcttctctc	4644
ABCD3	18	(intron 16 4310)	gaaaagtgaatgcgtgagtag G/T tttagccaggcttgatttaga	4645
ABCD3	19	(intron 20 273)	ttctaaaagttcagagaaac T/A ctgtagctcattattctctgg	4646
ABCD3	20	(intron 20 1664)	ctcaaaagaaaaaa A/C aaaaaacacatgatccataa	4647
ABCD3	21	(intron 20 6693)	cttaaggttgtgttttact C/T tgagcaattgatttccca	4648
ABCD3	22	(intron 21 7171)	atcataaacagagaaataat A/G tcttaaatgagctctgaaaa	4649
ABCD3	23	(intron 22 1220)	ctagaaatcaaaagcattta A/G aatatagccaagcctttatg	4650
ABCD3	24	(intron 22 1358)	agtagcaaaataatcatcac G/A ccagtgatcatgtgaaggag	4651
ABCD3	25	(intron 4 4448-4461)	taactttctgttagtttagc (T)11-14 aactgttttactttttagg	4652
ABCD3	26	(intron 5 268)	gttttttggcatttttttt T/Δ aaccttcagtcagggttttc	4653
ABCD3	27	(intron 5 891-902)	ttggtgtaaaacctgtagtg (T)10-13 aacaaatgcaaatatagtg	4654
ABCD3	28	(intron 7 1226-1227)	gggaatgggggtgtatcta (T) tacaactttccatgtaattt	4655
ABCD3	28	(intron 7 1226-1227)	gggaatgggggtgtatcta tacaactttccatgtaattt	4656
ABCD3	29	(intron 8 1129)	cagatttacttttttttt T/Δ aatcttgtaacttactagc	4657
ABCD3	30	(intron 13 1595-1596)	tgaacataataaagcacac (TA) gttatcattaatactttatg	4658
ABCD3	30	(intron 13 1595-1596)	tgaacataataaagcacac gttatcattaatactttatg	4659
ABCD3	31	(intron 16 7337-7351)	ttaattacttcacagactga (T)13-15 caggttcgatctggggctaa	4660
ABCD3	32	(intron 18 12)	gttcctcaggtgaagcctag C/Δ ttgagttatctttgatctaa	4661
ABCD3	33	(intron 20 1652-1670)	gcaagactctgtctcaaaag (A)17-20 cacatgatccataatagagg	4662
ABCD3	34	(intron 20 2262-2273)	ttaatccattttgttaaatc (T)11-13 accttaaatagcaactatc	4663
ABCD3	35	(3' untranslated region 2072-2079)	taaaataaagttgagcttag (T)8-9 aaaaaaaacaaagcaaca	4664
ABCD3	36	(3' untranslated region 2080-2091)	gttgagcttagttttttttt (A)10-11 caagcaacaaattaactag	4665
ABCD3	37	(3' untranslated region 3349-3368)	acttattttctgttcagatt (A)16-19 ctcatatctctatacaacc	4666
ABCD4	1	(intron 1 276)	tggcattctttttttgaaaa G/A aagaacctcaggtgcacaaa	4667
ABCD4	2	(intron 1 329)	cttctcagttcttgacaccc T/C gtgggcccaatgcaaggctcc	4668
ABCD4	3	(intron 3 171)	ttaagcacgttgatcttgct A/G ttggccacgtgggactgat	4669
ABCD4	4	(intron 3 449)	ctacccctcattcagtagg G/A gggctaccacctgtcactc	4670
ABCD4	5	(intron 5 273)	gacaggggctacctcagagag G/T aacaggagtcagggtgagg	4671
ABCD4	6	(intron 7 240)	tagtcttagtgccctagcgt G/A gggcctgaaattgtcaaatg	4672
ABCD4	7	(intron 7 267)	gaaattgtcaaatgaatgaa T/C gcctcactctcttgctggtg	4673
ABCD4	8	(coding region 910 (Ala 304 Thr))	tctatggagacctgagctccc G/A cagagcttagcacctgggtc	4674
ABCD4	9	(coding region 981 (Leu 327 Leu))	atcagctgcttcacccagct C/A atcgacctgtccacgacgct	4675
ABCD4	10	(coding region 1102 (Glu 367 Lys))	gcgagatcctggggcgagagc G/A agtggggcttgacacgtga	4676
ABCD4	11	(intron 13 191)	tggattggggccactactca T/C agcagctcctgaggcaggta	4677
ABCD4	12	(intron 13 262)	acgcgtatgtcaaacaccca A/G ggtcggattctggggccct	4678
ABCD4	13	(intron 17 848)	cctctgctcctctggcccat C/G cttctccctgaggcagggt	4679
ABCD4	14	(intron 17 946)	gtgggaggagaaagcagcggc G/A gcagagggcagggtttgat	4680
ABCD4	15	(intron 18 41)	ggcctgaggaggagaaagaa C/T ccaaaggctcagcctggcca	4681
ABCD4	16	(3' untranslated region 2)	gccacaggtctaggtttctgt G/A ggggacactgaatctccag	4682
ABCG1	1	(5' flanking region -386)	gcaataatcattggctagag G/A tattgtgatatgatgtcatt	4683
ABCG1	2	(intron 1 199)	caccaaatattggtgagctg C/T ctggatttgggagatgcagt	4684
ABCG1	3	(intron 1 291)	acttgggttcgggtgtgagg A/C tctctcactcgtttctgtg	4685
ABCG1	4	(intron 1 318)	actcggtttctgtgatgggtg T/A gtgcaggggagtcacaaagt	4686
ABCG1	5	(intron 1 468)	ggccccaacgggtttctaga T/C ccctccagagaagcctttgg	4687
ABCG1	6	(intron 2 434)	ctgggtacaggtttttgtcc G/A gttgtctctgtattgagtat	4688
ABCG1	7	(intron 3 1839)	ttaaaatgagttgtttttct C/G ctaaaagcctttaggagttg	4689
ABCG1	8	(intron 3 3076)	tttgctacttctctctgtctc C/T ggctctacttccctgggggt	4690
ABCG1	9	(intron 3 3352)	gttccttggaggaaacgtgg G/A gtacacagtggttccagtta	4691
ABCG1	10	(intron 3 8030)	acagtgagcacaaagcagc C/T gaagacacagcaggcaggtc	4692
ABCG1	11	(intron 3 8066)	aggtcaggtctgtgtgcaca T/C tggcaggctgc a/g tgcagacc	4693
ABCG1	12	(intron 3 8092)	ggctgc a/g tgcagaccagct C/T ggcccagggtggaagcaga	4694
ABCG1	13	(intron 3 8285)	ctggacatgtgactccctg C/T acccaccctcacaagcaca	4695
ABCG1	14	(intron 3 8860)	cagggtgataggaggtccaa T/C tggacacaggttcagtttgc	4696
ABCG1	15	(intron 4 2319)	gggggtgaacagaggcaga G/A gcctgggcatcttcactcag	4697
ABCG1	16	(intron 4 2557)	gaagggaagaagcagcagca A/G gaaagaagccctctggccct	4698
ABCG1	17	(intron 5 139)	tgaccacgggcacccctagag T/A ggcgcgcgtcccgatcgct	4699
ABCG1	18	(intron 5 177)	gctgccccctgccctccgcc C/A gggccacctggagcctcggg	4700
ABCG1	19	(intron 6 13)	cagttactgttaagtctgtt T/C ccaggggtgtgca g/a gaatct	4701
ABCG1	20	(intron 6 27)	gctgtt t/c ccaggggtgtgca G/A gaatctccctttctgtttt	4702
ABCG1	21	(intron 6 1191)	gctaagcagagttaggcccc G/A gctagtcttgaatgagaga	4703
ABCG1	22	(intron 6 1449)	atgctggagccctgagttc G/A gtgggcatacaaggggtggc	4704
ABCG1	23	(intron 6 2282)	ctcgcatcacgcagttttca C/T gatcctatttaattgggtgag	4705
ABCG1	24	(intron 6 3853)	cctgggcttcagcaggggcc T/C cacacctgcaatgggtg c/t ct	4706

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ABCG1	25	(intron 6 3871)	cc t/c cacacctgcaatgggtg C/T ctggggagaggggtgcagatg	4707
ABCG1	26	(intron 6 4175)	tccaaagcccagatttggtg T/C ttttggggctcttttggaaat	4708
ABCG1	27	(intron 7 4)	ctgggtggaggaagaaggtg G/A ggagggcggctgctttgtgt	4709
ABCG1	28	(intron 7 576)	agctcaggaggtgtctggaa C/T gccacacagtgaggagttt	4710
ABCG1	29	(intron 7 1426)	aattctccttctcaacttaa A/G gaaatattttatagaaaaat	4711
ABCG1	30	(intron 7 2342)	agagcctgcaatggggccgc G/A agggacctgccccatgactca	4712
ABCG1	31	(intron 7 2399)	gaggggttgacagacaggat A/G tgtctg c/g tgtgttccagctg	4713
ABCG1	32	(intron 7 2406)	tgacagacaggat a/g tgtctg C/G tgtgttccagctgctggttt	4714
ABCG1	33	(intron 7 2911)	ccctctctgtgcccactgtt G/C tcccaacaccagcctgttct	4715
ABCG1	34	(intron 7 4363)	tataatagattcctagcaga A/G aacataattgtgagaggaac	4716
ABCG1	35	(intron 7 4752)	gctttcagagccatttcaca C/T aaggggtctcattttattagg	4717
ABCG1	36	(intron 7 5026)	ccagggtctgtgggatttcag G/A ccaaaaggagcgtagcaag	4718
ABCG1	37	(intron 7 5532)	gggttaaatattccgggcag C/T gccaaagtcagattatctgta	4719
ABCG1	38	(intron 7 5681)	gctaaagtgcattggaaggca T/C catgaataaatcctttcagg	4720
ABCG1	39	(intron 7 9243)	gcctgagagcgctggcagta G/A gaagggtcgccagtgtggag	4721
ABCG1	40	(intron 7 11371)	gggtctcttgggagcccttt T/G tctctcccagcctgcgtct	4722
ABCG1	41	(intron 7 12420)	gggatttcgaatctcaacac T/C ctgagctctgtgctttcccc	4723
ABCG1	42	(intron 7 12985)	ctattggcagggtcgtgaaca T/C tgttcttggtatttgcataa	4724
ABCG1	43	(intron 7 20041)	acatggccggcttcccttct T/C cctc g/a gaatggcctggaatt	4725
ABCG1	44	(intron 7 20046)	gccggcttcccttct t/c cctc G/A gaatggcctggaattcgatc	4726
ABCG1	45	(intron 7 21058)	acaagacttagaatttgacc G/A tgattttaaaaactattctaa	4727
ABCG1	46	(intron 7 26189)	ttcttggatgtggccatgca C/T gggggcaagggtttgatgag	4728
ABCG1	47	(intron 7 27453)	atcatgtggtttgggggaaa G/C ctgggaccgccattggtaca	4729
ABCG1	48	(intron 7 29810)	attgtttctcctggttttgt T/C tgttgttgaatttccctttaa	4730
ABCG1	49	(intron 10 2116)	aaacagggcttgagctctcc G/A taaggacagagagaccttcc	4731
ABCG1	50	(intron 13 1196)	tgaaaagaaaatggatgagt G/A gaa a/c ccaaaagagagaaaaat	4732
ABCG1	51	(intron 13 1200)	aagaaaatggatgagt g/a gaa A/C ccaaaagagagaaaatgtgg	4733
ABCG1	52	(intron 13 2041)	aagcagaggcttttccaccc G/A gagactcaagaagctgctcc	4734
ABCG1	53	(intron 13 2490)	gtggtgaagttagagctgagc A/T caccggggagccctccatcc	4735
ABCG1	54	(intron 13 2822)	cagcaggctccgtgctgaag T/C cacagcaagccaggcccttg	4736
ABCG1	55	(intron 13 2850)	agccaggcccttggcctgcc G/A gagctggaagaccagaca	4737
ABCG1	56	(intron 13 2919)	gcctcccaggagtagctaca C/T gggaccgaaggcagatggc	4738
ABCG1	57	(intron 13 3506)	ggcagcctgggtgcccaga T/C cctccctggagcccccgcg	4739
ABCG1	58	(intron 13 3538)	cgccgcgcgggaagccccag G/A ggggctggagctaca a/g gtgg	4740
ABCG1	59	(intron 13 3554)	ccag g/a ggggctggagctaca A/G gtggccttgacaggtttttg	4741
ABCG1	60	(intron 13 3721)	ccagctcatgggcagggtg C/T ggagggaaggccaccacag	4742
ABCG1	61	(intron 13 3921)	gaagaccagcagtcgatgcc A/G gctgggaagagggtctctgcc	4743
ABCG1	62	(intron 13 3979)	accacaccagcctttccaga C/T agccttccagaagctgttct	4744
ABCG1	63	(intron 13 4291)	gagccgctggagtaggttcc G/A cttgctatggctcccagggg	4745
ABCG1	64	(intron 13 4968)	tattgactggacacettctc C/T gtatggggcactgggctagg	4746
ABCG1	65	(intron 16 672)	atcagtaacgggtcactaac G/A gatgtctgctgagtgggcag	4747
ABCG1	66	(intron 16 891)	tggcccaactgttgagggtgt G/A ggtgaccagaggggcctgga	4748
ABCG1	67	(intron 18 1616)	ctggaggagaagacaggata A/C agtctaagacgtg c/t tgtcac	4749
ABCG1	68	(intron 18 1630)	aggata a/c agtctaagacgtg C/T tgtcacagagttcagggtcc	4750
ABCG1	69	(intron 18 1674)	gcttccaaaggccgcatccg G/T gttgttctctgagc c/t gagga	4751
ABCG1	70	(intron 18 1689)	atccg g/t gttgttctctgagc C/T gaggacggctttgccaacgc	4752
ABCG1	71	(intron 19 446)	tgggtgacagtgaacacagc G/A gctgcttctccagaacttta	4753
ABCG1	72	(intron 22 243)	accgggagagccatggcagg A/C ccaagtgttctggacgttgc	4754
ABCG1	73	(3' flanking region 1257)	atgggggcccacagccctgcc T/C cagaagcagctttgtctcg	4755
ABCG1	74	(3' flanking region 1438)	gggggaagagcttgggaacc A/G tgagggtgttaggctgcaa	4756
ABCG1	75	(3' flanking region 1518)	tgaagggtgaactggagtag G/C tgaggattctgcagttgacg	4757
ABCG1	76	(intron 3 3754-3755)	ctccacctgcaacctccctg (G) cctccttgatttccctcatc	4758
ABCG1	76	(intron 3 3754-3755)	ctccacctgcaacctccctg cctccttgatttccctcatc	4759
ABCG1	77	(intron 3 7848-7854)	cagttttccagaatttggggg (A)6-7 tccataagctgtcatactt	4760
ABCG1	78	(intron 4 190-191)	tgtcgagagctccccttgcc (C) tggttgatcctcagggttct	4761
ABCG1	78	(intron 4 190-191)	tgtcgagagctccccttgcc tggttgatcctcagggttct	4762
ABCG1	79	(intron 4 198-206)	agetccccttgccctgggtga TCCTCAGGG/Δ ttctacttagaatgcoct	4763
ABCG1	80	(5' untranslated region (-713) - (-741))	cgacagctcaagcctgttccc (CGC)8-10 ccccggggcatggcctgtct	4764
ABCG1	81	(intron 6 376-387)	tcttgcttgagctcaagag (A)10-12 tagccagggtttctgcccag	4765
ABCG1	82	(intron 7 19944-19945)	ctgatgaggagggggggggg (CACCAGGCACGACACTCTGATGAGGAGGGGAGGGGG) caccaggcagcagactctga	4766
ABCG1	82	(intron 7 19944-19945)	ctgatgaggagggggggggg	4767
ABCG1	83	(intron 7 25136-25137)	catgaacttgcctgaccata (G) cctgtgaggagctagggt	4768
ABCG1	83	(intron 7 25136-25137)	catgaacttgcctgaccata cctgtgaggagctagggt	4769
ABCG2	1	(intron 1 152)	tcatttgaaagtgggtatgc G/A gttttaaaactgcagttcaa	4770
ABCG2	2	(intron 1 614)	agctagtcataataataac G/A ccagagttagtaaggaagaga	4771
ABCG2	3	(intron 1 10002)	cctcatgaatgggtatacatg T/A cccaacatatctctttgat	4772
ABCG2	4	(intron 1 10123)	acagtgttcccttgggtgc G/A tatacccaaatccctgcata	4773

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ABCG2	5	(intron 1 10768)	ataggaataattgagaacag G/A gtctgaagaactctgcagga	4774
ABCG2	6	(intron 1 10791)	ctgaagaactctgcaggaaa T/C g/a aaaatagttccctgctttt	4775
ABCG2	7	(intron 1 10792)	tgaagaactctgcaggaaa t/c G/A aaaatagttccctgctttta	4776
ABCG2	8	(intron 1 14183)	tcacttaaggctttgcaggg T/G gtctaggacacagaaagaga	4777
ABCG2	9	(intron 1 14934)	aaagtgtctcttaaaatttcc A/G tcttgagtcagtgagctatt	4778
ABCG2	10	(intron 1 14955)	tcttgagtcagtgagctatt G/T aaattcaagcaataagttat	4779
ABCG2	11	(intron 1 17251)	ctgttttgggaacagcaactc A/C atcataggcagagagaaagt	4780
ABCG2	12	(intron 1 17347)	atttcaaacctgtttcacaa G/A ttgttaagctcatcttaagg	4781
ABCG2	13	(intron 1 17626)	gaagggtcataacaacttcc T/G acataaagctctggagctata	4782
ABCG2	14	(intron 1 18369)	ctattgtctttctgtctgca G/T aaagataaaaactctccaga	4783
ABCG2	15	(coding region 34 (Val 12 Met))	atgtcgaagtttttatccca G/A tgtcacaaggaaacccaat	4784
ABCG2	16	(intron 2 36)	tgtaaaaagacagcttttta A/G tttacctacagtgaacctca	4785
ABCG2	17	(intron 2 4230)	caaccctaaattggagggcc C/T gggcggtggtgattgagaaag	4786
ABCG2	18	(intron 2 4518)	gttgacagacttttatagtg A/C gggacactgactgcacgca	4787
ABCG2	19	(intron 2 6278)	atgtatgtaccacgtcttca T/C attcttaaggatgacctta	4788
ABCG2	20	(intron 3 10)	ggcaaatctctgtgagata A/G gagagtataagtaagcggtt	4789
ABCG2	21	(coding region 421 (Gln 141 Lys))	tgacggtgagagaaaactta C/A agttctcagcagctcttcgg	4790
ABCG2	22	(intron 6 3203)	tcctattctgttttaataaa A/G gcattgaatttaggtttgct	4791
ABCG2	23	(intron 6 3287)	gtcaggtgaaactagagcaa A/G caatctaaaggcaagaatag	4792
ABCG2	24	(intron 9 5974)	tatactaataaatgtgtgt A/T taagtcttttatctctaattg	4793
ABCG2	25	(intron 10 1908)	gacgcttatgtgcagcctat G/T ttgatgtctggaaaggctga	4794
ABCG2	26	(intron 10 2094)	ccctgagggctgaggtatct G/A gattatttccagacttgcta	4795
ABCG2	27	(intron 11 20)	tgtgagtaggtctttgttct A/G ggaacggggctgtccagcag	4796
ABCG2	28	(intron 11 1447)	tgttcttcaaggaaagcccc C/T gtcaagaaggaaagaagc	4797
ABCG2	29	(intron 12 49)	atgtcttttagtcttgcctat G/T ggtgaagtcagttgcacctt	4798
ABCG2	30	(intron 12 1566)	tatgcagttacatggacaga C/T acaacattggagaccgaggg	4799
ABCG2	31	(intron 13 40)	gctctgataaggaaattgttt C/T ttctcttcatttcttctctgc	4800
ABCG2	32	(intron 13 1823)	ttactcaagcaggcctgact C/T ttagtatttgcctttttag	4801
ABCG2	33	(intron 14 497)	ctaataaaaacaaacagaa T/C gaaagattgtcactgtaaat	4802
ABCG2	34	(intron 14 815)	taactctttggaaacttctt A/G aaattttaaactgtttacct	4803
ABCG2	35	(intron 15 110)	ccaggggacactgaatttttc C/T gagctacgttttctcatcc	4804
ABCG2	36	(intron 15 566)	gccgcatagtcagtgtgtgt T/A gtttttaattaaacttgaa	4805
ABCG2	37	(intron 15 639)	aacaagaacacttgaataa G/A ttgagaaaaaaccccgttt	4806
ABCG2	38	(intron 15 1197)	tgagttagctgggattacagg C/T gccaccaccacacctggct	4807
ABCG2	39	(5' flanking region (-998)-(-995))	gttgggatggctacactcac TCAC/Δ aaagcctgatggcccgtttc	4808
ABCG2	40	(intron 13 405)	ctgctagtttattttttttt T/Δ aacatttttaattatgttt	4809
ABCG2	41	(intron 13 692-702)	tcaatatgtttctgcttacc (T)9-11 aatggttacttaaccta	4810
ABCG2	42	(intron 15 645-650)	aaacacttgaataaG/Attgag (A)7-8 ccccggttttcacataatgtt	4811
ABCG4	1	(intron 1 84)	ggcctgggtgtccatgttc G/A gaaagtcctgaccagtgagg	4812
ABCG4	2	(intron 2 77)	gaacacagaaggattctga A/G agggcattgacccccatcct	4813
ABCG4	3	(coding region 679 (Leu 227 Leu))	tgggtgtccctcatgaagtc C/T tggcacagggggccgtacc	4814
ABCG4	4	(intron 7 95)	ggcctcctaggggtagagat C/T tcaccgtcgctgctctccc	4815
ABCG4	5	(intron 7 158)	cttgcccttgggaagttagt G/A tgaatctaaactgagctctc	4816
ABCG4	6	(intron 8 106)	ccccagaggcattgcaacca A/G tgggtgctaggaagaaccta	4817
ABCG4	7	(intron 11 1120)	acgagataagtga t/c ggtcat A/G tggccaggaggagggggac	4818
ABCG4	8	(intron 11 1173)	gggggacagcttgaacaaga A/G tgtggaggcaggatggacac	4819
ABCG4	9	(3' untranslated region 2)	gagtgacaggcacatacatg A/C gaacaggccatctcagccct	4820
ABCG5	1	(intron 3 40)	ccctggcccccccgccccc C/A cgggggcttaggtacactg	4821
ABCG5	2	(intron 4 841)	gcttggaggcatcttgaatg C/T gctcatccaaactggactg	4822
ABCG5	3	(intron 4 1145)	gagcaaatccagccacagc G/A tgtaaaat c/a ctgataagtaa	4823
ABCG5	4	(intron 4 1154)	cagccacacagc g/a tgtaaaat C/A ctgataagtaattcagtg	4824
ABCG5	5	(intron 4 1690)	acagagatgagaaggaggct T/C gggaaatctaccctggctggt	4825
ABCG5	6	(intron 4 1806)	tcttttgtccagaatata T/C tatatctagtttatttatgc	4826
ABCG5	7	(intron 4 1878)	atttcagatatgtccattct C/T tgggtgggtgctaaagctacat	4827
ABCG5	8	(intron 4 2052)	gggtgtcttggaacaaaact C/T attaccatagagtatcttc	4828
ABCG5	9	(intron 4 2108)	tccccctggggtttctgcag A/T tagaggtaatcagtacaggg	4829
ABCG5	10	(intron 4 2230)	agcttctttagataaaatc G/A gtaagaatttttttttagtc	4830
ABCG5	11	(intron 4 2318)	ggagttacagggctttaagta G/C agcgaagagaaattggaagaa	4831
ABCG5	12	(intron 4 2367)	ttaaatgtggctgggggtta C/T aaattgggtccccattaaag	4832
ABCG5	13	(intron 4 2464)	gattatatgtctttgatgtg A/G actcacactgagattgtacc	4833
ABCG5	14	(intron 4 2586)	aaagcatttatgataataa G/A ttcaaaaacccaaacactta	4834
ABCG5	15	(intron 6 1318)	cagagacattcaaaagtgcat C/T gctaccctgtgatcacaca	4835
ABCG5	16	(intron 9 164)	caactattgagttaccaaca T/C gttaatatgaatgagctcac	4836
ABCG5	17	(intron 9 365)	gtaccgttagcttctctttg A/G agctgatttttaggacagcca	4837
ABCG5	18	(intron 10 64)	tcatggagctagtgggactc G/A tgcaggagagctccaggg	4838
ABCG5	19	(intron 10 2406)	tcaacaagcctgcttactgc G/A gttagtgtgaccattgtct	4839

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ABCF1	3	(intron 20 69)	tgactttaaccgaccacctc C/T ctctcttctcgggcagaaaa	4905
ABCF1	4	(intron 23 35)	agtgtgcctcctccctgct C/A catggggaccaagctgtagt	4906
ABCF1	5	(intron 7 342-354)	acagagcgagactccgtctc (A)10-14 gaaaaaaaaaaaaacattt	4907
ABCF1	6	(intron 7 356-369)	cgtctcaaaaaaaaaaaaag (A)13-15 catttcacagacctgtctt	4908
ABCF1	7	(3' untranslated region 2)	tcagccggcccgagagtg A/ Δ gctttcctccagaaagtct	4909
ABCF1	8	(3' flanking region 1067-1068)	attaatttgatcaattgtct (T) aatatgtcgtactctagatt	4910
ABCF1	8	(3' flanking region 1067-1068)	attaatttgatcaattgtct aatatgtcgtactctagatt	4911
OAT1	1	(5' untranslated region -1)	gcagctcggactcagctccc G/A gagcaaccagctgcggagg	4912
OAT1	2	(5' untranslated region -2)	gaaggcctcagcccccagcc A/G ctgggctgggctggcccaa	4913
OAT1	3	(intron 3 150)	caatagacaacacctttctc G/A ggctcatgcgcctgaccc	4914
OAT1	4	(intron 4 211)	ttctctggcttccccactc A/C gttctccagcctgcctgctc	4915
OAT1	5	(intron 5 33)	gagacttcccatgataacct C/T ccagggttccaccccaaac	4916
OAT1	6	(intron 6 168)	gaaccagatgcccccagct C/T gactcagtcctccatccac	4917
OAT1	7	(intron 1 58-71)	ggaagatggggcctttgtt (A)13-15 gtacatggagaaattaactg	4918
OAT1	8	(intron 3 1306-1319)	aataggttgaggaggagcag (A)12-15 tcaagagtgtggagggggca	4919
OAT2	1	(intron 4 842)	ttgacctccaaaagtgtttt G/A attacagggatgggcccattg	4920
OAT2	2	(intron 5 183)	ccacatccatcattcgagac A/C a/c actcgtctcagctgcccattg	4921
OAT2	3	(intron 5 184)	cacatccatcattcgagac a/c A/C actcgtctcagctgcccattg	4922
OAT2	4	(coding region 1269 (Ser423Ser))	actagactgctagtgtcctc C/T ggtgagcccagtcctcatagg	4923
OAT2	5	(3' untranslated region 17)	ataaatgtgtacatgagtg A/G tgaacacacatacataaggt	4924
OAT2	6	(3' flanking region 1386)	tgtagcagcccacatcgcca G/A tgttcacacctgagagagag	4925
OAT3	1	(5' flanking region -463)	ttcctgagaggcaaatccccc T/C tcccctactcgggaggtgcc	4926
OAT3	2	(5' untranslated region -1)	cctgcccacagctctggtc G/A tcttgcctccagtgccatgac	4927
OAT3	3	(coding region 153 (Pro51))	cctgtccaccactgtcgcgc G/A ccccaacaatgcctccacagg	4928
OAT3	4	(intron 2 177)	gcaccaagacccttggtctc T/C tccactcagagtcacagca	4929
OAT3	5	(intron 2 6201)	gtcctatctctctgtgtctt T/G tgcccagcagaggttctctc	4930
OAT3	6	(intron 3 79)	tctgtctccaccgtgcaccc G/C caaagaggcaagagctggg	4931
OAT3	7	(coding region 723 (Thr241Thr))	tggcggttggtgcagttaac T/A gtgtccattcccttcttctgt	4932
OAT3	8	(intron 5 524)	tcgaagtacaaaggaaagtt T/C aaagagaagcctgagcctgg	4933
OAT3	9	(intron 7 386)	gaccaatgggttttcagactc G/A aagacaaaaattatgtttat	4934
OAT3	10	(intron 9 81)	attgtcctgtcctctaccca G/A gggagccatcctttatgaac	4935
OAT3	11	(5' flanking region (-661)-(-660))	tacatttgggtccccaggggg (G) aagcggctgatcaggagaga	4936
OAT3	11	(5' flanking region (-661)-(-660))	tacatttgggtccccaggggg aagcggctgatcaggagaga	4937
OAT3	12	(intron 8 211-212)	tctgacttggaactgggcaaa AA/ Δ gtatggtggtatctgtagat	4938
OATP1	1	(5' flanking region -916)	acagagttagatgttcaataa G/A tatttgtgtatctgtgaga	4939
OATP1	2	(5' flanking region -843)	tagtgccagcagactatgcctt G/A atgtgtgtgtgtttgggatt	4940
OATP1	3	(5' flanking region -526)	aaatgtgtgcctgtatgtta T/C acatctgtacatatatttcc	4941
OATP1	4	(5' flanking region -172)	acaacacacactcaagtat G/A tgtgttattaaaagttagcta	4942
OATP1	5	(intron 1 206)	ttgattcaggcaagttagtc C/G taaatggctttagagagactt	4943
OATP1	6	(intron 1 454)	caacataacaataatttctc G/A taagaaaaatggccattttg	4944
OATP1	7	(intron 1 999)	gtttagcaaggttagatatt A/G atgtggatgttaagacaaa	4945
OATP1	8	(intron 1 1223)	ttgctagaagctagtaggac C/T agotttataaatcacagat	4946
OATP1	9	(intron 1 1326)	aactagtttaggcaaccatg T/C gtttttaggg g/a aaaagcaatg	4947
OATP1	10	(intron 1 1336)	gcaacccatg t/c gtttttaggg G/A aaaagcaatgaggtcatgat	4948
OATP1	11	(intron 1 1498)	atagtttgcctcttaagaata C/T actctgagaaggtttatagt	4949
OATP1	12	(intron 1 5041)	ttatgtctccgaggagttag C/T tctctaaatgcataaggaga	4950
OATP1	13	(intron 1 9532)	aaagactgggagcacttccc A/G atgacaaatactagactaga	4951
OATP1	14	(intron 2 961)	aaaaagttatatagaatat A/G agtgtcactcctttctagt	4952
OATP1	15	(intron 2 1110)	gtctactagtgttcaactcc T/C ttagatcttagcctgtatca	4953
OATP1	16	(intron 2 1419)	aaagcctaagaaggatgcag T/C gcaatagcctatgtgagaag	4954
OATP1	17	(intron 2 3339)	tatggtttgcaaaaaactta T/C tcgtatatattgttttttca	4955
OATP1	18	(intron 3 66)	caggaaatgaagtgtcactt T/C cctctctaggagcaatgctt	4956
OATP1	19	(intron 3 205)	tcagttttgtcaatttacac A/G atggggatttgggacctttt	4957
OATP1	20	(intron 3 6377)	aatgaatagactttgagtta C/T tggatttttagtggaataat	4958
OATP1	21	(intron 3 7238)	tgaatgtcacattttttaa G/A tttgtgttcccttatctcata	4959
OATP1	22	(intron 4 1016)	ttttattctggattcatgtt T/C gtggaaattgcagtagtcca	4960
OATP1	23	(intron 5 110)	tccacaatgatgtagtagt A/G tcttggcacagttggccttc	4961
OATP1	24	(intron 6 496)	agtgtctgaattataagcca A/G ttttatagtgtgttgggacc	4962
OATP1	25	(intron 7 1934)	aaagtgaaggaaattaaaa G/C tgagaacttgagcctgaatg	4963
OATP1	26	(intron 7 2140)	tagaatgtacaaatgaatc A/G gcattctctaggatgggacc	4964
OATP1	27	(intron 7 2365)	tgaatctctctttatcaact C/T gattttctccagactttac	4965
OATP1	28	(intron 8 88)	gcaaacctcctaagtgaagt G/C ttttaggatatatttttact	4966
OATP1	29	(intron 9 534)	tcataattttgtatttttaa G/A ttatctgggttttactgaaa	4967
OATP1	30	(intron 9 1286)	tattctctgagataaatca T/C tgaaggagtggctatgtggt	4968

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
OATP1	31	(intron 11 215)	ttcactcctattcctcgcta C/T tttcttctcttattttcttag	4969
OATP1	32	(intron 11 663)	ttcttctcttcttttgagctc T/A aaagttagagttcagttaatc	4970
OATP1	33	(intron 11 999)	atcatcactgcagtagagatt A/G gaattatctaaactttgtgat	4971
OATP1	34	(intron 11 16727)	ttttttttatttacaactt A/G tttacttttccaggtgtatga	4972
OATP1	35	(intron 12 48)	ctatcagaacaattattatta T/G tattattttttattacactt	4973
OATP1	36	(intron 12 686)	tatgttttgataaaactttgc C/A gtacaaaataagaaaattga	4974
OATP1	37	(intron 12 708)	tacaaaataagaaaattgaa A/G tattttccaaaataatcaagt	4975
OATP1	38	(intron 13 418)	tctctgggtctccaaaatcat A/G tattttctccctcttta c/a at	4976
OATP1	39	(intron 13 436)	at a/g tattttctccctcttta C/A attttgtctgaacaactcttc	4977
OATP1	40	(3' untranslated region 2	gtctttaagaaccttaaaaa C/A ctcttaactcaaaaataataa	4978
OATP1	41	(3' flanking region 57)	agtgaactaaagtttttctta C/A aaacaagtgtctgaatcaaa	4979
OATP1	42	(3' flanking region 572)	aatacactatggttattttat G/A tgtactataaatggagtgag	4980
OATP1	43	(3' flanking region 788)	atttctctaaatgatcagatg C/T atcatatgaaaaagaaagc	4981
OATP1	44	(3' flanking region 1356)	agggtgactgacataaatggg G/A gcagaggacataatgaggtt	4982
OATP1	45	(5' untranslated region (-189) - (-188))	attttctaactctgtattaaa (A) gcgttccaggtatttttcta	4983
OATP1	45	(5' untranslated region (-189) - (-188))	attttctaactctgtattaaa gcgttccaggtatttttcta	4984
OATP1	46	(intron 4 725-726)	tgatctttaaagcggggaa AA/Δ caggcaagtacgctatagtt	4985
OATP1	47	(intron 4 1082-1083)	attgagtcaggaaacccaaaa CA/Δ gtttcaaaaaatttgaaaaat	4986
OATP1	48	(intron 4 2301)	aatgtcatgtcttttttttt T/Δ aatgcagagtgtaaaaaagga	4987
OATP1	49	(intron 9 241-46)	attgtatgtgcatgtgggtg TGTGTG/Δ catgattgtctttgtgata	4988
OATP2	1	(5' flanking region -2574)	ggataaggcaaccctatgt A/G tcaactgctcaggagagggga	4989
OATP2	2	(5' flanking region -1723)	tctttcagacttcaaaagccc A/G tgatatttcatcagagctgt	4990
OATP2	3	(5' flanking region -1180)	tgcttatttaaacaggcataa T/G ctttgggtctcctgagccaga	4991
OATP2	4	(5' flanking region -811)	tatgtgcatatgtgtatata G/A gtaaaagtgtgtatatatgt	4992
OATP2	5	(intron 1 7188)	aatcatttgaaatttaagaa A/G aaaatatgttcagagaaaaa	4993
OATP2	6	(intron 1 7331)	gtgaaatgaggaaacaaagt T/C ccaccttttttctcctgaata	4994
OATP2	7	(intron 1 7391)	agagagatgtgaaatagat T/G tttctggggagtaggggaa	4995
OATP2	8	(intron 1 7886)	ttgttagtagaagaaaaatc G/A aagcctaaaactaaagggaag	4996
OATP2	9	(intron 1 7958)	ttgctattatataatttttt T/A a/t aaaaaagatttcttaatat	4997
OATP2	10	(intron 1 7959)	tgctattatataatttttt t/a A/T aaaaaagatttcttaatat	4998
OATP2	11	(intron 1 8036)	ggaaaaaatggggtgaaatt A/T atcaaaagggcagcttattac	4999
OATP2	12	(intron 1 9164)	acattatattctatataaaa G/T agtcagttgaagtaaaaagt	5000
OATP2	13	(intron 2 193)	tgattaagtatttctttggc G/A aaatttttgatgtcttaatat	5001
OATP2	14	(intron 2 1020)	ttgagtaaacatttaggccaa G/A tggcagtcataaggaaaaag	5002
OATP2	15	(intron 2 14865)	agagggaattaatcataagag G/T tttatttggctaaagtgaaca	5003
OATP2	16	(intron 2 14931)	gttagttaaataacagaaaa A/T tatcagaaatttttaaaaaat	5004
OATP2	17	(intron 2 15417)	ttctaaaaataagtaagctaa A/T tattctatattataactacta	5005
OATP2	18	(intron 2 20823)	ttgtataagagatacaaaaac A/C aattcctactaggggaaata	5006
OATP2	19	(intron 2 20852)	ctaggggaaataaagcttca G/C taaggaggtggcatttaagct	5007
OATP2	20	(intron 2 21360)	ttcaaaagctgtattttctca T/C tagtgctttttgtgaataaa	5008
OATP2	21	(intron 2 21467)	tatacacacaatacctgtcc A/G gaagatgtggtataagccaa	5009
OATP2	22	(intron 2 21621)	tatcaatacttatgaagaga A/G ctaactatttcaactaggga	5010
OATP2	23	(intron 2 22760)	ttccccacctcctgttggt C/G tctctttaaacttctccttg	5011
OATP2	24	(intron 2 23199)	cctatctgcacataacatta C/T aaacttatggcaattata a/g a	5012
OATP2	25	(intron 2 23218)	a c/t aaacttatggcaattata A/G aactcaatcacatattatact	5013
OATP2	26	(intron 2 23330)	gcccttggttctgttctct G/A tacctgctcaactacatag	5014
OATP2	27	(intron 2 23673)	ctggagacggtagctcaaac T/C gaggatgaaatagacattt	5015
OATP2	28	(intron 3 89)	ggttatcaactggggttaaat T/G tatctctcacaggcaatttg	5016
OATP2	29	(intron 3 224)	tgctaaatatcttataatgc A/G caaagaatgatgaactgaa	5017
OATP2	30	(intron 4 97)	ccctttaaattaggcagttac C/A ttttgagaagatacccca	5018
OATP2	31	(intron 4 568)	ttcatgatccaaattgtggc A/G acgtatttccaggcaacaa	5019
OATP2	32	(intron 4 599)	aggcaacaagatagaagaag A/G aaagaataagaagcaacaa	5020
OATP2	33	(intron 4 753)	aaaatagacattattccaag T/A taccaagttcccggttaaaa	5021
OATP2	34	(intron 4 781)	ttccccggttaaaaatcccaa G/C tataattactgtggaaggaa	5022
OATP2	35	(intron 4 1196)	aaggaccacaatctagatca G/T cattgctctaaatgccc	5023
OATP2	36	(intron 4 1229)	tatgccataatatgtgacac T/C tttgcaactgtgtattctac	5024
OATP2	37	(intron 4 1623)	catctagttagaaatggatta G/C attttatttttactacattt	5025
OATP2	38	(coding region 388 (Asn130Asp))	attctaaagaaactaatatc A/G attcatcagaaaaattcaaca	5026
OATP2	39	(coding region 452 (Asn151Ser))	taatcaaattttactctca A/G tagagcatcacctgagatag	5027
OATP2	40	(intron 5 165)	ttaatatcacagttcgccc A/T ttaacaacacaggttttaac	5028
OATP2	41	(intron 5 189)	acaacacaggttttaactac G/A c g/a ttttcaacttctatgcaa	5029
OATP2	42	(intron 5 191)	aaacacaggttttaactac g/a c G/A ttttcaacttctatgcaa	5030
OATP2	43	(intron 5 507)	atataactttgttttcttg C/T aaaaaggcaaaat a/g ttatatc	5031
OATP2	44	(intron 5 520)	ttcattg c/t aaaaaggcaaaat A/G ttatatcatttaagacttt	5032
OATP2	45	(intron 5 856)	agtcacataaatctaatag A/G ataaaaacacaaaaagaaa	5033
OATP2	46	(intron 5 1157)	acagataatttttacttggt T/C gtgcttttctgtatgatag	5034

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
OATP2	47	(intron 5 1226)	ccttgattgtaataatctcc A/C c a/c tgccaagagtggggccag	5035
OATP2	48	(intron 5 1228)	ttgattgtaataatctcc a/c c A/C tgccaagagtggggccaggt	5036
OATP2	49	(intron 5 1304)	actgttctcgtggaatgaa G/T aagtctcacaagatctgatg	5037
OATP2	50	(intron 5 1348)	ttataaatgagagtccct G/A caaagctctcttgctgccc	5038
OATP2	51	(intron 5 1407)	ttgctctctctctatcttcc G/A ccatgattgtgagggccccc	5039
OATP2	52	(coding region 521 (Val174Ala))	gtcatatcatgtggatatatg T/C gttcatgggtaatatgcttc	5040
OATP2	53	(coding region 571 (Leu191Leu))	gggagactcccatagtagca T/C tggggctttcttacattgat	5041
OATP2	54	(coding region 597 (Phe199Phe))	ctttcttacattgatgattt C/T gctaaagaaggacattcttc	5042
OATP2	55	(intron 7 33)	agaacaaggtaccatgataa C/T gtctttcttaagcacacatgc	5043
OATP2	56	(intron 7 267)	caaaataaccaaatgtaaaa T/A gtctcctcccaactgact	5044
OATP2	57	(intron 7 1260)	gtaactctcacatttctctgc A/G ttacacttggtaaaacttt	5045
OATP2	58	(intron 7 2273)	ttctcagtcctatctatcgc C/T gattatgacctttagttact	5046
OATP2	59	(intron 8 207)	gtggaagagaattaggtttg T/C acttttttagcagggaagaaac	5047
OATP2	60	(intron 8 546)	tcgggagaagtttctcccta T/C gtaattagagtaaatattt a/c t	5048
OATP2	61	(intron 8 565)	a t/c gtaattagagtaaatattt A/C ttttggttaattatctatcta	5049
OATP2	62	(intron 8 668)	taagtaatgtataattaggat G/T catcagcatttgacagtgcc	5050
OATP2	63	(intron 8 739)	tggaagaaccattgagagtca A/G taaacaaagagaatgacttg	5051
OATP2	64	(intron 9 112)	attttagtaatacaggataa G/C tataattttctgtattctt	5052
OATP2	65	(intron 9 266)	ttagaggtagtatctgtata A/G ttggatctttataatttagtg	5053
OATP2	66	(intron 9 305)	tgctaagatctgagacaaa C/G cttttgtaattataatcatt	5054
OATP2	67	(intron 11 10224)	tacactgtttccataaaaa T/C tctctatattattctctagt	5055
OATP2	68	(intron 11 10359)	attaatagattcaacgtgag G/C ttcccttaaaacttttagccta	5056
OATP2	69	(intron 11 10916)	cttatatagaaaagaatcca C/G aaaactattttaccttttat	5057
OATP2	70	(intron 11 10997)	aatatattagtttgaacaag T/C gagacttcactaaatataat	5058
OATP2	71	(intron 11 11018)	gagacttcactaaatataat G/A caatgtatttgcagcactgt	5059
OATP2	72	(intron 12 442)	aacattccaaaactttttaat C/T ga c/t t c/a acagcatgacttt	5060
OATP2	73	(intron 12 445)	attccaaaaactttttaat c/t ga C/T t c/a acagcatgactttta	5061
OATP2	74	(intron 12 447)	tccaaaaactttttaat c/t ga c/t t C/A acagcatgacttttata	5062
OATP2	75	(intron 12 907)	aatgaaaagaagctggcaga T/C tgaacatactgaatgagag	5063
OATP2	76	(intron 13 65)	tatatatatatatatata C/T acacacacatacatatatta	5064
OATP2	77	(intron 13 870)	aattctgagtatcttatttc G/A atgtatccaatctgtggcac	5065
OATP2	78	(intron 13 1935)	taaaaaaaagagctgc T/C ttacagcaattgagccaag	5066
OATP2	79	(intron 13 2261)	aacgaatctccaaattttt G/C aactttttttaaatacaaat	5067
OATP2	80	(intron 14 248)	tcaaggataataaccaactt G/A tcaaaaatcagagataatag	5068
OATP2	81	(intron 14 2463)	attgttttactaatatggaa C/G ctcttccaagacataatttt	5069
OATP2	82	(intron 14 2857)	tcacatgtatttctcaggac A/T cctggcaagatgcctctag	5070
OATP2	83	(intron 14 11458)	atctccagaggtcctgtgt C/T tccccaaagtcactgaccc	5071
OATP2	84	(3' untranslated region 22)	ataataaaacaaactgtagg T/C agaaaaatgagagtactca	5072
OATP2	85	(3' untranslated region 24)	tcttaataaaacaaatgagt A/G tcatacaggtagaggttaaa	5073
OATP2	86	(3' untranslated region 25)	cagagtttgaactataatc T/G aaggcctgaagctagcttg	5074
OATP2	87	(3' untranslated region 25)	gcctgaagcttagcttggtg A/G tatgtacataaatatctgt	5075
OATP2	88	(intron 1 457-458)	taattggcaaacataaaaa (A) cagggtgtctcaaaagtcacat	5076
OATP2	88	(intron 1 457-458)	taattggcaaacataaaaa cagggtgtctcaaaagtcacat	5077
OATP2	89	(intron 1 753 -7538)	gatcagcattacaaccaaga (G) atggagaatgacattcagga	5078
OATP2	89	(intron 1 753 -7538)	gatcagcattacaaccaaga atggagaatgacattcagga	5079
OATP2	90	(intron 1 10032-10035)	tgtgtgattctatattactt ACTT/Δ gtttcaattttctctccaca	5080
OATP2	91	(intron 1 10058-10061)	ttcaaatctctctccacaaa TTTA/Δ tttttctattaaattgtaat	5081
OATP2	92	(intron 2 413-423)	acttattttaaaaattctttt (A) 11-13 caaaaaacaggatttataaaa	5082
OATP2	93	(intron 3 1595-1603)	ttgccaagtaattcaagtgc (T) 8-10 gtattttaaaaaacacttttca	5083
OATP2	94	(intron 4 10-23)	ttcatgggatagtaagtgtt (A) 12-14 cctctgtgccactatcagta	5084
OATP2	95	(intron 5 1567-1572)	gtgaatataaattacttctga CTGTGTA/Δ aattaaaaaaaataagtag	5085
OATP2	96	(intron 5 1577-1585)	attacttctacttctgaaatt (A) 9-10 taagtagaataaataagagt	5086
OATP2	97	(intron 8 1939-1941)	ttctctaactctcttactct CTT/Δ atttcaagcagatgcaactg	5087
OATP2	98	(intron 10 3077-3078)	aaattctttatctacttttt (CTT) ttcctcttttctctgtcttc	5088
OATP2	98	(intron 10 3077-3078)	aaattctttatctacttttt ttcctcttttctctgtcttc	5089
OATP2	99	(intron 11 11011)	aacaag t/c gagacttcactaa A/Δ tataat g/a caatgtattt	5090
OATP2	100	(intron 12 1160-1169)	agcatgacatggttagagatg (A) 9-11 gcatttttaacatttgttaa	5091
OATP2	101	(intron 12 1310-1312)	tccatcttaataataaaatgt TGT/Δ ctactcaaaaggagaagtct	5092
OATP2	102	(intron 13 9-34)	tacgagcactaggtatgatg (A) 24-27 tatatatatatatatata	5093
OATP2	103	(intron 13 35-64)	aaaaaaaaaaaaaaaaaaaa (TA) 10-21 c/t acacacacatacata	5094
OATP2	104	(intron 13 1379-1387)	aaaattattccaccacaatc (A) 8-10 caaagtaaagttatgaacac	5095
OATP2	105	(intron 13 1916-1928)	aattctotttaaaataatgtt (A) 11-13 gtctgc t/c ttacagcaaa	5096
OATP2	106	(intron 14 588-596)	caattatactttactctctt (A) 8-10 ctaatttcaaaattcatatat	5097
OATP8	1	(5' flanking region -1413)	aataggggcttaataactct G/C aaacttatgattttctcatat	5098
OATP8	2	(intron 1 38962)	atgaaattagttttaaataa G/A caaccttaactatactctctc	5099
OATP8	3	(intron 2 253)	acagactttaccaacaaagaa T/G tatccttcccaaaatgtcta	5100
OATP8	4	(intron 2 329)	actcatggttggcaaatata C/G tttttaggaaactttatctc	5101

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
OATP8	5	(intron 2 2568)	ccattctggtgctttcttcc G/A tgaactattttccatcagt	5102
OATP8	6	(intron 2 2679)	ctcttattgctcttcttcca T/C gttttaatctaaataattta	5103
OATP8	7	(intron 2 2753)	caggaaactttcacaaagcc C/A ctaattaatttaagctccct	5104
OATP8	8	(intron 2 3132)	tgggttaatgtaggagagtt T/C accttcacagttaaattaca	5105
OATP8	9	(intron 2 3193)	aatgtcttgggcatatttgc A/G ttcatttggggca t/c tcaagt	5106
OATP8	10	(intron 2 3207)	atttgc a/g ttcatttggggca T/C tcagtcttactagatacaaa	5107
OATP8	11	(coding region 334 (Ser112Ala))	gaactggaagtattttgaca T/G ctttaccacattttctcatg	5108
OATP8	12	(intron 3 76)	agaattttattttttatactt G/A taagtgggcagttacctttt	5109
OATP8	13	(intron 3 2443)	tcaatttcatgttgctctta C/T agttataggtattctaaaga	5110
OATP8	14	(intron 4 67)	taatcacgtctataaagttt C/G tgatattctttaacaaaatt	5111
OATP8	15	(intron 4 91)	tattctttaacaaaattgat T/A taagaacaaataggaagaac	5112
OATP8	16	(intron 4 197)	ggtttgaactgcacctgttc G/A cttatatgcagcttttctcc	5113
OATP8	17	(intron 4 813)	tttaacagataaaaaaaa T/A attttgaacgcaaaaagaa	5114
OATP8	18	(intron 4 974)	atatgcaccttaaaaaaac C/G tggatttttaaatatgtaat	5115
OATP8	19	(intron 4 1003)	taaatatgtaagtacataa G/T gaattattgcatttttgt	5116
OATP8	20	(intron 6 155)	cattaataatcagaataaaa A/G agaaatttagctcctattta	5117
OATP8	21	(intron 6 750)	atccaactggggttttagatt T/G cctctttctgcctctctcc	5118
OATP8	22	(intron 6 780)	gcctctcctccatctgcacc C/T tctcttttctcgcagcaaaa	5119
OATP8	23	(intron 6 1248)	ctatgccctgtaatctcaca C/T ttcctcttattttaaaattgg	5120
OATP8	24	(intron 6 1500)	tcgtgtctgtgttagcatat A/G ataactcatcagggtttgtg	5121
OATP8	25	(intron 6 2008)	ataacataaatgagtaaga A/G tatcaaggcagggaattag	5122
OATP8	26	(intron 6 2087)	actactctcccatcacacac T/C aaaactcatgtctcccccag	5123
OATP8	27	(intron 6 12305)	tcactatggaggactgcaa T/C cattatcattatttcccaga	5124
OATP8	28	(intron 7 363)	taacaaatgataccgccat C/G atactattctctggttaatag	5125
OATP8	29	(intron 7 411)	cctttatttttggagaacct G/A gtggatgatattaaga c/a gta	5126
OATP8	30	(intron 7 428)	cct g/a gtggatgatattaaga C/A gtatatagatcactgtaata	5127
OATP8	31	(intron 7 634)	aaaatttatatatatacatat A/G taactctacctaagtattca	5128
OATP8	32	(intron 7 1791)	tgttttttaaaagggttagta T/C gtgaatagtaaaagcgaattt	5129
OATP8	33	(intron 7 2000)	agttgagcaaatgtctctca G/A gtatgataatgtcacttgaa	5130
OATP8	34	(intron 7 2043)	gtttattgattccatttttta A/G tggatcaacattgtagttag	5131
OATP8	35	(intron 7 2171)	atttattttgagcaaaaggct G/A c g/a actct c/t cttagaaagc	5132
OATP8	36	(intron 7 2173)	ttattttgagcaaaaggct g/a c G/A actct c/t ttagaaagcct	5133
OATP8	37	(intron 7 2179)	tgagcaaaaggct g/a c g/a actct C/T ttagaaagcctcaaaaat	5134
OATP8	38	(intron 7 2219)	atttgttaactttaagtctta T/G ataacttatatttacaataat	5135
OATP8	39	(intron 7 2261)	cagatattataatatatttt A/T ttattgaaatagtatttttt	5136
OATP8	40	(intron 8 150)	acaaaattttctccattctgt A/G ata t/a catcgttgtttctgcat	5137
OATP8	41	(intron 8 154)	aatttctccattctgt a/g ata T/A catcgttgtttctgcatgta	5138
OATP8	42	(intron 8 1303)	tttttttggagatggagtct C/T gctctgttgcacaggctggg	5139
OATP8	43	(intron 8 1372)	aagctccgcctcccagggttc T/G ccacccttctcttaagaaa	5140
OATP8	44	(coding region 1272 (Leu424Leu))	tccttctgttttcaacttct A/G tatttccctctaactctgca	5141
OATP8	45	(intron 10 63)	tcacagatttgatttaataa A/T tacttatcaaatcttccctat	5142
OATP8	46	(intron 10 911)	cttgcccaatatacctaccaa C/T gtattattaaacggcatgga	5143
OATP8	47	(intron 10 972)	tcctagtttctctgaagata G/A gctacaactttagtaaaact	5144
OATP8	48	(intron 10 1101)	tcctgtgtctctgtgtgttcc A/T g t/c agtgaagacctgaaagag	5145
OATP8	49	(intron 10 1103)	cctgtgtctctgtgtgttcc a/t g T/C agtgaagacctgaaagag	5146
OATP8	50	(intron 10 2027)	cccattttccatgagtggtcta A/G g/a ttttgtcccgtttcaaaact	5147
OATP8	51	(intron 10 2028)	ccatttttcatgagtggtcta G/A ttttgtcccgtttcaaaacta	5148
OATP8	52	(intron 10 2372)	tgtattttggcaaatgtattt G/T ttaatttttcaaaaactatt	5149
OATP8	53	(intron 11 10538)	caacagaggatcaatgtaaa T/G gaaatctcttaaaattaaaca	5150
OATP8	54	(intron 12 55)	ataaatattaatgttaata C/T taaagactgaatgcaattaa	5151
OATP8	55	(intron 12 1802)	taaaatgaatcggttaaaaca T/G tcaatgtataaatcaactgtca	5152
OATP8	56	(intron 12 2612)	ataggcatataaatactcttt C/A ttcctctgtatataggag	5153
OATP8	57	(coding region 1833 (Gly611Gly))	aacagctgtggagcacaagg G/A gctttaggatataataatc	5154
OATP8	58	(5' flanking region (-1590)-(-1587))	tacataacatatacctatat CTAT/Δ gttatgtgtctgcttatata	5155
OATP8	59	(5' untranslated region (-28)-(-11))	agcatcagcaacaattaaaa ATATTCACTGGTATCTG/Δ tagtttaataatggaccaac	5156
OATP8	60	(5' untranslated region (-7)-(-4))	tattcacttggtatctgttag TTTA/Δ ataattggaccaacatcaaca	5157
OATP8	61	(intron 4 213-214)	ttc g/a cttatatgcagctttt (T) gtccaaccaaacagaaggag	5158
OATP8	61	(intron 4 213-214)	ttc g/a cttatatgcagctttt gtccaaccaaacagaaggag	5159
OATP8	62	(intron 4 505)	tataactttctctttataaa G/Δ atgcaaaatgttatagcatt	5160
OATP8	63	(intron 4 616)	aatgaagtggaggaaaaaaa A/Δ tgatttcaagttttctgtct	5161
OATP8	64	(intron 4 804-812)	acatccatgttttaacagaat (A) 9-11 t/a attttgaacgcaaaaac	5162
OATP8	65	(intron 4 855)	agattgttttaacaaatttag G/Δ aaactattattcaaacacatt	5163
OATP8	66	(intron 7 619-628)	ttttatatatgaattaaaa (AT) 4-5 catat a/g taatcttaccta	5164
OATP8	67	(intron 7 1773-1779)	attttctatatattgaactg (T) 7-8 aagggtagtga t/c gtgaata	5165

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
OATP8	68	(intron 8 1270-1290)	tagtgtgocaccottetctc (T)19-23 gagatggagtct c/t gctc	5166
OATP8	69	(intron 10 665)	aactcaaaaggctttttttt T/Δ ccatgtgacacatatccgtg	5167
OATP8	70	(intron 11 247-250)	aaaaatcttaaggcacacac TGAT/Δ tgacagttgccttgattgta	5168
OATP8	71	(intron 12 1622-1630)	aaataaattgttggcatcta (T)8-10 atttttctaagggctcgctg	5169
OATP8	72	(3' untranslated region 2464-2465)	cctgatgccttttaaaaaaa A/Δ tgaacacctttggatgtatt	5170
TAP1	1	5'flanking - 673	agctaaagagtaaaagcacc G/C ctttttccaccagcctcgcg	5171
TAP1	2	5'flanking - 646	ccaccagcctcgctgctgctg T/G tcccttcacggacactctag	5172
TAP1	3	5'flanking - 563	ttgcaagcgctggctgtac A/C ggccacctccctcgctccc	5173
TAP1	4	5'flanking - 236	gctttgcgcggcgctaac G/T tgtgtagggcagatctgccc	5174
TAP1	5	intron 3 + 408	aaggaaactgaggccaagac C/T ctaaatgctgaaactgcaca	5175
TAP1	6	exon 4 + 153	ccctcaccatggtcaccctg A/G tcacctgcctctgcttttc	5176
TAP1	7	intron 4 + 289	gtatttcttttagcatccaag G/T ggcatagctgtgtctctttc	5177
TAP1	8	intron 4 + 291	atttcttttagcatccaaggg C/G catagctgtgtctctttctc	5178
TAP1	9	intron 5 + 1139	ttcttccaggttaagtactg C/T ggttctttgtgtccctcca	5179
TAP1	10	intron 7 + 375	gtctctgcctctgtctttgc C/T gcttctcttatctactcc	5180
TAP1	11	3'flanking + 71	agcgcaacttttcagctcgcg G/A tgtctctctttttatcatcc	5181
TAP1	12	3'flanking + 129	aactgcacacaccttttccct T/C aagcttttttaattctctatga	5182
TAP1	13	3'flanking + 459	cattcagggaggccagggtc G/A tgtgacgtcgacagttgctg	5183
TAP2	1	intron 3 + 8	tctcttttggcaggtaggtg G/A tgggcagctgggtccatttg	5184
TAP2	2	intron 4 + 104	cttcaccctgatgccaggac C/T tggggatgcttttctctgtg	5185
TAP2	3	intron 10 + 219	gcagcagttgtgtcctctcc A/G tgggcagccctcgaggtcc	5186
TAP2	4	intron11 + (317-319)	atgggtgccaggtgagtggtg GTG/Δ tccatctcattcctgctctt	5187
TAP2	5	exon 12 + 19	agctgcaggactggaattcc T/C gtggggatgcacagtgctg	5188
TAP2	6	exon 12 + (356-357)	aggtgggtgtgggtgtgggtg GG/TGGTGGGTGGA ggctgtctgtgctc	5189
OCTN1	1	intron1+6602	aggcgagccaggttatgtgg C/T gaaggataaggcctcttccc	5190
OCTN1	2	intron1+6790	gacaaaaaggggaaaaccttc C/T gtgataggcaggtttgtgga	5191
OCTN1	3	intron1+14019	cactgtctcccactgggccc G/A ccatgtcaactgttaaccaca	5192
OCTN1	4	intron1+14136	ccggtttcttaagaaaagcc T/C tttctaaggaccctctta	5193
OCTN1	5	intron1+14266	agctttccaaaaagacactt G/T cggcaccataactccccaaa	5194
OCTN1	6	intron1+14412	cttggggcaaacggccactg C/T gtgtgcattggctcttctctgt	5195
OCTN1	7	intron1+15776	acataggagacactctcttc G/A gatctcagttatccagaaca	5196
OCTN1	8	intron1+15817	ctgtgcttctgcgaataagc A/G gactacttcggatactgtaa	5197
OCTN1	9	intron1+15889	agagccagtttttggagccccc G/A tctggcaagcaggcagggccc	5198
OCTN1	10	intron1+16063	acctctgtctgtctgcagaat A/G aggtgtgatataaatatgtg	5199
OCTN1	11	intron2+1105	atatttccacaaggtccttg C/A gtacactgctccatgctttt	5200
OCTN1	12	intron3+1022	cttctgtcaagttgccagga T/C ggaaatattccaaactctact	5201
OCTN1	13	intron3+1217	tccccttctgcagggggaa G/A gagcggggcgaagattttctt	5202
OCTN1	14	intron3+1596	aagccagagaagctctctcc G/A tgggaatggggaacaaggtgg	5203
OCTN1	15	intron3+1720	ggagcctccaaagcctcccc G/A tgtgagcgggtgaggcaggg	5204
OCTN1	16	intron3+2104	tatgagactcgtgtgtgtgg G/A ttctcaggtctgaaagtta	5205
OCTN1	17	intron3+8323	cccttccccttttctaagtg G/C tgatagtttgaaactetaact	5206
OCTN1	18	intron4+926	tttttggaaactcacaattta G/T actagacctcatggttgccc	5207
OCTN1	19	intron4+1055	cacctgtctgacgagatagc G/A caggtcaggtggggtcactc	5208
OCTN1	20	intron5+ (1197-1202)	caacaacaacaacaacaaca ACAACA/Δ ttgggagtgcttaaaccttc	5209
OCTN1	21	intron5+ (2071-2083)	gttctgtctcattgctcatgc (T)11-13 caaaaaagaaactaaggca	5210
OCTN1	22	intron5+2781	tgatcattcttagaaaaag G/A acactcacattttggagagga	5211
OCTN1	23	intron6+ (882-917)	ttactactctatgatggcagc (AC)15-18 gatgatcgtcagaactggtg	5212
OCTN1	24	intron6+924	acacacacacacacgatgat A/C gtcagaactcgttagatttag	5213
OCTN1	25	intron7+511	attattgatagtaaatagaa T/C acatatttcttaataataag	5214
OCTN1	26	exon8+124	ggtoagggaacatggcggtgg G/A ggtcacatcccagggcctcca	5215
OCTN1	27	intron8+3514	acacacacacacacacacac G/A tatgaattctcaggaaaaggt	5216
OCTN1	28	intron8+3902	aagcaagatgaggatctgtt T/C ttctcctgtgtgagtaaacg	5217
OCTN1	29	intron8+ (4064-4089)	gtgaacataaacttagttg (T)18-26 gagtctcatagcctgtgga	5218
OCTN1	30	3'flanking+115	aaccaaatgatttatgcag T/A attctcatccagaaaacctt	5219
OCTN2	1	5'flanking - 225	cggcgctagaggagcgagtt C/T ggactcggaccaccaaggcct	5220
OCTN2	2	5'flanking - 124	gctggcagaggccgggcttc G/T ccaggtccccaggacaggcc	5221
OCTN2	3	5'flanking - 13	ggcgccgctctgctgccc C/G gggggcgcccttgcggccca	5222
OCTN2	4	intron 1 + 232	ggtggtcagtcgtgcccctcc G/A tctgtatggccactttgaag	5223
OCTN2	5	intron 1 + 314	atggccctgtgtgtgccagga C/T ttactctagttggggttggg	5224
OCTN2	6	intron 1 + 5055	catgtggtacatagcagcat G/A tctgactgttgatagcgtca	5225
OCTN2	7	intron 1 + 6437	gaagcttgccctcacacaca G/C aggcggccacccctgtcatca	5226
OCTN2	8	intron 2 + (173-174)	tagtaagaagagccaacaaa TC/Δ atctgactccgtaattcttg	5227
OCTN2	9	intron 2 + 608	agcaggttatttgtatatt C/A taaagcttttaactcaagga	5228
OCTN2	10	intron 2 + 4370	taattttatgatatccaagt G/A cctctataatagatgctca	5229
OCTN2	11	intron 5 + 969	caccagaaaggggtcctgtg C/T gcaaggtcaggcaggagtg	5230
OCTN2	12	exon 10 + (1028-1044)	ttagctcctggtttgtgtc (T)16-18 aaaaagaaactcactctggca	5231
OCT1	1	intron 1 + 7715	tagtctgactcacacatgg G/T tctgtgcttttctgctcct	5232
OCT1	2	intron 2 + 97	ggtggagaacatgaccagtt G/A gaattaactgcagaagctgc	5233
OCT1	3	intron 2 + 797	gtggagttgtgtgaacaact C/G tttaaaagagtggtggggagg	5234

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
OCT1	4	intron 2 + 1768	cgtagaactggagaggggtctg T/C gggcactgcccggctgagct	5235
OCT1	5	intron 3 + 1244	gcagatgctgaagaaggagca C/T gcggaagagcagcggtcaggg	5236
OCT1	6	intron 4 + 865	agcgctccagtggttaggaag G/C ctccacagggtgcgaactcca	5237
OCT1	7	intron 4 + 1028	gtcaatctctgtctctctccc A/G ctctcttcaattttatagtag	5238
OCT1	8	intron 4 + 1040	ctctctcccaattcttcatttt T/G tatagtagtactattggtattat	5239
OCT1	9	intron 4 + 1485	agcctcgcctctcccctgct C/T gtcccttggtgaacacagggatc	5240
OCT1	10	intron 4 + 1997	tgaggggattacagccccaac G/A tggggaggggcaggctgcact	5241
OCT1	11	exon 5 + 9	tggtgtgtgcgaggtgtgtgc C/T ggagtcctccctgggtggctgt	5242
OCT1	12	exon 5 + 20	gggtgtgtgcggaggtccctc C/G ggtgtgctgttatccacaaaa	5243
OCT1	13	intron 6 + 379	gaggaagtctccattctctat A/G tctaaacaccttagagacc	5244
OCT1	14	intron 6 + 2125	tattgaccccaaatctgtttct C/A acaatgtataatgactgtga	5245
OCT1	15	intron 6 + (2935-2953)	ttctctccatctgcgaggggc T/18-20 ctctcagtctgtgactcatgc	5246
OCT1	16	intron 7 + (6-7)	ttttatctccactggtgaagt (TGTTAAGT) tggtaagtgtctgtctttc	5247
OCT1	16	intron 7 + (6-7)	ttttatctccactggtgaagt tggtaagtgtctgtctttc	5248
OCT1	17	intron 7 + (1780-1781)	gtttttctttctctctttttt (T) catggagaaagacagagaa	5249
OCT1	17	intron 7 + (1780-1781)	gtttttctttctctctttttt catggagaaagacagagaa	5250
OCT1	18	intron 8 + 3247	ccaggcccaaacattctccat G/T tcatggccactgtggccagg	5251
OCT1	19	intron 8 + 10521	cccttaaccaaaggaacgccca G/A tggcagatccctcattctga	5252
OCT1	20	intron 10 + 393	tcagatgtcttttagtaacttt G/C ttccacaaaattcttttgaca	5253
OCT1	21	3'flanking + 1755	tcaatgatgttttttcaaatg T/C gttattaaaagtctctctct	5254
OCT1	22	3'flanking + 1799	ctttctttagaatctctcttgg G/A caaaactctctgaggagggcc	5255
OCT2	1	intron 2 + 1329	ctgcagcagaggggagagg G/A ataaaagtggtccacacaggc	5256
OCT2	2	intron 2 + 1867	cctctgtcaaggtgaagtac G/Δ attattcttcccccaaggc	5257
OCT2	3	intron 9 + (340-343)	cagcaggccctcaactctct CTCT/Δ gctgatttccacccctctctg	5258
OCT2	4	intron 9 - 396	atatacaattctattactttt A/G ttgtctagaaatgatctgaag	5259
OCT2	5	intron 9 - 386	cattactctttatttctctaga A/C atgatcccaattgtctcaagt	5260
OCT2	6	intron 9 - 86	atagaaaaatgctaaaaaaa A/Δ gttttaacaaaaatgaagg	5261
OCT2	7	intron 10 + 1725	tggaagaggcctttgaatcc G/A agcggcagctgcacactgcg	5262
OCT2	8	intron 10 - 195	caagataaatttttaggaataa C/T tctgtctgactgagttatca	5263
OCT2	9	exon 11 + 328	gtttttctggagggtttttt T/Δ ccatctttgtattttttttaa	5264
OCT2	10	exon 11 + 427	agggcaacaaaataaaaaa A/T gttgaaaaacagttaaaagt	5265
OCT2	11	exon 11 + 455	aaacagtaaaagtgtgggagag G/A agcatctattttcttaaaga	5266
OCT2	12	3'flanking + 34	agaatgtatgtccaagaattt T/A agataggccttttcagtaaca	5267
NTCP	1	exon 1 + 307	tatgggtcatagtcgccctac G/A gcctttgtgctgtggcaaggt	5268
NTCP	2	intron 1 + 607	cccagcaccactccagata G/C gccagcccatctccagccac	5269
NTCP	3	intron 1 + 702	gcagaaatcacgaagggtcc G/A ctctctggagacgcagcacac	5270
NTCP	4	intron 1 + (3950-3966)	cacatcacctacagcacttgc T/14-17 gagaataaggcatgttaaga	5271
NTCP	5	intron 1 + 9597	aaggacatattattcaggct C/G tgaagtgtcataattttattt	5272
NTCP	6	intron 2 + 4808	ccatgtggagaagcaactacc C/T gggggcacttgtctcagcag	5273
NTCP	7	intron 2 + 5032	acacctggagactagcagag G/C cagctttcccaccaggatca	5274
NTCP	8	intron 2 + 5046	gcagagcagcagctttcccac A/T ggcatacatcaattatgtg	5275
NTCP	9	intron 3 + (8-21)	gcctcaatggcaggttagtta T/12-15 aagaaagggtctcactctgt	5276
NTCP	10	intron 4 + (484-495)	tataataaccgacataaaag (A) 10-13 gattcctcaactctagttac	5277
NTCP	11	intron 4 + (728-754)	tgcaactttaacacaaatttt (A) 25-27 caggacatttcaaacacactt	5278
NTCP	12	intron 4 + 747	taaaaaaataaaaaaataaaaaa A/C aaaaaaacaggacattcaaa	5279
NTCP	13	intron 4 + 1339	ccccagtggaacactataat C/A aaagcaacgtattttcttgg	5280
NTCP	14	intron 4 + 1545	accagcagcaagaagaggtta A/T atcaattggggggttggagg	5281
NTCP	15	3'flanking + 559	caagacatattagtttttcgg G/A tatcagttttggcaaatgtgc	5282
PEPT1	1	exon 1 + 25	ctgccaggagcagctcccgc C/T ggcaggctgcgagcagcctg	5283
PEPT1	2	intron 1 + 88	caggggcccggggagggcgcaa G/A ggtcacggcgccggcggaagc	5284
PEPT1	3	intron 1 + 106	aagggtgcggcgggcgggga A/T cggggggagcccggaagggcc	5285
PEPT1	4	intron 1 + 248	cgagggtgcgattctctggccc G/A cccgcgcgtggggcactgta	5286
PEPT1	5	intron 1 + 326	tgaggcgggagcggaaccag C/A gggtagcgagcggggcgcca	5287
PEPT1	6	intron 1 + 1238	tttagcattctccagcatgc C/T aatcccgagactgcttagag	5288
PEPT1	7	intron 1 + 3001	tccttatgtctggggaagaag C/T gtcagtaagaaaaagcagcc	5289
PEPT1	8	intron 1 + 5673	ttgggaaagtgcacacagccac G/C gggcagcagggaacagggttc	5290
PEPT1	9	intron 1 + 5679	agtgccacagccacggggca C/G agggacaggggtcttccacag	5291
PEPT1	10	intron 1 + 5917	aaattcacaaaatgtacttc C/T ataagaaggctctgttaaaag	5292
PEPT1	11	intron 1 + 5966	ctaggcatttagaacttcta C/T aatctgcaccttagtgtaacag	5293
PEPT1	12	intron 1 + 9255	tggtcatttccaggcctcttc A/G gcctatgatttttagatagtt	5294
PEPT1	13	intron 1 + 10278	catgaccccatgtaggcgsga A/G aagcagccctgtatgcagcag	5295
PEPT1	14	intron 1 + 20251	aagaagagcctgtgtttatt C/T agtgattgtcaatgtgttbgg	5296
PEPT1	15	intron 1 + 20509	aaacacacactttctgacttg C/A gctttcttaagatgacatcc	5297
PEPT1	16	intron 1 + 20532	ttttctaagatgacatacttg T/C tgacacaggatgataactaagt	5298
PEPT1	17	intron 3 + 55	agagcgggagtgggccataac C/Δ agtctctaactttgtttccccc	5299
PEPT1	18	intron 5 + 1720	atctctctcttttacttgaaac A/A aataaagctacaaaaggaacc	5300
PEPT1	19	intron 5 + 1790	gctcattgtttattgttttcc G/A gatgtgtaaatatttagatgg	5301
PEPT1	20	intron 5 + 1860	agtttgcatttgactatcac G/A ctgcattctctgtgagctggc	5302
PEPT1	21	intron 5 + 1943	agggccactgagggaaaactg G/A gggaaaagagagggcctctcac	5303
PEPT1	22	intron 8 + 1478	tgttttcagatcttagtagt A/G catggaataggaccgttttcc	5304

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
PEPT1	23	intron 8 + 1898	ttaaatattagtggtataaag A/G aaacatagactcaatctctt	5305
PEPT1	24	intron 10 + 388	ttaaatagtttagacatttt C/T gattttctaaagaaaactgc	5306
PEPT1	25	intron 11 + 985	atccataaggtactcagtg C/T tggcctgtatgaagaactca	5307
PEPT1	26	intron 11 + (1022-1045)	ctcaaacaggggtagatttc (T)20-24 gagtcaagagctcactctg	5308
PEPT1	27	intron 11 + 1320	tgtgagccactgcacctggc C/T aatttctgactttctatga	5309
PEPT1	28	exon 16 + 107	tggagagatggtgacacttg G/C cccaatgtctcaagtaagta	5310
PEPT1	29	intron 18 + 6048	tttgttgttgggttttttt T/Δ gttgttgttgtttgttttg	5311
PEPT1	30	intron 18 + (6141-6142)	tcactgcagcctccgcccc (T) gggttcaagcaattatctg	5312
PEPT1	30	intron 18 + (6141-6142)	tcactgcagcctccgcccc gggttcaagcaattatctg	5313
PEPT1	31	intron 18 + (6241-6242)	tatttttagtagagacgggg (G) ttccaccatattggccaggc	5314
PEPT1	31	intron 18 + (6241-6242)	tatttttagtagagacgggg ttccaccatattggccaggc	5315
PEPT1	32	intron 18 + 12102	gtgggaattctagctaaagg C/T cgtgtggtctgtctcaggt	5316
PEPT1	33	intron 18 + 12203	gacctgagtttaattcatag C/A cattttctccagcacctaa	5317
PEPT1	34	intron 18 + 12307	gaaaggttaattattcttt A/G cactgtcagaggtgtacacta	5318
PEPT1	35	intron 20 + 79	tcacaaacacttaggacata A/G tatgatttaactagatgat	5319
PEPT1	36	exon 23 + (348-370)	tctttttctttttcttttc (T)18-23 gagacagagttttgtctctg	5320
PEPT1	37	exon 23 + 790	ccacatttggctatcttccct A/G tcacacaaatgatgttattt	5321
PEPT1	38	3'flanking + 2	aaataaatttctgttcttaa G/A cctaagtggttcatgtatctc	5322
EPHX1	1	intron 1 + 110	tgcaaaatgtgtcttactag C/T ttctagtgcataaaatattg	5323
EPHX1	2	intron 1 + 143	aaatatttgggtgagctcttc G/A ctgtgctgggcccagtcacca	5324
EPHX1	3	intron 1 + 1097	aatccagagagggagataga T/G tggagttcaaggggtggaca	5325
EPHX1	4	intron 1 + 1717	ttccaaagacagagcgagggg T/C gctgtggtgggctgtgttgc	5326
EPHX1	5	intron 1 + 1772	aactcgatgtcttctctccc G/T tctgggtcctcaactgcagtg	5327
EPHX1	6	intron 1 + 2054	gaaatgtaacagggcaact A/G tggacacagaaagttagata	5328
EPHX1	7	intron 2 + 1414	atttccaaaaatctgtttggg G/T gtaactgaaacacttgggaa	5329
EPHX1	8	exon 3 + 174	taccttcacttcaagactaa G/A attgaaggtatgtttgcaaa	5330
EPHX1	9	intron 3 + 6583	ctgtcaataccatgaagggg G/C ggcgggggacctaaaggggtg	5331
EPHX1	10	intron 4 + 34	agagggttccataactgcgcc G/A tcctcgccaaggggtggccc	5332
EPHX1	11	intron 4 + 63	aaggggtgggcccgggttccc C/T accaggctctctctccggcg	5333
EPHX1	12	intron 5 + 154	gcagtgctcagggacagcttg G/A cttggatcctctctgtctga	5334
EPHX1	13	intron 5 + 276	tgtgtgaccaaagctctggga T/C agccctgagcagaactcccc	5335
EPHX1	14	exon 6 + 130	gatgtggagctgtgtgtacc C/T gtcaaggagaaggtattcta	5336
EPHX1	15	intron 8 + 206	ggtgcctggctcccggggcg C/A cctcagtagcctcccaggt	5337
EPHX1	16	intron 8 + 353	tggccctcccagaaaagaga A/G ggcctcagtgaggggagag	5338
EPHX1	17	3'flanking + 708	aggtgcagactcatgcactc A/G gccctgaagggtgagagag	5339
EPHX2	1	5'flanking - (523-522)	aaagtcactggatagcccc (C) tccccgcgcccccaacacgg	5340
EPHX2	1	5'flanking - (523-522)	aaagtcactggatagcccc tccccgcgcccccaacacgg	5341
EPHX2	2	5'flanking - 522	aaagtcactggatagcccc T/C cccccgcgcccccaacacggt	5342
EPHX2	3	5'flanking - 521	aagtcactggatagcccc C/T cccccgcgcccccaacacggtc	5343
EPHX2	4	5'flanking - 516	actggatagccccctcccc G/C ccccccaacacggtcttatg	5344
EPHX2	5	5'flanking - 515	ctggatagccccctcccc G/C ccccccaacacggtcttatgt	5345
EPHX2	6	intron 1 - 74	tggctgtcttctcaatgaata T/C gaacagtgtctgtttccatg	5346
EPHX2	7	intron 3 + 72	gagccttaggtcagaatcca T/C tgaagttagctttgagatca	5347
EPHX2	8	intron 4 + 473	gtgtgtctctactttaatct A/G caaaaggtgattgaatggag	5348
EPHX2	9	intron 5 + 276	caagagtgggattgttcaagg C/T catcctgacctcacttttga	5349
EPHX2	10	intron 8 + 8	tctgtctctccccggtgggtg T/C gctgtcttgcagctgtctta	5350
EPHX2	11	intron 9 + 1573	atgtctgtgaagactgatgaa C/T gatggacgggtgcactgtctc	5351
EPHX2	12	intron 10 + 207	gaacaggatggagatgagct T/C gtttattgtcttttaataga	5352
EPHX2	13	intron 12 + 911	tgaagagacctcgacatgtc G/T catccacatactacagggga	5353
EPHX2	14	intron 12 + 2425	atcttctcagctgagcaaac C/T gaggctcagagggcttaacc	5354
EPHX2	15	intron 12 + 2460	ttaaccccaactggcccaag G/A ccaggtacatgattgggtca	5355
EPHX2	16	intron 12 - 281	aagtcctttcaagagattat T/C ataagtagtaccttctcatt	5356
EPHX2	17	intron 12 - 268	agattattataagtagtacc T/G tctcattataggaatattga	5357
EPHX2	18	exon 13 + 50	cctgagtcggactttcaaaa G/T cctcttcagagcaagcgatg	5358
EPHX2	19	intron 13 + 1739	ttgtctgaacaggggttttca G/T atgagcatatttcttttga	5359
EPHX2	20	exon 14 + 33	atgcataaagctctgtgaagc G/A ggtaagagacatgcttggga	5360
EPHX2	21	intron 14 + 314	ggatttgagacttacctcta T/C gggggctcactcgtgtatgc	5361
EPHX2	22	intron 14 + 878	attcccttattccttcacac C/T gctgtcactcattcattca	5362
EPHX2	23	intron 14 + 948	gcacaggctgggtatgaagc T/C ggggctgcatgctcagctac	5363
EPHX2	24	intron 15 + 259	agaggggttttactactttt C/T agtcatggctcctcagagaa	5364
EPHX2	25	intron 16 + 459	tcctcatttgtcaagcagaa G/C atgagtttccaatctctctggg	5365
EPHX2	26	intron 16 + 645	gtaagtgaacacactgttac G/A tgccagacttctgcccagac	5366
EPHX2	27	intron 16 + 985	gtcattatcatcatatgacc G/A atgaaaatgaccaaactgca	5367
EPHX2	28	3'flanking + 12	aggtggccttacacacatct T/C gcattggatggcagcattgtt	5368
EPHX2	29	3'flanking + 374	tgttcacggagaatgcacgg C/T atggggatgaacctttccc	5369
EPHX2	30	3'flanking + 544	tagccacctgcctttctccc G/A gcttccctagcagagtttgc	5370
COMT	1	5'flanking - 1287	cgtatgatattccccattct G/A agtccagaatacctagaaat	5371
COMT	2	5'flanking - 1217	tgtgagtatgggaaggggaa G/A cttttctgtctgtgttcccc	5372
COMT	3	5'flanking - 503	caggggctccaggaggacga G/A tgtgtatcctccattgtctc	5373
COMT	4	5'flanking - 425	gagaagttgggaagctctggc C/T agtggggccggtgccttggtg	5374

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
COMT	5	5'flanking - 277	cccagccccagtttccccc C/T tgggaagggggctactttgtg	5375
COMT	6	intron 1 + 12058	ctggcccatggaaggagg G/A agggggccccgacggggcca	5376
COMT	7	intron 1 + 12070	agggagggggggggccccc A/G cggggccacagtaaaggagt	5377
COMT	8	intron 1 + 18831	tgtgtatgttcttgggtaaa C/T agcccttggctttacacatc	5378
COMT	9	intron 2 + 832	cctctcctttggccaccgt G/C actaccccacactccgggccc	5379
COMT	10	intron 3 + 90	ggagaagctgttatcacc G/A tttccagggggctgggaacc	5380
COMT	11	intron 3 + 425	ccccaaaggtgggctgttcg T/G gattcagagagggcagctct	5381
COMT	12	intron 3 + 671	ggctcctgctctttgggaga G/A gtggggggccgtgctgggg	5382
COMT	13	intron 3 + 676	ctgtcttttgggagaggtg G/T gggcgtgctggggatcca	5383
COMT	14	intron 5 + 75	tcagcctcagcctctccaaa G/C agccaggcattccagtagag	5384
COMT	15	intron 5 + 310	accagacacagggcagaaa C/T ggcacaggaccaaggagatg	5385
COMT	16	intron 5 + 346	agatgggtgggggaaggccc G/A ctctggggccagcctgctct	5386
COMT	17	intron 5 + 3023	aaggcagccgctgtctcaa G/A gcctaggccattgtctctct	5387
GAMT	1	intron 1 + 429	ctcggaaagctgagctcagg G/A agacagctgtccccgggggtg	5388
GAMT	2	intron 5 + 1411	ggtagacctgggtccatcccc G/A accagagacgcaggtgccc	5389
GAMT	3	3'flanking + 626	cactgacctctctgcccga G/A agaagggcggctcctgtgct	5390
PNMT	1	5'flanking - 367	aagaggtgaatggctgcggg G/A ggctggagaagagagatggg	5391
PNMT	2	intron 1 + 35	ctgaggccagcagggacaaga G/T gtcgtcggggagtgaaagca	5392
HNMT	1	5'flanking - 211	cagaggcagatgacagctct C/T cgtaaaagatttcactgtg	5393
HNMT	2	intron 1 + 5409	aatataactgatataattgg A/G acatttcatgttggcctagt	5394
HNMT	3	intron 2 + 2561	cacttgtgcttgggacaaga A/G agaaggcctacaagaaaaag	5395
HNMT	4	intron 2 + 2895	caatcagaaaatgtaagaaa A/C ctccaagaaaaatttaagtt	5396
HNMT	5	intron 2 + 3977	accaaacttggaaagtgttaa G/A ttatgcatgtatgttcatgt	5397
HNMT	6	intron 2 + 5296	ttacatagtgagtttggag T/C cccaggattttatcttccct	5398
HNMT	7	intron 2 + 13317	caacctcatgaattcttag C/T tgggatgggtccctataaca	5399
HNMT	8	intron 2 + 14682	gtagatgagcaaatgagttc A/A ggagagatttaaatcccta	5400
HNMT	9	intron 2 + 15406	gtctatgcattcatgcacc G/A tctaaccagctgtctacctta	5401
HNMT	10	intron 2 + 28943	atgtgactttaacttcaggt A/G tatcaatctcccttgatgt	5402
HNMT	11	intron 4 + 49	cagaagaagacttttcaga A/G tatatatataatgaatatct	5403
HNMT	12	intron 4 + (1942-1943)	tttgagaaaaatttaaggta (A) tcttctatggcccacttcca	5404
HNMT	12	intron 4 + (1942-1943)	tttgagaaaaatttaaggta tcttctatggcccacttcca	5405
HNMT	13	intron 4 + 2405	ccctgtgaccaagcagataa C/A ctcatgctttatttagtcca	5406
HNMT	14	intron 5 + (80-81)	cctgtgtttgaaagaagctt (TT) atatattttgtcttctattat	5407
HNMT	14	intron 5 + (80-81)	cctgtgtttgaaagaagctt atatattttgtcttctattat	5408
HNMT	15	intron 5 + 235	ctttcttttgggaaaaatg T/C ctttctctctatatatgaa	5409
HNMT	16	intron 5 + (702-703)	tacttacaggttgatttttag (AT) acacagcagactctgtcttc	5410
HNMT	16	intron 5 + (702-703)	tacttacaggttgatttttag acacagcagactctgtcttc	5411
HNMT	17	intron 5 + 749	ttacaccagacccatactt T/G aacaccatagtccacaaaat	5412
HNMT	18	intron 5 + 1101	gtaggcagcctattcttgat T/G atattcatcaatcacaaga	5413
HNMT	19	intron 5 + 1137	acagaaaaagtattgtagac G/A gaaataacaattcattgaga	5414
HNMT	20	intron 5 + 1348	aaggagcatgaatagtcca C/G aagtaactgagaactgatta	5415
HNMT	21	intron 5 + 1673	caaaagaaaggagtaagaa G/C tcaacaatcagttagctttt	5416
HNMT	22	intron 5 + 2022	attttatttggggctttcta C/T gtctctctctcctaagccta	5417
HNMT	23	intron 5 + 2285	tgctcacttaactctttaa G/C atccagagataaatgatggag	5418
HNMT	24	intron 5 + 4159	taccagttgacccagcaacc C/T tcttatagagtattttaa	5419
HNMT	25	intron 5 + 4501	aatgatccacaaaattacta C/G tcattgttttctttcaatga	5420
HNMT	26	intron 5 + 5251	cacacacacacacacaca C/G caaatggaagcagccagaca	5421
HNMT	27	intron 5 + 5802	gaaaaagaaaatctggctta C/T atcatgttgaaaacaaaagt	5422
HNMT	28	intron 5 + 6189	ttcaattccaccttctccta G/C agcatatcctgagttacct	5423
HNMT	29	intron 5 + 6297	gtcttgggttcatctcttgag T/A taaattagatctgggaactt	5424
HNMT	30	3'flanking + 458	tatgtcactctcaagaactc C/T tataagaccaagagtcact	5425
HNMT	31	3'flanking + 993	ctgaaaatgaacactgaacc G/A ttaatcatactgatatgtac	5426
HNMT	32	3'flanking + 1793	gtggagcacagcatttttag G/A cttgatatttgcctttatata	5427
NNMT	1	5'flanking - 228	ataattttcctgacgagetc A/T agtgcctcctctggtctaca	5428
NNMT	2	intron 1 + 44	cccactaatgtgagtcata T/C agatggagctcagggcacg	5429
NNMT	3	intron 1 + 149	ggataaaaacgaatattggt A/G tagcgattccacagtttaca	5430
NNMT	4	intron 2 + 158	agataggcccatgtgtgtgc G/A tgttagtaaatttgtgtatg	5431
NNMT	5	intron 2 + 433	gctgtagccatccaagccta T/C agaacttggctgtgagtggt	5432
NNMT	6	intron 2 + 10826	atcatctgactgtgaagttc C/T agttctgtgtgaactcaagt	5433
NNMT	7	intron 2 + 13630	atttcatggagggaagtcca T/C ggtagaagcaggctgctagg	5434
NNMT	8	3'flanking + 71	ggctcagtggttggggccca A/G tggttcacttaggacggggac	5435
PEMT	1	intron 1 + (297-299)	attgtgtgagactcagaggt TGT/A ccgtgttagtctttgggatt	5436
PEMT	2	intron 1 + 817	tcatgaagcctgtgaaggcac A/G tctctgcccccaagcagcttc	5437
PEMT	3	intron 1 + 830	aaggcacatctctgccccaa G/A cagcttctaataccagttctt	5438
PEMT	4	intron 1 + 1035	gagttctctgaaggagctaa T/C accagtttagtgttttgaaga	5439
PEMT	5	intron 1 + 1573	agtgggcaggggagactaac C/T ggggtgtgtgaggggtgggct	5440
PEMT	6	intron 1 + 1759	gatttttcttaagaaagaa A/G gaaagaaacatacaacatac	5441
PEMT	7	intron 1 + 2768	gcattctgtctccacagge C/A ggggcacctccaggattcag	5442
PEMT	8	intron 1 + 2785	ggccggggccactccagat T/C cagaagatgactccagtagg	5443
PEMT	9	exon 2 + 162	agctcagcagacctcctggc C/T gtggtgggtagctcctttcc	5444

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
PEMT	10	intron 2 + 4598	ccgtgggttttttttttttt t/Δ ctctatttttttgggtgtg	5445
PEMT	11	intron 4 + 39	actgtccagacgggagtagt C/T cactgttggtagccccac	5446
PEMT	12	intron 4 + 1317	accgtccccagctggcccca G/A cctcctgacatgggctctg	5447
PEMT	13	intron 4 + 1355	ctggagccaggctgcagccg A/C agtgcctggccatcctggcg	5448
PEMT	14	intron 4 + 5925	gtccaggcactgtggcccta C/T gtggagttctccagtctcca	5449
PEMT	15	intron 4 + 6028	ggcagtggtccaaggaccag G/C atggactccctctctcacc	5450
PEMT	16	intron 4 + 6078	atctgtaccctcgcggactc C/T acctggcttcgtgccatcac	5451
PEMT	17	intron 4 + 6089	cgcggaactctacctggcttc A/G tgcctaccccccgccagat	5452
PEMT	18	intron 4 + 6379	tcaggtgtccctccctcat G/A cctcctcaccctgccctctc	5453
PEMT	19	intron 4 + 7339	tgtaaagaaatcctgccaaag C/T ggcagatgcacacggggtca	5454
PEMT	20	intron 4 + 7619	ctcctgcacatgtgctccag A/G gaggaaagggcatttgacagg	5455
PEMT	21	intron 4 + 8858	ggcatgtgtgtgtgtgtgt T/G gtgtgtgagtggtgtcatgt	5456
PEMT	22	intron 4 + 9029	ttcttggaaccagaaagcgtc G/A tctctgcgaaggccctcttg	5457
PEMT	23	intron 4 + 9056	gccagggcctcttgcacttg C/T gggaaagctgagctgagctg	5458
PEMT	24	intron 4 + 9512	ctgagctgggcagcagcatt A/G ctctgtgtgctgctggcact	5459
PEMT	25	intron 4 + 9523	agcagcattactctgtgtgc T/C gctggcactggcctgggtgg	5460
PEMT	26	intron 4 + 9622	gacaaagtgtacaacaagg G/A tctcgaactgggtcagctca	5461
PEMT	27	intron 4 + 10776	ccattcctgggtctctcttg G/A aggctgaatgaattccatg	5462
PEMT	28	intron 4 + 10912	tctgccccactttgtccaga G/C gtgcaacaaggccttcagga	5463
PEMT	29	intron 4 + 11590	ggacactggcctgatgcaga G/C gtgtgtgtctctcctgcag	5464
PEMT	30	intron 4 + 12090	ggccagggcaccctaccag G/C ctgagtcctcactgtccagc	5465
PEMT	31	intron 4 + 12263	taccgcctctccagatgga G/A cgggtgctctcatgggactta	5466
PEMT	32	intron 4 + 12448	tctgggtccctctcctgctt G/A tagtttctgggtgtaaaatc	5467
PEMT	33	intron 4 + 12730	tgggaccagtgcgccacca C/T ggcaccaaggacctgtgtct	5468
PEMT	34	intron 4 + 13240	gggtccagggcacacagcgg G/A ccagtcacacctgtcgttt	5469
PEMT	35	intron 4 + 13494	tccttggaactcagagatgg T/C acctcctgcgaggtggggc	5470
PEMT	36	intron 4 + 13817	aactctccctctgtgtctgag A/G cagatcttggagcctggccc	5471
PEMT	37	intron 4 + 14773	cgcctctgtgtctcatgccc C/T ctatgctctcactgctctg	5472
PEMT	38	intron 4 + 14951	gtcctgagggccctccccc G/A gagcctggggtgccctcaca	5473
PEMT	39	intron 4 + 16896	gctgtgactgtcttggagac T/C gggctctggcgggctgtgtg	5474
PEMT	40	intron 4 + 19439	ccaggagcctctgagggcagc G/A ggggtcttctcaaccacacac	5475
PEMT	41	intron 4 + 19557	atcttgcagcatgtcacgt C/T cctttcataatgaagcaagg	5476
PEMT	42	intron 4 + 20051	acagcactgcgggagccacg A/G catctgcagacgcatttgat	5477
PEMT	43	intron 4 + 20816	tggactctctggcgtccatc C/T agccacttcagtgccagctg	5478
PEMT	44	intron 4 + 21196	ggctggctgggcccctggat C/G atcgtgacaggtcttagtgg	5479
PEMT	45	intron 4 + 21528	acaggtgggagccagggctc G/T ggaagtgggcgggctgagc	5480
PEMT	46	intron 4 + 21596	ccgcttccccgtgctctggc C/T gtacagaaagtgtccact	5481
PEMT	47	intron 4 + 22672	agcctccactgccttgggg C/T tgaggggagggggcggggtc	5482
PEMT	48	intron 4 + 22713	tctaacgctgtctctcttgt A/T ctgaaacacaaacaccttct	5483
PEMT	49	intron 4 + 23010	tgccgggcagcggggagggg G/A ggcagtggttcccccaagt	5484
PEMT	50	intron 4 + 23588	gtgcaggcgcctctgcatccc C/T gcagccaagtctctggcgga	5485
PEMT	51	intron 4 + 23627	gacactgccttgagccagga C/T ggtgaggtgggacgccttcc	5486
PEMT	52	intron 4 + 23941	tgaggggttgggactctaca G/A aggagagtggaactcacgggg	5487
PEMT	53	intron 4 + 24091	gacacctcttctactgtcagc G/T ctgagacacgccccctgccc	5488
PEMT	54	intron 4 + 25348	caggccagttggaatccctac G/A tagagtgaagcatctcagc	5489
PEMT	55	intron 4 + 25603	taagcagtttaactactgatgc G/A tgatgaaaattccaacagca	5490
PEMT	56	intron 4 + 31540	cctccaggtggcaggaacac T/C gtgaggagcatgcaacgtgc	5491
PEMT	57	intron 4 + 31637	gtgggtctgggacgccaggac G/A gtgaggggttcaaggtgtg	5492
PEMT	58	intron 4 + 31642	ctgggacgcccaggacgggtga G/A gggcttcaaggtgtgtttgt	5493
PEMT	59	intron 4 + 35593	ggaggagctgaaagagctgg G/A gctcgggatcaggtgtgtca	5494
PEMT	60	intron 4 + 35647	actttgaggcaccaccgcac C/A tgtccgtgcgtgagggagac	5495
PEMT	61	intron 4 + 35862	tcccagtggtggtctctgcc C/T cgtctcagccagcactcag	5496
PEMT	62	intron 4 + 35882	ccgtctcagccagcactca T/G cggccaggggtggctggactc	5497
PEMT	63	intron 4 + 37141	ccacaggccggatgccttga T/C acttctcagctgcagggctg	5498
PEMT	64	intron 4 + 38862	tggagagaccacctcagaca C/G caaggacgggcatgccatgg	5499
PEMT	65	intron 4 + 38872	acctcagacagcaaggacgg G/T catgccatgggtcccggcag	5500
PEMT	66	intron 4 + 39140	atgtctcaaatctccctccc C/T gggaaatctaggcacaggtc	5501
PEMT	67	intron 4 + 39635	caggcccaggagcaggtggg G/T cctcctcacaggagcagggc	5502
PEMT	68	intron 4 + 39713	actctgagcatgctggctcc C/T tcttcttctccagggcagca	5503
PEMT	69	intron 4 + 40436	cctggttgtgtctcgacc G/A gaggcagacagaggagcct	5504
PEMT	70	intron 4 + 47485	acaatgactgttgagccct C/T gagcaggctgtgtcactgtg	5505
PEMT	71	intron 4 + 48131	actggggatcctgaatccc G/A cctcctgatgccaagtggagc	5506
PEMT	72	intron 4 + 48558	cacagtgtgaactgttaggc C/G acagccacatcttgcggag	5507
PEMT	73	intron 4 + 48702	gagatggggcggttccggga G/A gcaaaagcaggaagggcagaa	5508
PEMT	74	intron 4 + 50302	gcattgtcatgggcagagcc T/C gtctccactgtgagtgagcc	5509
PEMT	75	intron 4 + 54102	ggccgcgtgctcctgcagcc A/T tgggctcctctgagcttct	5510
PEMT	76	intron 4 + 54220	cccagggacagatcttctcc G/A ccagacgtctcttctgctc	5511
PEMT	77	intron 4 + 54371	gcagataatgtgcagctggg G/A tgcattgtgtgtgtgctcc	5512
PEMT	78	exon 5 + 79	tggcctgctactctctaac G/C tcaccatctgctcctgaac	5513
PEMT	79	intron 5 - 6796	ggaggaagtcagctctctac A/C gatggtggctcccagcttcc	5514

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
PEMT	80	intron 5 - 6636	ttttctctctcaccttttg T/C gttcagaggcagaggtgtgc	5515
PEMT	81	intron 5 - 6448	gttgggcccaggtctctgacag G/A accctcgggaccagctcctg	5516
PEMT	82	intron 5 - 5218	ggagccctggctgaagaagc C/G ttacgaccaaggcctggagg	5517
PEMT	83	intron 5 - 4824	ggacaggccgggggttgagc G/A gctgcatgaaggaggagg	5518
PEMT	84	intron 5 - 4249	tcaccagagtgatttctctcg C/A ggcaggtgcctggggtagcc	5519
PEMT	85	intron 5 - 4230	gaggcaggtgcctggggtag C/T cactgggcccgggtccatgag	5520
PEMT	86	intron 5 - 4182	ggagagtaagggtgggggg G/A cacttaggacagggaagctg	5521
PEMT	87	intron 5 - 3369	ccaggtggggccgtgtgcct G/C tggcctgtgtgtggccag	5522
PEMT	88	intron 5 - 2625	cagggaagctgggcccgtaa C/T gagctgggcttttgggccac	5523
PEMT	89	intron 5 - 1200	attattgtgagcatgggaag A/T gcacatttgggtcacacatgt	5524
PEMT	90	intron 6 + 606	gcctggctagaccccacca A/G tgaccctgatgatggcagca	5525
PEMT	91	intron 6 + 1229	tttggtccaggaagggggac G/A gcagccaggagcgtctggtat	5526
PEMT	92	intron 7 + 716	atggagatgtgctcccccg C/G gggtcagaggacctgcggtc	5527
PEMT	93	intron 7 + 1537	ctctgggggacgcataagcc G/A cctccagaggacatcagcca	5528
PEMT	94	intron 7 + 1718	gggcttcacagtgcttgagc T/C ccccgcatgtaggaccacca	5529
PEMT	95	intron 7 + 2695	ggctttgggggacctggac C/T catttctagaaaacagcctt	5530
PEMT	96	intron 8 + 140	ccagggtctccaggtcagag C/T ggccatggtagcttacaatg	5531
PEMT	97	3'flanking + 179	tacttaggagcgctcagggg C/T tcacctggccatggccatgg	5532
PEMT	98	3'flanking + 394	gatgacactgtcattcctaa A/G tgaatggcctgtgtgctgacc	5533
ALDH1A1	1	intron 1 + 564	cattattttcttcagccaagt T/C tgttgccattggagcagatg	5534
ALDH1A1	2	intron 1 + 710	gttctgagagtaactctgaa C/T tttgctgtttcacactgct	5535
ALDH1A1	3	intron 1 - 3868	ccctttttatataccagaata C/G agcctaaactcttctctcg	5536
ALDH1A1	4	intron 2 + 2933	taagtatgctatactatatt T/C gatagatactatactata	5537
ALDH1A1	5	intron 2 - 1646	caatgtgattaaactgaatgc C/T gcaaatatgcactgtatatg	5538
ALDH1A1	6	exon 3 + 54	caggcttttcagattggatc C/T cgtggcgtactatggatgc	5539
ALDH1A1	7	intron 3 + 157	taggccccttaacattgaac T/G attctcaaatagtaactctgc	5540
ALDH1A1	8	intron 3 + 339	tgagtctctctagaatgat G/A ttaggttttattcaagcattt	5541
ALDH1A1	9	intron 3 + 655	agcagtttagatgagtcagag C/A ataataatgtgggggaggg	5542
ALDH1A1	10	intron 3 + 735	gaagccaatttaacataaac C/A aataccaagatcaggtttca	5543
ALDH1A1	11	intron 3 + 863	gcaagtatggttaatacaag G/A accattttactcaaatat	5544
ALDH1A1	12	intron 3 + 1757	agatgacaagatttcttcta T/A ttcaaaaattccctagcaca	5545
ALDH1A1	13	intron 5 + 90	ttctctaaacagatggatg C/A ttatgtatttggtaaatgtg	5546
ALDH1A1	14	intron 6 + 213	caggaagccaaacacaagg T/C ttgggtgcaaacagtcact	5547
ALDH1A1	15	intron 6 + 1323	ttttgaattaaattcttata C/T tgaacttttaaacctttta	5548
ALDH1A1	16	intron 7 + 638	gcaaaagaaagtgggtggaag C/A atactgtaccatgcataaaa	5549
ALDH1A1	17	intron 9 + (1462-1463)	aatggaattctatgtttttt (T) gttgtgattattttatctatc	5550
ALDH1A1	17	intron 9 + (1462-1463)	aatggaattctatgtttttt gttgtgattattttatctatc	5551
ALDH1A1	18	intron 9 + 1757	tgatctagaatttagtttct A/G taaatgaatagaatccagtg	5552
ALDH1A1	19	intron 12 - 1383	aatcccacttattactctcc T/G gagagcttcaagtcctata	5553
ALDH1A1	20	3'flanking + 40	ttttaagtacaagttttggt T/C acagtgattttcttctgtca	5554
ALDH1A2	1	5'flanking - 716	cagggtatctctattctgagc C/G cgaggcgaggggactcgca	5555
ALDH1A2	2	intron 1 + 314	cgttcccgactgcgcgggg G/Δ aaggcgtcggaacccgttag	5556
ALDH1A2	3	intron 1 + (664-675)	ttttgaactgaagaacttac (T)11-13 ataacgaactgtgacatctt	5557
ALDH1A2	4	intron 1 + 1370	gcattgcagcttagaagtttt A/G ttttatgaggggtctctaaac	5558
ALDH1A2	5	intron 1 + 1557	ggtagcttttttcagaattta A/Δ ttgggaagctcttccagttc	5559
ALDH1A2	6	intron 1 + 1934	tcagctcttttagtgagactt C/G taaattttctaaagacaagca	5560
ALDH1A2	7	intron 1 + (1971-1980)	agcatgtgggacaagcagta (T)9-11 aaactgtgaagagcagaagct	5561
ALDH1A2	8	intron 1 + 2295	tactgtaagacaatatgtta T/C tgtttttgtcttgcataac	5562
ALDH1A2	9	intron 1 + 2387	ttgggcccacatagagtgca C/T tacttaaaataaatgaccag	5563
ALDH1A2	10	intron 1 + 2841	aggaatgtgcttttttaaac T/Δ agatgggtgttagtcaaggag	5564
ALDH1A2	11	intron 1 + 3035	gacttttataattttgtata A/G ctgatattataggaatacac	5565
ALDH1A2	12	intron 1 + 3319	aaagagttatgttttttttt T/Δ ctgcatctgatattatattg	5566
ALDH1A2	13	intron 1 + 3474	ttgtctttttattattcat T/C taaacttctgttttctgggg	5567
ALDH1A2	14	intron 1 + 4186	ccctccaaaccttttaactaa G/C attgtctgttttgggtcataa	5568
ALDH1A2	15	intron 1 + 4222	cataaattgtcagtcataact A/G catgttaatagaggacttca	5569
ALDH1A2	16	intron 1 + 4254	aggacttcaagtttttttttt T/Δ aaatacttttccataactat	5570
ALDH1A2	17	intron 1 + 4397	cccttccactacatgggctt A/G tgttaccatgtggaattatc	5571
ALDH1A2	18	intron 1 + 5935	aactccaggttgcaaataga T/C gtttctgtgtatttttaagtag	5572
ALDH1A2	19	intron 1 + 6206	ttttgaaagccctcttagca T/G ttctttaatttctttattga	5573
ALDH1A2	20	intron 1 + 9559	agataaattgatgaattatt C/T actctgtgctgctgatagat	5574
ALDH1A2	21	intron 1 + (9631-9632)	taaaaagaattttctaaaaga (AAGA) ccttttttttgaataactct	5575
ALDH1A2	21	intron 1 + (9631-9632)	taaaaagaattttctaaaaga ccttttttttgaataactct	5576
ALDH1A2	22	intron 1 + 12731	ctgaaatagaaacctttcag T/A gtacctgacagagcagtgaa	5577
ALDH1A2	23	intron 1 + 13442	cagtgctcataaagatccagc G/A gaaatcaaatgtttcatat	5578
ALDH1A2	24	intron 1 + (14173-14176)	tctaaaaataaataaata AAAA/Δ gagaaaattaagtttaagat	5579
ALDH1A2	25	intron 1 + 14586	actcatttattgggtcaaac C/G cttcttcaaccttaggatag	5580
ALDH1A2	26	intron 1 + 14595	ttgggttcaagaccttcttca A/G ccttaggatatgcattgagg	5581
ALDH1A2	27	intron 1 + 14711	gtttgagacattaacttcta A/G ttaactgaagatgctagtt	5582
ALDH1A2	28	intron 1 + (15327-15337)	gaagagcacagtagaaagac (T)9-11 aacctagcaataactattga	5583
ALDH1A2	29	intron 1 + 17258	atcagtcacatgtgttgggc A/G tacaacacttaatttaaat	5584

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ALDH1A2	30	intron 1 + 18277	taatacaaatcatttgaagc A/G tttactattaaaaaaca	5585
ALDH1A2	31	intron 1 + 18734	ctttgagcactactgcatt T/A taagtgcgtgtaagatgtgg	5586
ALDH1A2	32	intron 1 + 19081	ttaatcacctcaatctttaa C/T gaatttcttgattttcttt	5587
ALDH1A2	33	intron 1 + 21514	aatcaggatattgggggttc G/A tctttattctgccacaaat	5588
ALDH1A2	34	intron 1 + 21732	cattttaaaatagtgcttta A/G taggacttggtgttaag	5589
ALDH1A2	35	intron 1 + 21865	tggcatagggttataaatgt C/T tgtgttaggactctttcca	5590
ALDH1A2	36	intron 1 + 26282	taaagaaggagaaaaaaa A/Δ ctaatctgagactttgcagg	5591
ALDH1A2	37	intron 1 + 27805	ggatgatgctacccaaggaa T/C tgcacacttccagacagtac	5592
ALDH1A2	38	intron 1 + 28204	tcactccatttttaactgt C/G cttcctaataatgtgtggttaa	5593
ALDH1A2	39	intron 1 + 28521	tctttgttacacttctttaa T/C cggggtatcagataatcttc	5594
ALDH1A2	40	intron 1 + 49478	gaataaaaggataggacat G/T ggtaagaccactttttccct	5595
ALDH1A2	41	intron 1 + 49834	gcctctcaattttctcatgt G/T taatagagagaaaacctgc	5596
ALDH1A2	42	intron 1 + 50351	gactgactgggttcataagtt C/G agaaatttcaactgtgtgtct	5597
ALDH1A2	43	intron 1 + 51181	tggtattaccatagtagttc C/T gtaacacttggcgtgtgact	5598
ALDH1A2	44	intron 3 + 654	ttaacctctcttgagtaaaa G/A gaatccttcagaaccagg	5599
ALDH1A2	45	intron 3 + 668	gtaaaaggaaatcctcagaa C/T cagaggggatgtgtacggacc	5600
ALDH1A2	46	intron 3 + 712	catacacttctgtctcgttt G/T cctctgctattctgtgagcca	5601
ALDH1A2	47	intron 3 + 1273	tattcactgtgtaaaaagg T/A gtttcatgggtgaagaaatc	5602
ALDH1A2	48	intron 3 + 1743	ccacacctaaatgagattcc C/T gttttaaacactctcaagct	5603
ALDH1A2	49	intron 3 + 2891	tgcacatatatactcattgt A/G gtttttactaggaactagac	5604
ALDH1A2	50	intron 3 + 2919	ctaggaactagaccacactg G/A cagtactagaaatcttttta	5605
ALDH1A2	51	intron 3 + 3054	tggaaagtctctggggactta G/C tatctctccatttctcttc	5606
ALDH1A2	52	intron 4 + 290	cattgtgctagattaggtgc T/C ggggttaggtatgaaggggca	5607
ALDH1A2	53	intron 4 + 380	ctccttgccctcctgaacaa C/T ataagatctactctttggaa	5608
ALDH1A2	54	intron 4 + 461	gattatggctgattttcagt T/C tcttttaataattttctct	5609
ALDH1A2	55	intron 4 + 506	tctatatttctcgaacggcc G/A tgaattactttcataatcta	5610
ALDH1A2	56	intron 4 + 1952	ttggtccctcactccactgt C/G atttcattattaaaaaca	5611
ALDH1A2	57	intron 4 + 2079	ctctatttggcctaaccgta C/T cttgggtttcttttacttcc	5612
ALDH1A2	58	intron 4 + 2519	ttgggtcataagagctctct C/G catgggtctcacaacagatg	5613
ALDH1A2	59	intron 4 + (2840-2851)	ttgtctctgcatacttggc (T)11-13 cacagtgaagtctggaatat	5614
ALDH1A2	60	intron 4 + 7231	aataggatacaaatacacaa A/T gatagtgttcagatcctaa	5615
ALDH1A2	61	intron 4 + 7958	taaaatcgtttttattgtta C/T taggtatataaaattgtcta	5616
ALDH1A2	62	intron 4 + 8090	tctgattttatcactgttta C/T agattgcttagtcatactca	5617
ALDH1A2	63	intron 4 + 12823	tgttagcctgtagctaaatg C/T ttttcaaatatgtgaacggt	5618
ALDH1A2	64	intron 4 + 12939	atgagggtccgacttttaaga T/C ttttgcctacattttcttc	5619
ALDH1A2	65	intron 4 + 14935	tattgtaggagtctttttaa T/G aaatggacttttacccttct	5620
ALDH1A2	66	intron 4 + 15321	gcattttgggtgtctgagaga C/T atatccagaaatgtctatg	5621
ALDH1A2	67	intron 4 + 15412	tttcaagtttatttctgttt T/G tttttttttttttttttttg	5622
ALDH1A2	68	intron 5 + 1888	aatccaaacatctgtacttt G/T tagtggaacagatttatgtc	5623
ALDH1A2	69	intron 7 + 9166	gaaaagctactttattcaaa G/A ataaaagtattttaagaaaa	5624
ALDH1A2	70	intron 7 + 9914	aaagctggagaaaatactagg C/T tttcctcaacagtgtttcc	5625
ALDH1A2	71	intron 7 + 18942	tttgagggggaactaatccc G/A tgacttctaggttatctctt	5626
ALDH1A2	72	intron 7 + 19820	ttcaccctcatttttaggtt A/G ggggaggtggctgtctacag	5627
ALDH1A2	73	intron 7 + 19826	cctcatttttaggttagggga G/A gtggctgtctacagttttag	5628
ALDH1A2	74	intron 7 + 19913	cgtgaatcattcagttatttt A/G tttaaaaataccagtttgaa	5629
ALDH1A2	75	intron 7 + (20110-20111)	catgatttattctctaacta (ACTA) tgctaagtcaaaagattctgc	5630
ALDH1A2	75	intron 7 + (20110-20111)	catgatttattctctaacta tgctaagtcaaaagattctgc	5631
ALDH1A2	76	intron 7 + 21857	acaatgaaaattaagaagg A/T gaagagggaagaagcagaga	5632
ALDH1A2	77	intron 7 + 21929	tacaagacacaggcatcttt A/G actagtttactgggatctct	5633
ALDH1A2	78	intron 7 + 23308	ggctttgacttcggaaacct G/T tgggttataacaaagtactg	5634
ALDH1A2	79	intron 7 + 23554	gacattgggtgaaaaccagg C/T tgggttaggagtgctctgtcc	5635
ALDH1A2	80	intron 7 + (23701-23703)	catctgagatttgccttctg GTG/Δ tttaccaggttagtggtg	5636
ALDH1A2	81	intron 7 + 26479	gatacatgaacaatttgggt T/C atctcatgatattcttcaa	5637
ALDH1A2	82	intron 7 + 26561	taaaggccacaatgcagtga T/C tgaatctccagttacattt	5638
ALDH1A2	83	intron 7 + 26662	tttcttagtctctccatca C/T gaaactaaagctgtcttcca	5639
ALDH1A2	84	intron 8 + 76	tttatatctccacttttgat G/A ggacactagcaaaagatatt	5640
ALDH1A2	85	intron 8 + (700-711)	accatctcatcagtgatcc (T)11-12 cctccacttgttggcaggc	5641
ALDH1A2	86	intron 8 + 724	ttttttttccctccactgt T/C gccaggcagagctgtttcc	5642
ALDH1A2	87	intron 8 + 800	cagattgcttgaatttcagc C/A ccagcttggaaatttgcagag	5643
ALDH1A2	88	intron 8 + 1251	gatttctgtgaaaattgaga G/A gatctggcaacctggggctc	5644
ALDH1A2	89	intron 8 + 1627	ggccctcccccaggcaaacg G/A gtgagaacatggctgtttcc	5645
ALDH1A2	90	exon 9 + 141	tggagcggggccaagaggcg G/A tagtggggagctccctttgac	5646
ALDH1A2	91	intron 9 + 778	aaccagctcggacagatccc T/C tgtagcttgtgaaagtgtag	5647
ALDH1A2	92	intron 9 + 801	tagcttgtgaaagtgttaga A/G gtgaaggctgggtcacttc	5648
ALDH1A2	93	intron 9 + 868	tctgaaggcctcgtgtact T/C agtgggggtggggaggccac	5649
ALDH1A2	94	intron 9 + 1338	aatttttgcctcttttact A/G tcaatacaacttgcctaagtt	5650
ALDH1A2	95	intron 10 + (227-229)	ctatgtgcttatgattatta TTA/Δ gccaacagaacaatcagaat	5651
ALDH1A2	96	intron 10 + 316	ctaaatgtgggtcactggga T/C gttaaccaggagagagaatc	5652
ALDH1A2	97	intron 10 + 368	ctttacatctgtgcaagaga G/A ggacaaggagcaaatcagcc	5653
ALDH1A2	98	intron 10 + 660	gtaaacttgcattgaaatgt G/A gaaagcaggtaaaggaatga	5654

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ALDH1A2	99	intron 11 + 104	tggggaataccaaaagcaac C/T aaagttcaccagaaaagggg	5655
ALDH1A2	100	intron 11 + 229	aaacttctaaaagaaatacc A/G tgccagtcagattatgtgct	5656
ALDH1A2	101	intron 12 + 117	catacattcaacaacattt C/T gtggagcacatgtactata	5657
ALDH1A2	102	intron 12 + 691	gataggggaagatcactgtga A/G ctggaaaaatctgggaaacc	5658
ALDH1A2	103	intron 12 + 1934	catcttgtctagattgcacg T/C ttgtttgtttgtttgtctct	5659
ALDH1A2	104	intron 12 + 1973	ctacttaccctccaaaacatg T/A ttctctttcttctaaatgacc	5660
ALDH1A2	105	intron 12 + 2722	ccagagtgactccagtatac C/A tcaactgcccaggaccacag	5661
ALDH1A2	106	intron 12 + 3855	cacttgaaagcaaccataat T/C gtgaggtttctgatgctgta	5662
ALDH1A2	107	intron 12 + 4185	ttgtcttaagcgaaatgaac T/C atacggacagaggaacacgcc	5663
ALDH1A2	108	intron 12 + 4991	acaggaacacttagacatgc A/G acccactccaccctccgtc	5664
ALDH1A2	109	intron 12 + (5018-5019)	cccaccctccgtcttggggg (G) aggaagcacactactgtcc	5665
ALDH1A2	109	intron 12 + (5018-5019)	cccaccctccgtcttggggg aggaagcacactactgtcc	5666
ALDH1A2	110	intron 12 + (5051-5052)	actgtcccaagaactaata (A) ctgaaccagtgctgccttgt	5667
ALDH1A2	110	intron 12 + (5051-5052)	actgtcccaagaactaata ctgaaccagtgctgccttgt	5668
ALDH1A2	111	intron 12 + (5300-5302)	ttaaagtttttaaaaaactt CCT/Δ taaaaactactcatgagatg	5669
ALDH1A2	112	intron 12 + 5405	catcccaggacttgcgttgc G/C caggtgataaactgcacctc	5670
ALDH1A2	113	intron 12 + 5435	aactgcacctccccaggact C/A ccgctgcactcacatgcagc	5671
ALDH1A2	114	3'flanking + 449	tttgggcccgggaacaatttt T/C caaggttgtaaagccaaatt	5672
ALDH1A2	115	3'flanking + 597	acctgggatattctctgaccc A/C atctgggtttcttttaccga	5673
ALDH1A2	116	3'flanking + 669	atagagactggaagtcatca T/C gtgcagttcacccgttctga	5674
ALDH1A2	117	3'flanking + 1122	cgctgctccactgagctcctc T/G gtcacacccattcttggccc	5675
ALDH1A2	118	3'flanking + 2214	tgcagctgttaaaagaaatc T/C gtaaatgggtgacgtactac	5676
ALDH1A3	1	5'flanking - 1425	cagtgtagccagccgatat C/T ggtcaaggctgccccgctcg	5677
ALDH1A3	2	5'flanking - 1379	ccattatccccctttcccccg C/T ctcagctgtgcactccaggc	5678
ALDH1A3	3	5'flanking - 1270	aacttaccctctatccagc T/A ctatccagaaggacaccagg	5679
ALDH1A3	4	5'flanking - (1214-1213)	acggaggcctcaaacaggga (GGA) aaataaggagaccctcccc	5680
ALDH1A3	4	5'flanking - (1214-1213)	acggaggcctcaaacaggga aaataaggagaccctcccc	5681
ALDH1A3	5	5'flanking - 1103	gcacagcttttgcagagtg C/T cgctgctccgtctcttggct	5682
ALDH1A3	6	intron 1 + 986	gccttaactttccccacctt T/G ggcttctcttgatttttgct	5683
ALDH1A3	7	intron 1 + 1462	gtacaggatttcaaaatact G/A tatatagaaccagacagta	5684
ALDH1A3	8	intron 1 + 1661	cctgtgtcttgggtgggtgc G/A caacctttgcagttaaagg	5685
ALDH1A3	9	intron 1 + 2360	agaggatagaagtcctcttct A/G atttagaggccctcttctct	5686
ALDH1A3	10	intron 1 + 2516	tgaatacatattctttttga G/A tttagctgagtgccctgttg	5687
ALDH1A3	11	intron 1 + 2624	cctgagacaccttacagctc C/T gtccctgcttccatgtcatc	5688
ALDH1A3	12	intron 1 + 3255	tttcatctttctacaaatgg G/C cccctcttctgctgcact	5689
ALDH1A3	13	intron 1 + (3643-3656)	gcttcagagggtttttgtggg (T)12-14 aacattctatcaacttttaa	5690
ALDH1A3	14	intron 1 + 4265	ccaaaagccctctctttttaa T/C atgacattaataagacaatt	5691
ALDH1A3	15	intron 1 + 5187	caagatggataagacgtcac C/T taaggtccttagcatgtga	5692
ALDH1A3	16	intron 2 + 43	ctotaagtaattcaattatg G/T atgaccaaaaggataaggaaa	5693
ALDH1A3	17	intron 2 + 127	cagggcctgggctagctgcg T/C gaattggcatgtggttctca	5694
ALDH1A3	18	intron 2 + (285-300)	aggaagggttttcttttttc (T)16-17 atcaattatttggacctgga	5695
ALDH1A3	19	intron 2 + 778	cggtgtcagagtaggcttgg A/G ttttatcttgcctatgagtt	5696
ALDH1A3	20	intron 2 + 1216	actcggtagagtcactcctg A/C ctggtgtcccacatccactc	5697
ALDH1A3	21	intron 3 + 81	accatgggggtatgggaaaaa A/C gatcacggctcctggttttg	5698
ALDH1A3	22	intron 3 + 236	gctcagcttcttgaccagt T/G gttgtctataggcagttgag	5699
ALDH1A3	23	intron 3 + 1467	ggcccgggttaggggagga G/T atctcctttctgaccttga	5700
ALDH1A3	24	intron 3 + 1725	ccacatgttccccgggtgag A/G gtgactcctcccagggttaa	5701
ALDH1A3	25	intron 3 + 3777	gccagaagtagatgcccca A/G ttcagctgctgcattactgg	5702
ALDH1A3	26	intron 3 + 3829	caagtcactgggcccgttagc G/C tccgtgctgcaccttgaag	5703
ALDH1A3	27	intron 3 + 4299	tcaatttccacagccacact G/A gccagcctggccgagaagga	5704
ALDH1A3	28	intron 4 + 84	agagccccccctgactgttt C/G cctaaggcaccattcccaac	5705
ALDH1A3	29	intron 4 + 126	ccactccctctccaaatggt A/G ctgccaaattcttcttctaag	5706
ALDH1A3	30	intron 6 + (290-291)	tagagaattttcaggggggg (G) tcaaccaagaggagccaaa	5707
ALDH1A3	30	intron 6 + (290-291)	tagagaattttcaggggggg tcaaccaagaggagccaaa	5708
ALDH1A3	31	intron 6 + 705	aacagctggttagagccaa T/G ttccactttcctttgttga	5709
ALDH1A3	32	intron 7 + 56	ggggcgtgttatttgacacc C/T gtgagcttttcttcttgacag	5710
ALDH1A3	33	intron 7 + 1107	gatgctgttactctctctgg A/G gacagacactgacctgtgga	5711
ALDH1A3	34	intron 7 + 1610	aagagccacacagaccacc C/G ccctactgggtgtgtggaat	5712
ALDH1A3	35	intron 7 + 1820	cacctgtaagtggagcggt T/C agaccaagatcccaggatg	5713
ALDH1A3	36	intron 8 + 963	gagaaaggacaggaggagga C/T acaggctctcaggaaaggaaa	5714
ALDH1A3	37	intron 8 + 1824	accattcttattccactaagc G/A tgtcccccagatcttattc	5715
ALDH1A3	38	intron 8 + 2384	cgctccctctgcccctcccc C/A tccagtggaactggcagtg	5716
ALDH1A3	39	intron 9 + 24	atccccctggtgtgtgtgaa A/C ccattggtgctgtctagggg	5717
ALDH1A3	40	intron 9 + 91	gcctacaggggtccctctccg T/C gaaaggaatgctgacctgtc	5718
ALDH1A3	41	intron 9 + 219	actgaggcatgggaggagg C/G gctattcccagggcagaaagg	5719
ALDH1A3	42	intron 9 + 435	ccagacggagagagcctggg G/A caggagaatgtatctccagg	5720
ALDH1A3	43	intron 9 + 1472	ttgactttttagggccagata C/T accgattttctccaagagaa	5721
ALDH1A3	44	intron 9 + 2038	taacaatgtgttctctacgg G/A ctctccaggaggtgtggagt	5722
ALDH1A3	45	intron 9 + 2124	caaacagggtctgccagatg G/A catatgccacagcagccagg	5723
ALDH1A3	46	intron 9 + 2154	agcagccaggaggacctgc G/C gttgggccaagccctgtgt	5724

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ALDH1A3	47	intron 9 + 2197	cttttggcccccagggagg G/A gaagagcagctcagcagcat	5725
ALDH1A3	48	intron 9 + 2466	ttcttagttcctcatgtttc C/T ctctagaatgttttcgtgtg	5726
ALDH1A3	49	intron 9 + 3655	gatttggtcaagtgccatgca C/T ggtttatgccctctctcctg	5727
ALDH1A3	50	intron 9 + 3954	gggtgcgcttttgacaactg C/G tcagtagcgtgttcacaagc	5728
ALDH1A3	51	exon 10 + 88	tggaaatcgggggctcagcc A/G tggaaagacaaggggctcttc	5729
ALDH1A3	52	intron 10 + 8	tgccaaagaggaggtacaag G/A gggctgtggcaaggctacga	5730
ALDH1A3	53	intron 10 + 307	ctctctgatttttctaacaca A/C ccggtccccagtcagtcac	5731
ALDH1A3	54	intron 10 + 378	gtgggttttgccaggaatca G/A ttcaagaacctgtggattca	5732
ALDH1A3	55	intron 10 + 975	aatattgtgtcattctctcc C/G ctggtagtattatggaaac	5733
ALDH1A3	56	intron 10 + 1088	cagtgcaggagccaggggg C/T ctctccagatgactctgag	5734
ALDH1A3	57	intron 11 + 105	ttgtttacattgtatattat A/G taccagccctgtctcagtg	5735
ALDH1A3	58	intron 11 + 274	agggctccagtcactgtgcc T/G gtggccctgtgctgtactg	5736
ALDH1A3	59	intron 11 + 1088	cagtgcaggagccaggggg T/A ctctccagatgactctgag	5737
ALDH1A3	60	intron 12 + 96	ctccaatctgctgacacccc G/A tccccccacaccgccgctc	5738
ALDH1A3	61	intron 12 + 1537	gggccttggttgggggccttt G/T tgggtctctcttttgagatt	5739
ALDH1A3	62	intron 12 + 1660	gtccccctccacactcagtc C/A tggcttgtagtccatccctg	5740
ALDH1A3	63	intron 12 + 5642	tctgtgctaactctgcttc T/C ctcatgcccccttaggctggc	5741
ALDH1A3	64	exon 13 + 104	gggcctctctctcaaacatc G/C gacggcggaatgtggcagat	5742
ALDH1A3	65	exon 13 + 281	ataggttgtctgtgaaatcg C/T agtccgtcctggggaggag	5743
ALDH1A3	66	3'flanking + 743	gtgagcaggaaactgtagga G/A aaggatattttccctcattt	5744
ALDH1A3	67	3'flanking + 1145	gcctccagctacccccacc G/A cctcaggaggggtcattcca	5745
ALDH1A3	68	3'flanking + 1185	aacctagggtgtctgagaatc T/C ggggtgggattaccagcaaaa	5746
ALDH1A3	69	3'flanking + 1600	acaccacgcccctgcaaatg T/C tgggaaactgtcgggtggcaa	5747
ALDH1A3	70	3'flanking + 1847	caggagccctcgccgtgcc C/G ggttctgtgaaatggcagtg	5748
ALDH1B1	1	intron 1 + 134	cgttgcactgtaggactctc C/T ccacgtccccctaatcccatc	5749
ALDH1B1	2	intron 1 + 367	gcagttccccggtatagaga A/G ggtccggtccttccccctgt	5750
ALDH1B1	3	intron 1 + 405	tgtgggtgaactgttaaaaa C/T tgcctgtattcaggaggata	5751
ALDH1B1	4	intron 1 + 2002	cttcaactaatctgggaaca C/T tacactctgtttaattttca	5752
ALDH1B1	5	intron 1 + 2157	tgggaaagctgaaaaggat G/T ctgagacctgtggtggggg	5753
ALDH1B1	6	exon 2 + 192	ccgacggtcaaccctaccac T/C ggggaggtcaattgggcagct	5754
ALDH1B1	7	exon 2 + 265	cgtgaaagcagcccggaag C/T ctcccgctgggggtccccat	5755
ALDH1B1	8	exon 2 + 329	gcggggccggtgtgtgaacc G/T cctggcagacctagtggagc	5756
ALDH1B1	9	exon 2 + 614	acttgccccggcactcgcca C/T aggcacactgtggttatga	5757
ALDH1B1	10	3'flanking + 168	aaagtgcacactgtaagacc G/A tagagaaaaactctggttcc	5758
ALDH1L1	1	intron 1 + 252	cgcagcgcaggactggccc G/C ccgaggatctggccggccgc	5759
ALDH1L1	2	intron 1 + 544	ctcaggggctgcgtgtgagt C/T ccagctccagccactgcct	5760
ALDH1L1	3	intron 1 - 6596	cagatttttcttaaggtgca C/G tagccactgaggatattttt	5761
ALDH1L1	4	intron 1 - 6513	caattatggtttatcttagg G/A acatgtttatagagatagta	5762
ALDH1L1	5	intron 1 - 6478	atagatttcttaacttagctt G/A cattctaaattttgttccct	5763
ALDH1L1	6	intron 2 + 240	gtggcattaggtcctggag A/G agggctatagagaagcccag	5764
ALDH1L1	7	intron 2 + 1326	gaggaggagaccggagagga G/C agccagctccagtcaggggcc	5765
ALDH1L1	8	intron 3 + 386	gtcctaetcttaacttccact G/A ccgctgctctgggcagcaca	5766
ALDH1L1	9	intron 4 + 271	gggcccgttcaatagacaag G/C aaggctaaaggcagggactg	5767
ALDH1L1	10	intron 4 + 356	taggattctatttctctctc C/T ttcaactcgttgattctcctt	5768
ALDH1L1	11	intron 4 + 608	gtgctctgataggctgtctc A/C gtcacatgcttctgctggg	5769
ALDH1L1	12	intron 4 + 664	ggtcacatggcctgagcggc A/G gggcggtcagtcacctggg	5770
ALDH1L1	13	intron 4 + 785	gagggtctgttgcctctgcc C/G gaggacaggctggcagggaac	5771
ALDH1L1	14	intron 4 + 874	ccctggggagcccttctgtg T/G tgggcgcagcaggaagagca	5772
ALDH1L1	15	intron 4 + 1349	tcctcaggctcttctgtcac G/A tggggccagactccttggct	5773
ALDH1L1	16	intron 4 + 1799	ctggggctgggaaggaggca G/A ggtcctattgctggggatag	5774
ALDH1L1	17	intron 4 + 1815	ggcagggtcctattgtgtgg G/A atagcaaccactggatctc	5775
ALDH1L1	18	intron 5 + 272	aaagcccacaggagataag A/G gtgggaggttagggggcaaaa	5776
ALDH1L1	19	intron 5 + 301	tagggggcaaaacgtcagcc G/A tagtgcgagcagctcttcaag	5777
ALDH1L1	20	intron 5 + 343	caagggtgtgaggagacagtgc G/A ggtctctggagcaatagcca	5778
ALDH1L1	21	intron 6 + 926	cctgcctgggctactggctt C/T gggggctctctctcaccac	5779
ALDH1L1	22	exon 7 + 41	aacgctgaacacttcaggcc T/C ggtgccgaggagacgctt	5780
ALDH1L1	23	intron 7 + 305	cctagaatcagagagaagcc C/T tcccaggagcctgggttca	5781
ALDH1L1	24	intron 7 + 837	gtccggacaaacccctggg C/T gtggatccccagccgtgtt	5782
ALDH1L1	25	intron 7 + 866	cccagccgtgtgtgtgtgc C/T ggcctaccagagttaggcgt	5783
ALDH1L1	26	intron 7 + 884	tccggcctaccagagttagg C/T gtggcagtatggggcctggc	5784
ALDH1L1	27	intron 7 + 1118	aatgttccagaaaatcatgc G/C aggcagtaagggcagaggaa	5785
ALDH1L1	28	intron 7 + 1168	aaagtaaaaggttcaggagaa G/A tctagcctggggctgctccc	5786
ALDH1L1	29	intron 7 + 1451	cagggcacccacagcatctg T/C ccagagacctgcaaaagacag	5787
ALDH1L1	30	intron 7 + 1489	caggaaatgcaagaaggcaa T/C taagtgtcttaaggaggagc	5788
ALDH1L1	31	intron 7 + 1579	tcagggtgggaggggagtga G/A gagagaccagctgagcacac	5789
ALDH1L1	32	intron 7 + 1691	ctggctgggctttagcttgc A/C gaaagctccagaacatcttt	5790
ALDH1L1	33	intron 8 + 1632	tcagggttgcatttgttcc T/C gtgcacattcagagttccag	5791
ALDH1L1	34	intron 8 + 1799	gctcaagtctctcttagct G/C ttcaccgtgcagccccctaa	5792
ALDH1L1	35	intron 8 + 1986	ggtggaggggcctggcctgt G/T gctgttcaggagaacgctcc	5793
ALDH1L1	36	intron 8 + 2002	ctgtggtgttccaggagaac A/G ctccaagagcctgctgtggg	5794

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ALDH1L1	37	intron 8 + 2627	aaagaggagagccgggggtg C/T ttgtgccaggggttggggga	5795
ALDH1L1	38	intron 8 + 2646	gcttggtgccaggggttgggg G/A aactggttctgattgggctt	5796
ALDH1L1	39	intron 8 + 2925	ctgctgccctccataggtcc C/G agactgaatcctctcagagga	5797
ALDH1L1	40	exon 9 + 4	caggtcttctgtttgcagagt G/T ttgtgcagcggatcctcccc	5798
ALDH1L1	41	exon 10 + 109	cagctgttagtgaggaagct G/T cgaggggacgatgaggaggg	5799
ALDH1L1	42	intron 10 + (671-672)	tggcatttttctctgtctga (AG) gtcctcttagccaccctaa	5800
ALDH1L1	42	intron 10 + (671-672)	tggcatttttctctgtctga gtcctcttagccaccctaa	5801
ALDH1L1	43	intron 11 + 8	caccgatggaagtgtgagtg C/A agggccagcaccctctctcc	5802
ALDH1L1	44	intron 11 + 447	atgagccaaagcagccctat G/A gtatgatacacacgtgaacat	5803
ALDH1L1	45	intron 11 + 601	ctcaaatgagtcatttgag A/G ggagttaatgaaagactcat	5804
ALDH1L1	46	intron 11 + 639	catctgcaaggagagggga G/A ggggttagggacacagacagg	5805
ALDH1L1	47	intron 12 + 66	ctgggcagtgccagggggg G/A acttctgtggagccctttt	5806
ALDH1L1	48	intron 12 + 478	ctattaaaaaaaaaaaaaa A/A ttttaagccaggagaaaggg	5807
ALDH1L1	49	intron 12 + 684	tcctgggagaagagaggggtg C/T gggcagatgagccgagaaca	5808
ALDH1L1	50	intron 12 + 767	cgctaggggtgcgaagcca A/G gttatggcggtgtcccaacg	5809
ALDH1L1	51	intron 12 + 1014	tcataaggttccagtcctctt C/T gcaagccctcaattctaga	5810
ALDH1L1	52	intron 12 + 1359	ctggttctgcctcagctcag C/T acagcagaggctgggtctag	5811
ALDH1L1	53	intron 12 + 1734	gggtggtccagctgctggtg G/T tcagtagggcgccgagacc	5812
ALDH1L1	54	intron 12 + 1901	ttcagcagcctaactgaatt G/A acaatagaatagtcctgcaa	5813
ALDH1L1	55	intron 12 - 470	gggatggggccacctctcca T/C ctctggagatgccaggctca	5814
ALDH1L1	56	intron 12 - 334	aaggcgagcctcttggggca T/C gaccccttctgtctctgag	5815
ALDH1L1	57	intron 12 - 325	ctcttggggccatgacctctt T/C gctgtctgcagcaagtgggt	5816
ALDH1L1	58	intron 12 - 221	gaagggaagcgaggaagatc G/C aggaaggagagagggagacag	5817
ALDH1L1	59	intron 12 - 4	cccgcttccccctcaccctgg T/C caggttgccagatctcatgg	5818
ALDH1L1	60	intron 13 + 34	tcccaccagctgtgagcaca T/C gcagactggcccagccatat	5819
ALDH1L1	61	intron 13 + 58	gactggcccagccatatagg A/G gaactccaagggcagcacag	5820
ALDH1L1	62	intron 13 + 125	ccacaactggtggtctggaa T/C gacacctgtttattagcttg	5821
ALDH1L1	63	intron 13 + 126	cacaactgtggtctggaaat G/A acacctgtttattagcttg	5822
ALDH1L1	64	intron 13 + 281	acctgcattccagacaggttc T/G ggtgttgacagagttcagtt	5823
ALDH1L1	65	intron 13 + 299	tcggggtgtgacagagtcca A/G ttccgtgtggatgcagggct	5824
ALDH1L1	66	intron 14 + 121	catttatcaaacagccatcc A/G tgtgcttcttgagcactgc	5825
ALDH1L1	67	intron 14 + 167	gccaggcattgtgttaagga C/T ttgaggacaattgtatttaa	5826
ALDH1L1	68	intron 14 + 205	taatctcccagtaaacactgg A/C tcagtcaggtccacgggtggg	5827
ALDH1L1	69	intron 14 + 219	cactggatcagtcaggtcca C/G ggtgggaacaagagtaaac	5828
ALDH1L1	70	intron 14 + 2275	tctcatctgtgatgcattcc T/C cagacctctgtcccagcct	5829
ALDH1L1	71	intron 14 + 2431	agaatgactgagtgatoca C/G ctagagagccccagccccgg	5830
ALDH1L1	72	intron 14 + 2660	agccaaagcatttcttgggga C/T accaagaacaccttgccttgg	5831
ALDH1L1	73	intron 14 + 2740	aaactccacctcaccgtcca T/C gcagctccccaggagcgctca	5832
ALDH1L1	74	intron 14 + 2756	tcacatgcagctccccaggag T/C gtcagagggcagagagggg	5833
ALDH1L1	75	intron 14 + 2805	ccgcacagcaggagaatggc T/C ccaaggaggaggaggacggg	5834
ALDH1L1	76	intron 14 + (3636-3637)	tctcctgggtgtgtgtgggg (G) tgtggggcagctccccatc	5835
ALDH1L1	76	intron 14 + (3636-3637)	tctcctgggtgtgtgtgggg tgtggggcagctccccatc	5836
ALDH1L1	77	intron 14 + 4347	tccaggacagaaacagcagg C/T gtgagctgcctctcagaggg	5837
ALDH1L1	78	intron 15 + 380	atgtcccttatgtggcttcc A/G agaccagaaagtcctggagag	5838
ALDH1L1	79	intron 15 + (1055-1056)	gccacaatctgcagctactc (C) tcccagcttgcctgctgggct	5839
ALDH1L1	79	intron 15 + (1055-1056)	gccacaatctgcagctactc tcccagcttgcctgctgggct	5840
ALDH1L1	80	intron 17 + 15	gaaaaggtgcgtggctgggg G/C tggagcagagggagggctgc	5841
ALDH1L1	81	intron 17 + 44	aggaggggctgctgtgagtg C/T gcctgggacatggcagtgct	5842
ALDH1L1	82	intron 17 + 51	gctgctgtgagtgccctgg G/A acatggcagtgctgtccaca	5843
ALDH1L1	83	intron 17 - (2224-2223)	ctggtgtcatctcccagact CT/Δ gtcactaaaccacaatatga	5844
ALDH1L1	84	intron 18 + 140	agcgtcatcacaagcatagc G/A tggcaggcagcaggcttagg	5845
ALDH1L1	85	intron 19 + (51-52)	tgggtcactgggacagcagc GC/Δ ctggctggaggggttggag	5846
ALDH1L1	86	intron 19 + 399	tcaggtcagcctgggctga C/A catggacagggggccctggag	5847
ALDH1L1	87	intron 19 + 608	ccaccagatttatccactca A/G ccacacctgggaagagcaggc	5848
ALDH1L1	88	intron 19 + (669-670)	atggggccatcctgagtcctc (C) ttgggaggtttgtaatgcct	5849
ALDH1L1	88	intron 19 + (669-670)	atggggccatcctgagtcctc ttgggaggtttgtaatgcct	5850
ALDH1L1	89	intron 19 + 1794	gtcctgtctgggggtcttaa G/C ggagtcagtagactccaca	5851
ALDH1L1	90	intron 19 + 1969	tgatcgggggtcggtttggg G/T cgacaggacaggagcagaga	5852
ALDH1L1	91	intron 19 + 1972	tcgggggtcggttttggggcg A/G caggacaggagcagagaata	5853
ALDH1L1	92	intron 19 + 2083	tgagaagagcagaggggtgt G/T ccgggtgctcgagtcacacc	5854
ALDH1L1	93	intron 19 + 2119	acacctgtgtctgattagg G/T tgattaggggtgcagagttt	5855
ALDH1L1	94	intron 20 + 1388	ttacctcttcccactccc C/T tggactgtgagttccatgag	5856
ALDH1L1	95	intron 20 + 1564	cccaggaaaccaggaaacagtg G/A ggagccatcaccggccctg	5857
ALDH1L1	96	intron 20 + 1873	tcagtggttaaacatcattt G/A tgtatgtatgaaaaattatg	5858
ALDH1L1	97	intron 20 + 2427	actaggattggatggacttg G/C gatcaggtctcagctctgtc	5859
ALDH1L1	98	intron 20 + 2458	cagctctgtcactgcccaac C/T ggcggggccatttccctcaa	5860
ALDH1L1	99	intron 20 + 2544	ccaggtgggagagccatctg C/T agcgtggtgacaccatcac	5861
ALDH1L1	100	intron 20 + 2573	gacaccatcacacgggtgc C/T gtgacccgggtgcttatgtcg	5862
ALDH1L1	101	intron 20 + 2574	acaccatcacacgggtgcc G/A tgacccgggtgcttatgtcg	5863
ALDH1L1	102	exon 21 + 33	agccaaactgtttcacagac G/A tggagaccacatgttcata	5864

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ALDH1L1	103	exon 21 + 87	ccttcggggcctgtcatgac A/G tctctcggtttgctgatggg	5865
ALDH1L1	104	intron 21 + 323	ccatgcattaaccaccccc C/G acactgagtggcttgggaata	5866
ALDH1L1	105	intron 21 + 361	ataatcagagattattttta C/G tcacggctcaggttcaatga	5867
ALDH1L1	106	intron 21 + 478	gtcttgcgggagggttcctc C/A gcgtggcagcctcgggggttg	5868
ALDH1L1	107	intron 21 + 1086	caacccaatcttgcctcccg C/T gctgcagcccgccacatttt	5869
ALDH1L1	108	intron 22 + 235	gggcctggaggagacactcc A/C gccaggaggcactggggggc	5870
ALDH1L1	109	intron 22 + 313	atagcaggggaggagttggcc G/A tgaagaccagggggcccggt	5871
ALDH1L1	110	intron 22 + 1214	tggggccacttatgaatcct G/C cccgagttccctcagctccc	5872
ALDH1L1	111	intron 22 + 1226	tgaatcctcccccaggttccc T/C cagctccctcctaaccctag	5873
ALDH1L1	112	intron 22 + 1623	ggggcttcccactgtccaga C/G aaggcgggtgggagctgggga	5874
ALDH1L1	113	intron 22 + 1698	attctggggagtcctggccc A/G ctatccactgccagggaata	5875
ALDH1L1	114	3'flanking + 145	gagagacaggaggaaatggg C/T gtgggtcatctcagggccca	5876
ALDH1L1	115	3'flanking + 239	tgggaaacaggtgggaagac G/A gggattgagctgggtgagcc	5877
ALDH1L1	116	3'flanking + 288	gggaagcagctcagactccct C/T agcagatggggccggggcct	5878
ALDH1L1	117	3'flanking + 1513	agggtcggctcagaccccg A/C gtgctcctggcatgtccagc	5879
ALDH1L1	118	3'flanking + 1707	cggtgggacttgccctagca C/T gtgccactataccagaaca	5880
ALDH1L1	119	3'flanking + 1709	gtgggacttgccctagcagc C/T gccacttataccagaacaga	5881
ALDH1L1	120	3'flanking + 1745	acagatgagtcacatgtcaac C/T gcttccctgagttccctttgt	5882
ALDH1L1	121	3'flanking + 1843	ctgcctctcagccacagcc G/A ggccgctcacactcctccca	5883
ALDH2	1	intron 3 + 1766	aaattggtggctcatctgc C/A tggccccccttctcctcctc	5884
ALDH2	2	intron 8 + 52	gaaggtagccctggccacct G/C tgttgtggctccagccgac	5885
ALDH2	3	intron 8 + 69	cctgtgtgttggtccagcc G/A atcctgtcggcccccagtg	5886
ALDH2	4	intron 9 + 5197	gctttcttatgacttggct C/A atttccagttgtcttgttg	5887
ALDH2	5	intron 11 + 114	gagctgggctcagtttctcc T/C gggtcagggtgtgatgtcga	5888
ALDH2	6	3'flanking + 411	ggatgatgatttctgcccctc T/C tctgctgtgggtaaacagct	5889
ALDH2	7	3'flanking + (432-433)	tctgctgtgggtaaacagct TC/Δ tgtttcatgcattactttt	5890
ALDH2	8	3'flanking + 488	ccaataaagatgtgcttga G/T gtttcatgcatttaatttgt	5891
ALDH3A1	1	5'flanking - 758	ctgcaggcggttgagggtgg C/A gggaaagccctggtgagagg	5892
ALDH3A1	2	5'flanking - 308	agtcctggaaagctggaaag C/T tccatgccaggctgaatcaa	5893
ALDH3A1	3	5'flanking - 294	gaagagctccatgccaggct G/A aatcaatcagcagccccac	5894
ALDH3A1	4	5'flanking - 3	gtcccccttggctcttggcc G/A ttccaggagccccagttacc	5895
ALDH3A1	5	intron 1 + 2323	actgtctcctttcttccgga C/T ctttgggagttttacaatac	5896
ALDH3A1	6	intron 1 + 2499	cccgaatttgccactatact T/C cgtgtattggtagcaggaaat	5897
ALDH3A1	7	intron 1 + 2943	caggggctagcaaggcagcc A/G gggccaggcgtctgagtgga	5898
ALDH3A1	8	intron 5 + 72	cacacatgactgcacctcat G/C ctgtgggtccactctgagta	5899
ALDH3A1	9	intron 7 + 633	cgctgggggtctctgcgcc G/A tccaactctggcttgtttcc	5900
ALDH3A1	10	exon 8 + 36	cggacgtggacccccagtc C/G cggtgatgcaaggaggagac	5901
ALDH3A1	11	intron 9 + (40-41)	gctgcctcctctgggcccc (C) agggctggggcacactcacc	5902
ALDH3A1	11	intron 9 + (40-41)	gctgcctcctctgggcccc agggctggggcacactcacc	5903
ALDH3A1	12	intron 9 + 322	cacagtggtgatgccctggg G/Δ acacccatagacattggccac	5904
ALDH3A2	1	intron 1 + 39	gggtgtggggaaactggccc C/T cgccgcgcaactgtggagctg	5905
ALDH3A2	2	intron 3 + 2491	tgccgcgaagaattggcac T/A gctgagttctacatgcagtt	5906
ALDH3A2	3	intron 3 + 2595	ttctgtacatcaacttgtga T/A ggattgaggccagttctgtg	5907
ALDH3A2	4	intron 3 + 2775	taccgctttggccctgacca G/A gggtaaatcttcttaataact	5908
ALDH3A2	5	intron 3 + 3424	aggcaacttctgcacacacc G/A cgtctcatgcattttccctg	5909
ALDH3A2	6	intron 3 + 3676	atgttgaaagagattgctgat G/A ttagacgttaggatttattt	5910
ALDH3A2	7	intron 4 + 481	tagaaaaataagaggtttcag G/T ttctctctgctaaatccggg	5911
ALDH3A2	8	intron 4 + 769	atcctgctttatacctgaac G/A tcttgaggcagagccaaaa	5912
ALDH3A2	9	intron 4 + 796	aggcagagccaaaaggcaca A/G ccaggagagctgtaccgaa	5913
ALDH3A2	10	intron 5 + 254	attagttgtggcatatact T/G ttttaaaaaagttaataat	5914
ALDH3A2	11	intron 6 + 137	aatcctgctttctggtatac T/C gtacctgtagcttttgttat	5915
ALDH3A2	12	intron 6 + 923	aggctaataagtgtaagag G/A aaggggctatcctgatttagc	5916
ALDH3A2	13	intron 7 + 331	tgctttctgtatgttaatcc A/Δ cagggcattgctgaataaca	5917
ALDH3A2	14	intron 8 + 643	tttagaacatgacctgacct C/T ctctcccatgtgagatga	5918
ALDH3A2	15	intron 8 + 666	ctccacacatgtgagatgact G/A actcagctttttatttctcc	5919
ALDH3A2	16	intron 9 + 2129	tgttttcatttttaaaaaaa G/T gtttgactttggaattcatg	5920
ALDH3A2	17	exon 10 + (1894-1895)	ttggcttgctactaataca CA/Δ tctgcttcaaaatgaacata	5921
ALDH3A2	18	3'flanking + 31	gtatttgtcaacttttttt T/Δ ctatttttaaaattcttagc	5922
ALDH3A2	19	3'flanking + 106	gtgtgttgggggtgtgtgt G/A gtactatagtaaataggtt	5923
ALDH3A2	20	3'flanking + 1630	aaaagcacgtgggaacaca A/G ttaatcatgtcttaccgat	5924
ALDH3B1	1	5'flanking - 1455	ctgcctgtccacacccacag C/T agcttgacatcatccccac	5925
ALDH3B1	2	intron 1 + 464	catgaatgactctgggaag A/G atcattcttagcaatggact	5926
ALDH3B1	3	intron 1 + 2269	aaatggaatccaaacagcaa G/C agacctccctcaccggtca	5927
ALDH3B1	4	intron 2 + 1349	actgagcttttgcacccgc C/T gectgcccgccttcatgaga	5928
ALDH3B1	5	intron 2 + 1820	tcctgttggaaggacacct C/G cccagcctcagtggttagga	5929
ALDH3B1	6	intron 2 + 2046	aaactcaggcgctgcctcag C/G caggagaccagctggcccc	5930
ALDH3B1	7	intron 2 + 2939	aagcacgcactgaacatgga G/A tgagtgtgtgaacgaatgaa	5931
ALDH3B1	8	intron 3 + 7	tgcccaagaacctggtgagc C/T gggcggtgaggggggag	5932
ALDH3B1	9	intron 4 + 36	gccccctccgggtcacccttc T/C ccgctcaggcctcagggcc	5933
ALDH3B1	10	intron 6 + (116-117)	attctctctctctctctct CT/Δ ggaccaggctgggagcagtc	5934

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ALDH3B1	11	intron 6 + 263	cagaccctcatacgtgaacc T/C gctgccccccaggctcttag	5935
ALDH3B1	12	intron 6 + 1298	gtagacagagctggactcca T/G ccttgggtgataagggatcc	5936
ALDH3B1	13	intron 6 + 1411	gccagggtcacaagcagagg C/T gggaggagccaaggggtttg	5937
ALDH3B1	14	exon 7 + 185	acctgctggcccccgacta C/T gtcctatgcagccctgagat	5938
ALDH3B1	15	exon 7 + 339	tgccggcattgctgggtgc G/A gcgtgtggccattgggggcc	5939
ALDH3B1	16	intron 7 + 249	ccagggtccaggggtcagc G/A tgctaagatgaatcccatc	5940
ALDH3B1	17	intron 7 + 277	atgaactcccatccaccac C/T ggctatcctgaaagctgta	5941
ALDH3B1	18	intron 7 + 498	gaccaaggtcggggattct C/T tgtgtccacagggcctgag	5942
ALDH3B1	19	intron 8 + 14	cagccaggtgggggtgcgc C/T gggctgggcagggtcaggag	5943
ALDH3B1	20	intron 8 + 49	caggagcccgagtggtgg C/T acaagtgtggcagcaggg	5944
ALDH3B1	21	intron 8 + 111	tcaggactttgggatggtgg A/T cctcttggtctgtctctgc	5945
ALDH3B1	22	intron 8 + 3219	atcctgatggggctcaaggc A/G gcctcagcacatcctgttc	5946
ALDH3B1	23	exon 9 + 33	gtgctgacccagaccagcag C/T gggggctctgtgggaaca	5947
ALDH3B1	24	intron 9 + 946	tcaccagggccccagagctgac C/A cttcttggtggccgtggccc	5948
ALDH3B1	25	intron 9 + 1067	aggctccccaagcctgggtc C/T cctctggccccaccactct	5949
ALDH3B1	26	exon 10 + 137	ccgcaatcgccgcgcgcgcct G/A aggatgctggtgtggccat	5950
ALDH3B1	27	exon 10 + 397	cgctcccaaccatgagagcc G/A aggtgggaggcatgggaac	5951
ALDH3B1	28	exon 10 + 1198	ctcttccccatgctgctcat C/T ctcctggggccccaccactc	5952
ALDH3B1	29	exon 10 + 1475	cagggtgtggactgagtttc G/A tctcctgtctctctgtgta	5953
ALDH3B1	30	3'flanking + 15	cctggcaataacttacatctc A/G gtgatttcttctgtgcat	5954
ALDH3B1	31	3'flanking + 60	caacaggactctggaccaag G/C ccttggcgttgggttaacaat	5955
ALDH3B2	1	intron 1 + 98	agggaaggggatgtgtgcc G/A tggccctgggtcagggggc	5956
ALDH3B2	2	intron 1 + 157	atggctgcaggggcatggg T/C acggggctgtctcaggagag	5957
ALDH3B2	3	intron 1 + 354	tctgtggacagacaaggatt C/G ggtcgggggaccagggtg	5958
ALDH3B2	4	intron 1 + 851	tatgacaggtccatcaggcc T/G cacttctgtgtgtcttat	5959
ALDH3B2	5	intron 1 + 894	ctcagcatctgccccacag T/G gcttttgacacgttggttc	5960
ALDH3B2	6	intron 1 - 463	aaagaacctccagagtcct C/G gtttagtcccagaaggagg	5961
ALDH3B2	7	exon 2 + 61	gccttcaactgaggcgac G/A cggccggccaggttccgggc	5962
ALDH3B2	8	intron 2 + 8	ggacctgcataagtggtggc A/G tggagagtgggccccggcag	5963
ALDH3B2	9	intron 2 + 23	gggcccgtggagagtgggcc G/C ggcaggggctggagcagct	5964
ALDH3B2	10	intron 2 + (180-181)	ttcactcctgaacactcaca (A) gccaccctgtgatgcaggct	5965
ALDH3B2	10	intron 2 + (180-181)	ttcactcctgaacactcaca gccaccctgtgatgcaggct	5966
ALDH3B2	11	exon 3 + 72	gactacgctctcaagaacct T/G caggcctggatgaaggatga	5967
ALDH3B2	12	intron 8 + 375	ctgcagcatcctaaccctac C/T gtcgcgactcaaggctgccg	5968
ALDH3B2	13	intron 8 + 463	aatcacccccatggcacc G/A accgtcactgagaggtgct	5969
ALDH3B2	14	exon 9 + 33	atgctggagcggaccagcag C/A ggcagctttggaggcaatga	5970
ALDH3B2	15	exon 10 + 428	aggtgtctctactcacccca C/T cctcccaattccagccctt	5971
ALDH5A1	1	5'flanking - 1303	gaaattgattaaactctact G/A ttatcacttctgcatatgt	5972
ALDH5A1	2	5'flanking - 301	gtgaaaaggtgacagcagtc C/T gcagggtgcatctactggcga	5973
ALDH5A1	3	5'flanking - 221	ggtcgcgccaggagagaagc C/T gcgcggcgcttagggcaagg	5974
ALDH5A1	4	5'flanking - 175	agggcgccgcccgggtgcag C/G gagaagagcgggagagagg	5975
ALDH5A1	5	5'flanking - 174	ggcgccgcccggcggtgcagc G/A agaaagacgcggagagagg	5976
ALDH5A1	6	exon 1 + 106	gcgcgctgtgctccctgcctcc G/C ggcctgcgcggccggcc	5977
ALDH5A1	7	intron 1 + 326	cctaaccgtggagggcgccg G/A agaaaggggaggggtgtgac	5978
ALDH5A1	8	intron 1 + 5551	gtctgtacaaaaaaatttt T/G ttttaattagctgagcatga	5979
ALDH5A1	9	intron 1 + 5555	gtacaaaaaaatttttttt T/Δ aattagctgagcatgatcat	5980
ALDH5A1	10	intron 2 + 306	gttttggtgtgttttttttt T/Δ aaactgtttttgtacattt	5981
ALDH5A1	11	exon 3 + 107	cggagacattatccacaccc C/T ggcaaggacagggcgggccc	5982
ALDH5A1	12	intron 3 + 201	gtggtggcagtgagtggaat G/T atgcatttctaatgcctgca	5983
ALDH5A1	13	exon 4 + 42	atcaccgggaaggtgggggc C/T gccctggcagcggcgtgtac	5984
ALDH5A1	14	intron 4 + 2306	atcgtgtcttataaatcagtt T/C tgctaggatataaatccttg	5985
ALDH5A1	15	intron 4 + (2334-2346)	tataaaatccttggtccaca (T)11-13 acttgattatcttaaatgta	5986
ALDH5A1	16	intron 4 + 2456	tataagttcaacttttttttt T/Δ acctagatcacaaaaagtgt	5987
ALDH5A1	17	intron 4 + 2501	tttggtttttttcccccttt A/G tctttaaagaccaataatgt	5988
ALDH5A1	18	intron 4 - (64-46)	atctattttttctcttttc (T)16-18 cagtttggttaattgttggc	5989
ALDH5A1	19	intron 4 - 27	ttcagtttggttaattgttg G/C cacatgtttgctgtttctct	5990
ALDH5A1	20	intron 5 + (4621-4624)	tttgaatagataaacactta CTTA/Δ tatggttgaataatgaac	5991
ALDH5A1	21	intron 5 + (4677-4678)	accatgacaagttctcacct (C) accccaacctgactcactc	5992
ALDH5A1	21	intron 5 + (4677-4678)	accatgacaagttctcacct accccaacctgactcactc	5993
ALDH5A1	22	intron 7 + (432-443)	aaaaaatgatgttaaaaggc (A)10-12 tgaatacaaaaaagtcattt	5994
ALDH5A1	23	intron 7 + (3243-3244)	cagtcctgtgtgtgtgtgt GT/Δ cccccaaacactgctgga	5995
ALDH5A1	24	intron 7 + 4987	tttttgaataaagaaaaaaa A/Δ tggaactagtatatgttttc	5996
ALDH5A1	25	intron 8 + 2717	gatcacctggaaactcacagg C/T gtggtaggagacgtgcagcc	5997
ALDH5A1	26	3'flanking + 2711	cagtgtgtgcttggggag G/A agccagcatgtgaaatgatg	5998
ALDH5A1	27	3'flanking + 2777	gtccatggtgtgcgttata G/A aatgtttgtctaagctgaact	5999
ALDH6A1	1	5'flanking - 1303	ctctaaagcagaaacagag G/C aaaagcatgggagatacca	6000
ALDH6A1	2	5'flanking - (1273-1270)	ggagtataccaaaacactt AATT/Δ gttacttgaaatgacttgca	6001
ALDH6A1	3	intron 1 + 437	tgccattgtctctctccccc A/T cctacttctactatccgttg	6002
ALDH6A1	4	intron 1 + 835	gttccacccccaaaatcagc T/Δ cttctagtgtacacacct	6003
ALDH6A1	5	intron 1 + 1294	atatttctgtgctgcgactct T/C gttctgttctagtatctttt	6004

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ALDH6A1	6	intron 1 + 1447	gagtcattgagaaccttaag A/G aagtattttgtccttttcca	6005
ALDH6A1	7	intron 1 + 2536	agtcttggccatctcttttcta T/C gttaggcactgacataggct	6006
ALDH6A1	8	intron 1 + 2703	caggagaggaaggaggttct G/T ataaaggatatagcaagtag	6007
ALDH6A1	9	intron 1 + 2802	gcaacaatgctaattgggtgt T/C tcttaggaaatgaagaaaag	6008
ALDH6A1	10	intron 2 + 2333	gtttgtttgtttgtttgttt G/Δ ttttttcagccaaactgtaa	6009
ALDH6A1	11	intron 4 + 138	gactctctccctgtactgc A/G tctctccagctcttattctt	6010
ALDH6A1	12	intron 4 + 200	aaagagggaacattcttgcat T/C aatttctatttgtgtgtctt	6011
ALDH6A1	13	intron 5 + 291	ggcaagtcagtgtaacctgc G/A ccccttcattggcctgaacc	6012
ALDH6A1	14	intron 7 + 209	tcccggttccaagcgattct C/A ctgcctcagcctcccgagta	6013
ALDH6A1	15	intron 8 + 287	gcctctctgagcagcttgga C/T acaggtgcggggccaccact	6014
ALDH6A1	16	intron 9 + 877	gatacaaaaataaataca C/T agacatatattggaggagcaaa	6015
ALDH6A1	17	intron 9 + 885	aataaaacatacagacata T/G ttggaggagcaaggagtgaa	6016
ALDH6A1	18	intron 11 + 40	ttttgtcttttcttttaaga A/C attttctaaagatattcag	6017
ALDH6A1	19	3' flanking + 520	cctgcaaaagttttcttttagc C/T cctcttttatcccaataac	6018
ALDH6A1	20	3' flanking + 1026	cgtgttgggtcaggtgtgtct T/C gaactcctgacacctcaggta	6019
ALDH6A1	21	3' flanking + 1035	caggctgtgtctgaacctct G/C acctcaggtgacccctgc	6020
ALDH8A1	1	5' flanking - (837-836)	gctgaacattgttaatat (AT) tcattagccaattgtgttcc	6021
ALDH8A1	1	5' flanking - (837-836)	gctgaacattgttaatat tcattagccaattgtgttcc	6022
ALDH8A1	2	5' flanking - 702	gggactctgaagccttgcta C/T atgtgtcacacatgtttttg	6023
ALDH8A1	3	5' flanking - 642	gcacatctaggaagatgtga G/A cagccactgtggccccggt	6024
ALDH8A1	4	5' flanking - 84	atgctctctgagagcgtcag G/T tgcctctccacattcactga	6025
ALDH8A1	5	intron 1 + 5437	gcattggtgaaatggagcg T/C gtttctttgtttctatggtta	6026
ALDH8A1	6	intron 1 + (5836-5855)	gtgagaatccatctaaaaaa (CAAAA) 4-5 atgaggtgtgtggagacct	6027
ALDH8A1	7	exon 3 + 146	cactacacgggtgcggggccc G/T gtgggagtcggtgagtgctg	6028
ALDH8A1	8	intron 4 + 1033	aggctcttttctctatgtcac C/T ccacggccaggcaggagtg	6029
ALDH8A1	9	intron 4 + 1037	ctttttgctatgtcacccca C/T ggccaggcaggagtgctgg	6030
ALDH8A1	10	intron 4 + 1662	tctctctctgagaccaagaac G/A tctggatagatgatgagtta	6031
ALDH8A1	11	intron 4 + 2046	agtccttgggcattttaaacag A/C ctgacagataaaacttctt	6032
ALDH8A1	12	intron 6 + 1146	ttttccagatgcaagagact C/G ccttgttctctctctctctg	6033
ALDH8A1	13	intron 6 + 1744	ttcttcttcttcttcttctt C/T tttcttttttaacatgtact	6034
ALDH8A1	14	intron 6 + 9802	tgagtggtgaattctaacctt A/T ctgtttattagctctatgaa	6035
ALDH8A1	15	exon 7 + (1089-1098)	tacagtgagacctgtctt (A) 9-10 tgcgtgcaaaacaaaaataa	6036
ALDH8A1	16	3' flanking + 848	ctcagctgagctcccttgac T/C ttaatcatttagtgaagaa	6037
ALDH9A1	1	exon 1 + 121	actgtgtgggttatggcggg G/A tgggtgggagaaatgtgtgt	6038
ALDH9A1	2	intron 1 + 67	cgcggatttcccgccagcc C/G ccgttctctgtgttctgcag	6039
ALDH9A1	3	intron 1 + 103	tgcagcgttgacttgagcac A/G agacagtgacagtgagag	6040
ALDH9A1	4	intron 1 + 1818	gaatttttgagaaaaaa A/Δ tgttcttttaggggtgcctt	6041
ALDH9A1	5	intron 2 + 5891	tcaggaacaggaaagtaaga G/A gtttacatttctaaattctt	6042
ALDH9A1	6	intron 2 + 6398	atcaaaaaacacttgtctgat T/G atcgtgtctgtaacctgcct	6043
ALDH9A1	7	intron 2 + 9677	atgacgctgagtttgggtgt A/G ttcttttgttttcttgcct	6044
ALDH9A1	8	intron 2 + 9991	gggagagtgaggagacctac C/T ctggcttctaatcttctt	6045
ALDH9A1	9	intron 2 + 10198	ttgtcagagacacttttgat A/G atccttacgtactatcac	6046
ALDH9A1	10	intron 2 + 10256	ttagtagataacttttttt T/Δ gtaaggatggagaataatag	6047
ALDH9A1	11	intron 2 + 11382	catattcaatttttttatgt T/C ctttagaccaagaagagca	6048
ALDH9A1	12	intron 2 + 11455	taaaccttttaagctcatcat C/T ggaccatctattgaattct	6049
ALDH9A1	13	intron 2 + 12044	atttaaaagtgaagctattt C/T tagtttttaaaattgagcag	6050
ALDH9A1	14	intron 3 + 334	ctatttagcaaaactttttt T/Δ gacagtgtataaagttttca	6051
ALDH9A1	15	intron 3 + 368	gttttcaacaattgatattg G/Δ aaggttggtagggcctagga	6052
ALDH9A1	16	intron 4 + 191	ccctcaaggagcttatagtt T/A aggttgtacacaaatcatgtc	6053
ALDH9A1	17	intron 4 + 557	tagaaaaaatgttaattgtta A/G aaagcattactgttaggaca	6054
ALDH9A1	18	intron 5 + 830	agttcaagatgattttgtag G/C ttcagggcctagttgactta	6055
ALDH9A1	19	intron 5 + 838	atgattttgttaggttcagg C/T ctgattgacttagcatgcaa	6056
ALDH9A1	20	intron 6 + 120	agaaaaagttgcacaaatagt A/C caaagaattcccatgtacct	6057
ALDH9A1	21	intron 6 + 2569	attaaaaatctgctttaata T/C ttttttggggagaggacac	6058
ALDH9A1	22	intron 8 + 1414	ccgatcttcaaaaaattagc T/C ggggggtggtgtgcacactg	6059
ALDH9A1	23	intron 9 + 664	aaagtctcacattttttttt T/Δ ataacttcatggtcaagagc	6060
ALDH9A1	24	intron 9 + 2170	taatgcacacattttttttt T/Δ ctccatagggacatccaacg	6061
ALDH9A1	25	exon 11 + 587	aaaacaaaaacaaaaaa A/Δ ccttgttctttataggttc	6062
ADH1	1	(5' flanking region -55)	atcatgtgtgggaactggaat C/T gggtgttattcaagcaaaaa	6063
ADH1	2	(intron 1 268)	acatttgcggtaaacgcgata A/G tttattccaagctaatactg	6064
ADH1	3	(intron 3 443)	aatgga g/c gctacatggctat G/A gctgaatgagcatgacctt	6065
ADH1	4	(intron 6 56)	tacaacttggaggatgcatt T/G aggtctgcagaataatgtttt	6066
ADH1	5	(intron 8 74)	gtctagcagaaaaatgaaaag G/A tggaaaggatgagaaaaatta	6067
ADH2	1	(intron 2 340)	ctatttttaaaagcgtgcac T/C cttacataagacttaaatat	6068
ADH2	2	(intron 3 91)	aaaggcaatgagagacgaaag T/G gcttgacaaagtcaccg	6069
ADH2	3	(intron 3 205)	atgtattgtaccctccaacc A/G ttatgtaccgagtatctact	6070
ADH2	4	(intron 7 108)	acaattgacaaggcaagatt T/C tgaacacaaatcaaaaaataa	6071
ADH2	5	(intron 3 1721-1723)	actgcatagaatttaagaa GAA/Δ cttgttttatctctctccag	6072
ADH2	6	(3' untranslated region 2305-2306)	gttaaatgctttccactctc AG/Δ gggaaggatttgcattttga	6073

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ADH3	1	(5' flanking region -254)	tgagagaagagaagcaggaa C/G ttgagagaggaggaagagag	6074
ADH3	2	(intron 2 355)	tatgcattcttctatattat A/G caagacaaaaatcttaggat	6075
ADH3	3	(intron 3 32)	acactcaggggaacatgcctt G/A gtccaccatcacagattag	6076
ADH3	4	(intron 4 6)	ctgcttgaaaaatgagtaag C/T ttctgatgctttctttgcac	6077
ADH3	5	(coding region 453 (Thr 151 Thr))	agcaccttctccccagtacac A/G gtgggtgatgagaatgcagt	6078
ADH3	6	(coding region 815 (Arg 272 Gln))	ttcgtttgaagtcacgtgc A/G gcttgacaccatggtatgat	6079
ADH4	1	(5' flanking region -482)	acagccagagaccagaacc A/G tcagggtggttgatggact	6080
ADH4	2	(5' flanking region -437)	catcaggtgggacaaaaaga G/A tagctccttagcagtgaacta	6081
ADH4	3	(5' flanking region -234)	actcaagcatatgtgcaacc A/G agtaccatgaaaagaatttgt	6082
ADH4	4	(5' untranslated region -3)	ggtaagttaaatggcgatt C/G tgaggagtagaaaatttccct	6083
ADH4	5	(5' untranslated region -2)	ttcaataaaaaaagaa T/A ttaaaaaatcttggagctca	6084
ADH4	6	(intron 1 707)	ttatatttgaattaaaaat A/G taatttgaggctagaaaaaa	6085
ADH4	7	(intron 5 619)	tcaaagagggatctcacaat T/C ggacatctcaacctgcttat	6086
ADH4	8	(intron 5 1755)	tttcgcacacaaattactca T/C taataaaaaatcttaaaaaat	6087
ADH4	9	(intron 5 3425)	actgagactctggagcaata T/C attaagaatcatactgaaca	6088
ADH4	10	(intron 1 1181-1189)	ggtaaacctttaatacacttg (T)9-11 caagaaataaaaaatgtaat	6089
ADH4	11	(intron 5 2828)	tccagtcaaaagtcgacctaa A/Δ ttccaggaggtgttctctcc	6090
ADH4	12	(intron 7 15)	ttgggtgctcagtttttttt T/Δ ctctcatagctttaattctt	6091
ADH5	1	(5' flanking region -115)	taactgctgtaagttacac G/A g/a ggaagccctttcccgacaa	6092
ADH5	2	(5' flanking region -114)	aactgctgtaagttacac g/a G/A ggaagccctttcccgacaaa	6093
ADH6	1	(intron 3 249)	tgaaactggacttgaaagta C/A aaatgagacaaaaatttatg	6094
ADH6	2	(intron 6 1072)	taaccctctatactgtattgc A/G tcactttctaacaggcagct	6095
ADH6	3	(coding region 885 (Val 295 Val))	gtctgtgtggttgttgggt G/A ttgctgtccagtgcttcaact	6096
ADH6	4	(intron 7 1292)	gttgagaacactgccttagt C/A ccgtctgtgttcttagaatt	6097
ADH6	5	(intron 7 1616)	ctatcacagaataatccgca T/C agaactaagcagattacg	6098
ADH7	1	(5' flanking region -528)	tgtgcagacacagaaagttt T/C acttaactttctacacctaa	6099
ADH7	2	(intron 1 361)	tcagtagcatgtgtgcact C/T gctgcagtagttcaatggga	6100
ADH7	3	(intron 3 183)	aacctcaaccttttagaaggc A/G aaccttacgggtttataaa	6101
ADH7	4	(intron 4 76)	tgaattgaattaattataac G/A tgtatttgatgatcaacaa	6102
ADH7	5	(intron 6 615)	tggcatagcgtaaagagact T/A ggaataatggaataaagcca	6103
ADH7	6	(intron 8 532)	aagtctaacacatcacccaa T/C ttagtagccattgtactat	6104
ADH7	7	(intron 8 651)	gctgctatttatttcaagta G/A gccacaaaatttccctattt	6105
ADH7	8	(intron 8 727)	ttcagatccctgtgaagccag G/A tattatttttaccattttta	6106
ADH7	9	(intron 8 1207)	tctccacattttggtctagcc T/C acaggatcatcatattatga	6107
ADH7	10	(intron 8 1691)	tcctctatctcattgccac G/A ctctattgttttaattcagtc	6108
ADH7	11	(3' untranslated region 13)	atttaccattttgtgaaggcta T/C aattgtatctttttaagaaaa	6109
ADH7	12	(3' untranslated region 14)	gatatagtaaatgcactccc T/C agagtaataattcacttaaca	6110
ADH7	13	(3' untranslated region 15)	aaacacttggttatgagttaa C/G ttggattacattttgaaatc	6111
ADH7	14	(3' untranslated region 18)	aatataaacatagagctaga A/G tcatattatcatcattatca	6112
ADH7	15	(3' flanking region 865)	tacatcaaaaagaataaatac C/T aagaaggataaacacattt	6113
HEP27	1	(5' flanking region -191)	tcagcactctgtgtctagct A/T aaggtttgttaaatgcaccaa	6114
HEP27	2	(5' untranslated region -1)	gaacccatcaattccgtaca C/A attttggtgactttgaagag	6115
HEP27	3	(intron 1 1941)	aaatttaccctaacaccagct G/C actctctgaccttttctgtt	6116
HEP27	4	(coding region 289 (Ala 97 Thr))	ttgtgtgccacgtggggaag G/A ctgaggaccgggagcagctg	6117
HEP27	5	(intron 4 1070)	tgctcagtttcacagatca T/C gactctttttctcgaaactg	6118
HEP27	6	(3' flanking region 362)	ggctttgtgtgtgtctcatt A/G tctgaactgggctgctggg	6119
UGT1A1	1	(5' flanking region -1337)	tctttcccttttgacttcaa A/C tcagtcacagaatttcccc	6120
UGT1A1	2	(coding region 211 (Gly 71Arg))	cctcgtttgtacatcagagac G/A gagcattttacaccttgaag	6121
UGT1A1	3	(intron 1 2925)	gcatttgggaagggaataac T/G aattaaaaagcctaaactaaa	6122
UGT1A1	4	(intron 1 3442)	agactcggccttttccagat G/T agcttcagtgtaagagtggg	6123
UGT1A1	5	(intron 1 3512)	ttaagtaagccattttaccaa C/T gctcagaagaaagaaacttga	6124
UGT1A1	6	(intron 1 3665)	tcttgctacaaaacaaaaaa T/C gcagcatggttggtggggagg	6125
UGT1A1	7	(intron 2 15)	cagacagtaagaagattcta T/C accatggcctcatatctatt	6126
UGT1A1	8	(intron 4 574)	agattttaaactccaattta C/T ataaaaagttgccataatag	6127
UGT1A1	9	(3' flanking region 125)	tatagaggttcacacacaca C/T gccttcattgcgtgtgcctg	6128
UGT2A1	1	(5' flanking region -1602)	ataacatcttctgcagagaa A/C ctccaatggaaatacactca	6129
UGT2A1	2	(5' flanking region -1480)	tacagattatcttttgggtgat G/C ggagagcttagaagagacat	6130
UGT2A1	3	(5' flanking region -1406)	atttcagaagatttataaac A/T tgaaaaggatcactctg c/t tt	6131
UGT2A1	4	(5' flanking region -1388)	acatgaaaaggatcactctg C/T ttatttcacagacatattgcatt	6132
UGT2A1	5	(5' flanking region -935)	aaattattcaatctcttttgg G/A cagtggtttctttttctttg	6133
UGT2A1	6	(intron 1 535)	cattgatcagggtgatttat C/T catgctaagcttatttattt	6134
UGT2A1	7	(intron 1 642)	tatattgatcatgttgatac A/C ttatatacacatatttgccta	6135
UGT2A1	8	(intron 1 1448)	aggtgcttacaggcaacatc C/T acatagcagtcgtggctgg	6136
UGT2A1	9	(intron 1 2000)	gacacattagcttcttttctt A/G cagatctctgtttctaaaaa	6137
UGT2A1	10	(intron 1 3118)	cttaaaattctttaaataa T/G cattgcaacaaatttatatc	6138

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
UGT2A1	11	(intron 1 3191)	ataaatagaacaactcccta A/T gtttacttctctgcagtgga	6139
UGT2A1	12	(intron 1 3770)	atcaccagataatttactat C/T cattaaggagtaggtcatca	6140
UGT2A1	13	(intron 1 4584)	tgattgggttagaatcttga A/C aaatcttctagtatcatcc	6141
UGT2A1	14	(intron 1 4854)	tactctgtgcattgttaata G/A cctatcactgtgtgtctgcc	6142
UGT2A1	15	(intron 1 -19146)	ctgtttaaattctcattcaa C/T gggccacatgggttaaaataaa	6143
UGT2A1	16	(intron 1 -19085)	tagacaaagaccctttcaat A/C aacaaagttagaatgtgtt	6144
UGT2A1	17	(intron 1 -18346)	atggcaatatttttagaata G/A ttaactcccaataatgaata	6145
UGT2A1	18	(intron 1 -18218)	tatatcattatttttaactta T/G agatagcactagccctaatt	6146
UGT2A1	19	(intron 1 -17937)	ctccataaatttggactca C/T cactatttaccagcactatc	6147
UGT2A1	20	(intron 1 -12585)	ttccacacagggacaaagta A/G cagaggaaatttttcttgc	6148
UGT2A1	21	(intron 1 -11430)	aacaaaggtttattttctta C/G agttctgtatggctagacgtc	6149
UGT2A1	22	(intron 1 -10761)	tttaaaatagcatgtattt T/G ccacttttaaaaactatct	6150
UGT2A1	23	(intron 1 -381)	aaatcctcctccttctctc C/T tttccaggcccccactctac	6151
UGT2A1	24	(intron 1 -329)	ttccctttctccttttctcc A/G tctctctctcttctctctc	6152
UGT2A1	25	(intron 1 -41)	ttttctctcagcaaacata T/A aagctaatttctccatccca	6153
UGT2A1	26	(intron 2 263)	caccttgatactggacttgg T/C gggacagaaacacagatcat	6154
UGT2A1	27	(intron 2 454)	agaaagcccatgaaataag G/C cagggttttttaggtttta	6155
UGT2A1	28	(intron 2 554)	aaaaacttttttaggtgac A/T atgggtgagtttagtttctga	6156
UGT2A1	29	(intron 2 1113)	ctgcaggcaagctctagtga A/T tgtttattataggaaataat	6157
UGT2A1	30	(coding region 922 (Gly308	gtgtgtgtgtgttttctctg G/A gatcaatggtcaaaaacett	6158
UGT2A1	31	(intron 3 -217)	aagcttagaagtataaata T/C caaaacaataatactatact	6159
UGT2A1	32	(intron 3 -194)	aaacaataatactatactgg G/A tagactattatagacaagact	6160
UGT2A1	33	(coding region 1171 (Val391Ile))	acggagtcctctatgggtgga G/A ttcccatgtttgtgatcag	6161
UGT2A1	34	(intron 5 1546)	tttttaaaattcagaaactc A/G g/a ttatgtgttattcttcaaa	6162
UGT2A1	35	(intron 5 1547)	tttttaaaattcagaaactc a/g G/A ttatgtgttattcttcaaa	6163
UGT2A1	36	(intron 5 2505)	taattgacttttattataac G/A tacatgttgataagtcata	6164
UGT2A1	37	(intron 5 2639)	tagactattacaaagtgttt A/G gttgctgcacaaattttgttca	6165
UGT2A1	38	(intron 5 4009)	gaatccaggctggaaactttt C/A ttccagacacaaacaaaa	6166
UGT2A1	39	(intron 5 4311)	atcacagactgtcttttcc G/A tcacaaacacacagatgtgt	6167
UGT2A1	40	(intron 5 4616)	acttttttatgtctacattt G/C atcatactgtgttaagcata	6168
UGT2A1	41	(intron 5 4717)	tgcaagaatttatattttctc C/A acgtaactatggccttaaac	6169
UGT2A1	42	(coding region 1524 (Gln508Gln))	gctatatttttgggtcataca A/G tgtgtgtgtgttttctgtca	6170
UGT2A1	43	(3' untranslated region 1	aaggagtttaacaaaaaac G/A tctccatctctgtttccaaa	6171
UGT2A1	44	(3' flanking region 685)	aatctagaaaataattatca T/C ttttataaaatttttagtca	6172
UGT2A1	45	(intron 1 (-18967)~(-18965)	ctcccaattagattgattag TAT/Δ gagttctctgggttactggt	6173
UGT2A1	46	(intron 1 (-18862)~(-18803)	aatacattcttcccccctca (AC)14-17 atgcttactggcctattta	6174
UGT2A1	47	(intron 1 (-17463)~(-17447)	aaacttagaaacctctatcc (A)16-27 gtaagaaaaatggcagagaa	6175
UGT2A1	48	(intron 1 -10860)	attcaatgcaactttttttt T/Δ gtaatggcagaattagaaca	6176
UGT2A1	49	(intron 2 528-538)	ctgttaggaaacaaattgggtt (A)8-10 ctttttttaggttgacA/Tatg	6177
UGT2A1	50	(intron 2 1514-1533)	ttgtgtgtatgtgtatgttt (GT)9-11 tattttaaatgaatttaatac	6178
UGT2A1	51	(intron 5 916-917)	gcttagtatattatataat AA/Δ gtctatatataatagcttagt	6179
UGT2A1	52	(intron 5 1163)	caatatttatgtcatttttt T/Δ ctccactattactctgtttcc	6180
UGT2A1	53	(intron 5 3819-3838)	agacagacagacacacaaac (AC)8-12 tcaacacatgtaaacactc	6181
UGT2A1	54	(intron 5 4785)	tatcttcaatgaaaaataaaa A/Δ caaaaattgtctaatttctg	6182
UGT2B15	1	(5' flanking region -277)	cgaacaggcaggagcctct C/A acttgccactgtttcttaaca	6183
UGT2B15	2	(intron 1 670)	catcaaaagaaaataggggcc A/T aattaagggagagcacatat	6184
UGT2B15	3	(intron 1 775)	ctaatttatataagatctta A/C gatgaaccaagacagtagta	6185
UGT2B15	4	(intron 2 2183)	cagagtttccactgttggc C/T aggtgtgtcttgaactcctg	6186
UGT2B15	5	(intron 2 2430)	tatttcaaaagataaagact C/G ttgccaaaaagatcaagtg	6187
UGT2B15	6	(intron 2 4806)	aaaaaattactccaatagct C/T ctga c/g tttctcatcttagat	6188
UGT2B15	7	(intron 3 129)	ctaatttatctcagacatctg T/C tcaaa g/a caaaaacatatatg	6189
UGT2B15	8	(intron 3 424)	caataacaataagcaggtat T/C gaaaaaactttgaaatgcat	6190
UGT2B15	9	(intron 3 493)	ggc t/a gtttttacttccatg C/T attggaataggtctatttag	6191
UGT2B15	10	(intron 3 906)	gccctctctgaatgatctat G/A caagtttttctgtgaaacac	6192
UGT2B15	11	(intron 3 1036)	tcagtaccttagtttggtag T/C agacatggttaagactggct	6193
UGT2B15	12	(intron 3 1544)	aataaatatataaggttatta C/G taatttgcacttttttatt	6194
UGT2B15	13	(intron 3 5550)	gtgtgtgtgaatcaatgtgtg C/T tgccttggggcagtagtcca	6195
UGT2B15	14	(intron 3 5720)	tttttcaaaagttaattttt C/A ttggggatttccctgcaggg	6196
UGT2B15	15	(intron 4 134)	atcaaaatttaactactttat A/G tttattttccagctttagta	6197
UGT2B15	16	(intron 5 6627)	ttttaatgttgatattctta T/C atttactcttcagctataaa	6198
UGT2B15	17	(coding region 1568 (Lys23	tttccgaaagcttgcacaaa A/C aggaagaaagaaagaaagag	6199
UGT2B15	18	(3' untranslated region 1	ggatttaatacgtacttttag C/T tgggaattattctatgtc a/t at	6200
UGT2B15	19	(3' untranslated region 1	ag c/t tgggaattattctatgtc A/T atgatttttaagctatgaaa	6201
UGT2B15	20	(intron 2 1980-1981)	aagagagtagcagaataagg (AGG) acaagggataaatgactagt	6202
UGT2B15	20	(intron 2 1980-1981)	aagagagtagcagaataagg acaagggataaatgactagt	6203
UGT2B15	21	(intron 3 605-618)	ctagccaaagtagatttagag (A)11-15 cttgtctgtctgtgctgactt	6204
UGT2B15	22	(3' untranslated region 1957-1968)	aagtataatttaaaaaagc (A)11-14 tacaactcttttttttaaac	6205

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
UGT8	1	(coding region 677 (Pro226	gcagaagtacaacctgctgc C/T ggagaagtcctatgtatgatt	6206
UGT8	2	(coding region 741 (Ala247	atgctgtgtactgacgttagc A/G ctggaattcccaagaccac	6207
UGT8	3	(intron 2 53-54)	ttgacaatcaatctctcctt GT/ Δ ttagtgcacaggtccagta	6208
GSTA1	1	(5' flanking region -266)	ttgcaaaagagcaaaatct C/A ggtgaaatgtattgtgtaaa	6209
GSTA1	2	(intron 2 1220)	gagacacaggctttcctaag A/C tatgacaacaccataactag	6210
GSTA1	3	(intron 4 1813)	aaaggcaccactggagggtg A/C attattttgcatcacctga	6211
GSTA1	4	(intron 5 732)	gaagagtgtgtcatgaagg T/C ggagtcactgcccaaggag	6212
GSTA1	5	(intron 6 333)	ttatcccatatgtgccaca A/G tgagccggtctgagcagagc	6213
GSTA1	6	(3' flanking region 412)	ctttcttatgtcatttgcata A/C caatgattctgtctgtgtg	6214
GSTA4	1	(intron 1 280)	gcattggtggaaggtgggt C/T ggatcgctcccggtctggc	6215
GSTA4	2	(intron 3 176)	ggaaatcactcttatttcaa T/C agttccataaaaagctggccg	6216
GSTA4	3	(intron 4 94)	acaccacatttactttatgt C/G ttacatagtttagtgagatca	6217
GSTA4	4	(intron 5 1062)	cacacttgtgcacatgcaga C/T acccatgggcatccaagagt	6218
GSTA4	5	(coding region 487 (Thr 163 Ala))	catagtgtgattttactccaa A/G ccattttagctctagaagag	6219
GSTA4	6	(intron 6 595)	tgagctctgagagcaaatga G/A agatgtt a/g gcacctaaaca	6220
GSTA4	7	(intron 6 630)	taaacatcaccccaaggat T/A cctaccattctccttctgag	6221
GSTA4	8	(intron 6 3943)	tcttcgtagtatcatataacc T/C tttttgttagccttaaaagt	6222
GSTA4	9	(3' untranslated region 10	taataacacacccaagtgtcta G/A taaatgactctcctctgagc	6223
GSTA4	10	(intron 5 370-371)	gtgtctgaacagctgtctca (TA) gctgacatcctcctgataa	6224
GSTA4	10	(intron 5 370-371)	gtgtctgaacagctgtctca gctgacatcctcctgataa	6225
GSTM1	1	(5' flanking region -694)	tacgaagtggttaatttaca C/T agtacttagccagatgaccg	6226
GSTM1	2	(5' flanking region -661)	gatgaccgaaggactcagta C/T ccgagggcccttaacagaaa	6227
GSTM1	3	(5' flanking region -658)	gaccgaaggactcagtagcc G/A agggcccttaacagaaaaca	6228
GSTM1	4	(5' flanking region -656)	ccgaaggactcagtagccga G/A ggcccttaacagaaaacaca	6229
GSTM1	5	(5' flanking region -537)	tagaggggagactaagccct G/C ggagtagctttccggatcaga	6230
GSTM1	6	(5' flanking region -525)	taagccctgggagtagcttt C/G ggatcagaggagtcctgct	6231
GSTM1	7	(5' flanking region -465)	aattaaattccaggttggg G/A ccaccacttttttagctgac	6232
GSTM1	8	(5' flanking region -383)	gcggagagaaggctgaggga C/T accgcgggcaggaggagaa	6233
GSTM1	9	(5' flanking region -382)	cggagagaaggctgaggga A/T ccgcgggcaggaggagaa	6234
GSTM1	10	(5' flanking region -378)	gagaaggctgagggaacacg C/T gggcaggaggaggagaa	6235
GSTM1	11	(5' flanking region -343)	agggagagaagccttctgccc G/A ttaggatctggctgtgtct	6236
GSTM1	12	(intron 2 118)	tgctggagctgcaggctgtc T/C cttccctgagcccggtgag	6237
GSTM1	13	(intron 3 233)	agtgagtgcccggtctctc T/C ctgctctgtcttatgggaag	6238
GSTM1	14	(intron 4 26)	tgtgggtggctgcaatgtgt G/A ggggggaagtgccctcctcc	6239
GSTM1	15	(intron 5 140)	actatcagcagttattctca C/T gactccaatgtcatgtcaac	6240
GSTM1	16	(intron 5 577)	ctgccacccattagaagga A/G ctttctactttccctgagct	6241
GSTM1	17	(intron 5 645)	gctgggtctggatccagaggg T/A gccagggtcttgggctctc	6242
GSTM1	18	(coding region 519 (Asn 173 Lys))	caccgtatattttaggccaa G/C tgcttggagccttcccaaa	6243
GSTM1	19	(coding region 528 (Asp 176 Asp))	tttagcccaagtgccttga C/T gccttcccaaatctgaagga	6244
GSTM1	20	(intron 7 2421)	cagcaccgtgtagaattctc A/G taagtgttagctgttactgt	6245
GSTM1	21	(3' flanking region 42)	atttgcctctggccatctac C/T cagactgtctgtctgtctgt	6246
GSTM2	1	(intron 1 7)	ggaaacatccgggggtgagc C/G agggctccgtggcggtggg	6247
GSTM2	2	(intron 1 45)	gggacgggggtgcgtggggg C/T ggggaagtgtggagcagctg	6248
GSTM2	3	(intron 3 70)	gactgcattctcctctccca G/C cttagaggtgttaagatcag	6249
GSTM2	4	(intron 3 224)	agcagggccctgtctcctc T/C tgcccttgcatatgggaagg	6250
GSTM2	5	(intron 5 100)	ttgatctctctgtgtgagtt C/A ttggtcttgctgactctaag	6251
GSTM2	6	(intron 5 341)	tctcttgggtgggttcatgg T/C ctggctgggttcaggagtg	6252
GSTM2	7	(intron 5 696)	accttttagctagacacagag C/T gctgatttgtgcatttaca	6253
GSTM2	8	(intron 5 723)	ttgtgcatttacaatcctt A/G gctaggcagaaaagttctcc	6254
GSTM2	9	(3' untranslated region 10	ctcagcccccagctgtctccc G/A tgttgcatgaaggagcagca	6255
GSTM2	10	(3' flanking region 139)	ttctgtctggcatagtaagg C/T gcttgagaattcttgcctcc	6256
GSTZ1	1	(5' flanking region -546)	agcagggcccccagccgcac C/A gcctcgaagcgcctgagcc	6257
GSTZ1	2	(intron 1 321)	tgtctgaccagccgccccgc T/C aaggagtcacaaagaggcag	6258
GSTZ1	3	(intron 1 2890)	aaaatactgcataaaacca G/A gccacgtctgttgggggga	6259
GSTZ1	4	(intron 1 2896)	ctgcatcaaaaaccagccac G/A ctctgttggggggacacaa	6260
GSTZ1	5	(intron 2 255)	tctcccaacactgctctcca A/G agcccttggaaccatgtt	6261
GSTZ1	6	(intron 2 1560)	caccactgtttaagccctg G/C gggggcagagttaaacacaa	6262
GSTZ1	7	(coding region 94 (Lys 32	cettgaaagggcatgactac G/A agacggtgcccatacatctc	6263
GSTZ1	8	(intron 4 297)	agaaggaggagtttgcctggc C/T ctgtccctctgggtccagg	6264
GSTZ1	9	(intron 6 94)	tatctgaacacagctccacg G/A ctgcttgggctgacagtt	6265
GSTP1	1	(intron 1 269)	ctccccggggtccagcaaa C/G ttttcttggctgctgcagt	6266
GSTP1	2	(intron 2 134)	ccccgggctccttctctgt C/T cccgcctctcccgccatgcc	6267
GSTP1	3	(intron 5 438)	gtgtgtgctgctgctgtgc G/A tgtgtgtgctgtgtgtgtg	6268
GSTP1	4	(intron 6 162)	cccgctggctgagtcocctag C/T ccccgctgctgcagatctc	6269
GSTP1	1	(5' flanking region -103)	taaagagtgtcccaggcgtc C/T gtgcccaccaatggggcaca	6270
MGST1	1	(promoter region -1879)	ttaataaatgtttattcaat T/G aaaccaactgctaattctc	6271
MGST1	2	(promoter region -508)	tctggaccctgaacaggagg G/C gacatcgtgacaaagcaaat	6272

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
MGST1	3	(promoter region -314)	cctggagatttttaactttct G/A cgaagtttttaaaaaaact	6273
MGST1	4	(promoter region -131)	atcagcaggcgatgggtact G/C tggcggggtaaatcaggtga	6274
MGST1	5	(intron 1b 36)	ggagaaggggacggcatgca A/G aggggtggcaggcagggaagg	6275
MGST1	6	(intron 1c 456)	ccccttgggaacgggttctcac C/T tgtgcccacttccccagtc	6276
MGST1	7	(intron 1c 719)	gcccgaagcattgctgtat A/G gcacccaggcctccagtgag	6277
MGST1	8	(intron 1c 985)	cgagtaaaatttttctaccc G/C tttgttttagagtggtgtct	6278
MGST1	9	(intron 1c 1428)	gtaaggggaagggcggttcc T/A caactgagaagtgaagattc	6279
MGST1	10	(intron 1c 2914)	ctcatcagggtgtgtgcaga T/G gcttgggtgctggccagttct	6280
MGST1	11	(intron 1c 4274)	attgtaataagattaacaaag G/T tgatgaaagtagtgtacata	6281
MGST1	12	(intron 1c 4276)	tgtaataagattaacaaaggt G/T atgaaagtagtgtacataat	6282
MGST1	13	(intron 1c 4767)	gccttctctcttcagcacatt C/T ccaattatacttccaattcc	6283
MGST1	14	(intron 2 2379)	ttctcaaatcttcattatata G/C ttttcttcaacccaaagttt	6284
MGST1	15	(intron 2 2767)	tttaactatagatgccttct T/G ctctcttctgtgtttgattta	6285
MGST1	16	(intron 2 2974)	tcactgcagcctcaacctct C/T gggctcagggtgatctcccaa	6286
MGST1	17	(intron 2 3083)	aaaaaattttagatagatggg T/G actccctatgttgcacaggc	6287
MGST1	18	(intron 2 3106)	tcctatgttgcacaggctg A/G tcttgaaattcttgggctcaa	6288
MGST1	19	(intron 3 1495)	gtcagacaatggccttcagc G/A tctctctcttgcagaatatg	6289
MGST1	20	(intron 3 1703)	ttctcttctaagaagaagtc T/C gtgcagatcatttagcagaaa	6290
MGST1	21	(intron 3 2528)	ttttggagacacttttcaga G/C agagcgtttccagcatcttc	6291
MGST1	22	(intron 3 2557)	tcacgatcttcccttccca T/C ttttaagttagacttttttt	6292
MGST1	23	(intron 3 2731)	atacacatatgggaacaatta A/C ctaaaaaacttaaggtaatat	6293
MGST1	24	(intron 3 3032)	agagacatttagaataatatt C/A cctttaaaggtagagaataa	6294
MGST1	25	(intron 3 3045)	atatattcccttttaaaggta G/C agaataaaccttccactgaga	6295
MGST1	26	(intron 3 3289)	ggtttatagtggttccccccc T/A ccccgcccccaaaagaccca	6296
MGST1	27	(intron 3 3976)	ggaaagctgggggaactgtt G/T cctggaacagagtcctcaaaa	6297
MGST1	28	(intron 3 4288)	ccatttctatttgcactgc G/A taacacaggcgtagaagtg	6298
MGST1	29	(intron 3 4298)	tgtcaactgcgtaacacagg C/T gtagaagtggacattgtttt	6299
MGST1	30	(intron 3 4429)	attggagggtgacgatatctc T/C gtgatgctgggggagaaatc	6300
MGST1	31	(intron 3 4519)	tttaataaaaaatggtaatt C/T tgtcttttcttccactctc	6301
MGST1	32	(intron 3 4817)	attgctatagaagagagtaa C/T gtaagcagaaatagttttc	6302
MGST1	33	(intron 3 6077)	tttgaattagtgtctttaa T/C agttatctttttccacagag	6303
MGST1	34	(3' untranslated region 60)	gggttaaaccttcttctctc T/C tagcatttcccaatctcgt	6304
MGST1	35	(3' flanking region 147)	tatttgcttctctctctctc C/T tgttttcttcttctctgaaa	6305
MGST1	36	(3' flanking region 237)	cagcacgtttttctctatgaa C/T aagacattctccaaataact	6306
MGST1	37	(intron 1C 904-923)	tgcgattatcttggtaatt (A)16-19 ggcaaatcagtcacaaattg	6307
MGST1	38	(intron 1C 3433-3434)	cccttcaataactagaacaa (AA) gcagacacattaaatgttac	6308
MGST1	38	(intron 1C 3433-3434)	ccccttcaataactagaacaa gcagacacattaaatgttac	6309
MGST1	39	(intron 1C 5146)	actatttcaattttttttt T/Δ ggagggggagacagagttct	6310
MGST1	40	(intron 2 552-563)	cccagcattataagaatgac (T)10-12 aagtgcagatgtggggagg	6311
MGST1	41	(exon 3 172-173)	tagcatttggcaaggagaa AA/Δ tgccaagaagtatcttcgaa	6312
MGST1	42	(intron 3 152-158)	agaaaactggatgtctgaaa TTGACA/Δ (GTCCAAATAT)	6313
MGST1	42	(intron 3 152-158)	cactgcacttgtatgtgtt	6314
MGST1	43	(intron 3 2198-2200)	ggatttttagattcttcccta CTA/Δ ttctttccgaccttccaccc	6315
MGST1	44	(intron 3 2567-2568)	ccctttccatttttaagtt (A) gactttttttttccacctt	6316
MGST1	44	(intron 3 2567-2568)	ccctttccatttttaagtt gactttttttttccacctt	6317
MGST1	45	(intron 3 2571-2580)	tttccatttttaagtttagac (T)9-11 caccctctctgttacctcag	6318
MGST1	46	(intron 3 3288-3289)	ggtttatagtggttccccccc (C) tccccgcccccaaaagaccc	6319
MGST1	46	(intron 3 3288-3289)	ggtttatagtggttccccccc tccccgcccccaaaagaccc	6320
MGST1	47	(intron 3 4682-4683)	tcctcttcatgtctctatgt (GAGATGTTGTGGCTCACAT)	6321
MGST1	47	(intron 3 4682-4683)	agtcactctcttctgtgagac	6322
MGST1	47	(intron 3 4682-4683)	tcctcttcatgtctctatgt	6323
MGST1	48	(3' flanking region 1359-1)	acacacacacacacacacac CC/Δ tgctctggagttgggcaact	6324
MGST1	49	(3' flanking region 1889-1)	ttagaatagtttcttaactat ACT/Δ tttactcccaagagaagctt	6325
MGST1L1	1	(5' flanking region -105)	tgctgcccgtgcccgtggggc G/A gggcggtggcggtgtggt	6326
MGST1L1	2	(intron 1 277)	agtgtctgtgagagaagcag G/A ttctggagggtggagtggtg	6327
MGST1L1	3	(intron 2 8030)	ggggttatagagagccctc C/G gccccaccacacatatgca	6328
MGST1L1	4	(intron 2 8499)	gtatggcaggagtggtgtcc C/T ggcaagccatagaggtatgg	6329
MGST1L1	5	(3' untranslated region 46)	cgccacctgtgaccagcagc T/G gatgcctccttggccaccag	6330
MGST2	1	(5' flanking region -46)	ggtcagcattcaagtcag A/T agcgccatttatcttccct	6331
MGST2	2	(intron 1 176)	ggtcacccatgcccgctgct A/C cctccttcccaaggggcaag	6332
MGST2	3	(intron 1 204)	tcccaggggcaagcagagac T/C gagaacattccagagattag	6333
MGST2	4	(intron 1 373)	ttacaagtgttccaaaggaa A/T cgtgcctgtctttaaaccctg	6334
MGST2	5	(intron 2 -3245)	cctcgtgatttgcacacctc G/A gcctcccaagtgctgggat	6335
MGST2	6	(intron 2 -1998)	aggccgaggtggggcgatca T/C gaggtcaggagatcgagacc	6336
MGST2	7	(intron 2 -1640)	tgtttattccttgcagatgcc A/G taatataaagtagtaattt	6337
MGST2	8	(intron 3 41)	actgtgttctaagtatgact A/G tgatgcttaaacgattaaag	6338
MGST2	9	(intron 3 453)	atcagagtgctatgttgcag A/G tatatgaacttttgcttcac	6339
MGST3	1	(5' flanking region -520)	acaaaaaggccctaacagc A/C taaatccattcacttcggga	6340
MGST3	2	(5' flanking region -355)	cgccataaacccgctacgggt G/A ctctgctggggacaaattat	6341

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
MGST3	3	(5' flanking region -234)	ctgggggagtagatatatgt T/A ttgagaatgagaggagtaa	6340
MGST3	4	(intron 1 74)	agcctttgagcaggcactcc C/T atatttcagcctatgcgagc	6341
MGST3	5	(intron 1 682)	agaaaatgcccttctttat G/C tggggtggcagcagcgagcc	6342
MGST3	6	(intron 1 832)	cgagtttacaagctacataa T/C agcgtcgggggcaagtaagt	6343
MGST3	7	(intron 1 1919)	aataaaattcctgagtttct G/C tcaactgctcttacagtacc	6344
MGST3	8	(intron 1 1991)	tgtaattaggcaacaggaaa A/G ttgtactatctttcaaatgc	6345
MGST3	9	(intron 1 4458)	tcttccatcctcctaacata T/C agttagcttccactctccaa	6346
MGST3	10	(intron 1 4676)	tgaatatgcaatgcaattgt C/G gggggatagttacttttcat	6347
MGST3	11	(intron 3 278)	cagcatgaccatctaaacc G/C atgttgactctcccaggcct	6348
MGST3	12	(intron 4 423)	cttgccctttttgtgtgggg T/G gtggggtgtgcacagagaag	6349
MGST3	13	(intron 4 506)	gtgcagagaagaaaacaaag T/C ggggaagggtggaaggggat	6350
MGST3	14	(intron 4 -162)	tcacagatattttattttcc C/T gactgaaactaacttaattc	6351
MGST3	15	(intron 4 -130)	acttaattctacctaatttg C/G gtggggagtagttggccaaa	6352
MGST3	16	(intron 4 -105)	ggagtagttggccaaatcat C/G aaattgttaactttttgcta	6353
MGST3	17	(intron 4 -65)	aacatattgtgtaatacaacc C/T taggtgttaaaaaaggtttg	6354
MGST3	18	(intron 5 105)	atcccagcactttgggaggg C/G aaggcaggcagattgcttga	6355
MGST3	19	(intron 5 197)	aaaaaatacaaaattagcc G/A gatgtggtgtgtgcacacctg	6356
MGST3	20	(intron 5 222)	tggtgtgtgcacacctgtagt C/T ccagctactctgggaggctga	6357
MGST3	21	(intron 5 374)	tcttatgctactatattttt T/C ttcttgggaatttgagaaaa	6358
MGST3	22	(3' untranslated region 51)	atgacttacctttattttcca G/T ttacattttttttctaaata	6359
MGST3	23	(3' flanking region 166)	agtcgtattgtgtgatgta G/T gtatagtcagtcacacagta	6360
SULT1A1/ST	1	(5' flanking region -1597)	gcagagtaaaagggaactcact C/G aagaagaggaacgtgggggt	6361
SULT1A1/ST	2	(5' flanking region -1491)	gaggggtatattcatgaaga G/T tccaggaaaaggttaagatt	6362
SULT1A1/ST	3	(5' flanking region -1376)	cggtttcattatgttactgat C/T a/g taca a/g tgagatcctaggt	6363
SULT1A1/ST	4	(5' flanking region -1375)	ggtttcattatgttaactgat c/t A/G taca a/g tgagatcctaggt	6364
SULT1A1/ST	5	(5' flanking region -1370)	catatgttactgat c/t a/g taca A/G tgagatcctaggtgaaacc	6365
SULT1A1/ST	6	(exon 1B -65)	aaccctgcattccccacaca G/A caccacaatcagccactgc	6366
SULT1A1/ST	7	(intron 1B 442)	gagccaccctgcctaggcct G/A tgcttttctgtagtcatcag	6367
SULT1A1/ST	8	(exon 1A -197)	gctgggggtcccagcaggaa A/G tggtagacaaaagggcgctg	6368
SULT1A1/ST	9	(exon 1A -159)	ctbgctggcagggagacagc A/C caggaaggtcctagagcttc	6369
SULT1A1/ST	10	(exon 1A -95)	gagaccttcacacacctga T/C atctgggctctggcccgaca	6370
SULT1A1/ST	11	(intron 1A 60)	ctggttttcagccccagccc C/T gccactga c/g tggcttttga	6371
SULT1A1/ST	12	(intron 1A 69)	agccccagccc c/t gccactga C/G tggcttttgaagtgccggca	6372
SULT1A1/ST	13	(intron 1A 174)	tgtgatgtgtgttaagggaa G/A ggcctggctctggccctga	6373
SULT1A1/ST	14	(intron 6 11)	catgaaggaggtgagaccac C/G tgtga a/t gcttccctccatgt	6374
SULT1A1/ST	15	(intron 6 17)	ggaggtgagaccac c/g tgtga A/T gcttccctccatgtgacacc	6375
SULT1A1/ST	16	(intron 6 35)	gaagcttccctccatgtgac A/T cctggggcccgccactcac	6376
SULT1A1/ST	17	(intron 6 71)	ctcacagggagccaccagg T/C caccagcccctcccttgg	6377
SULT1A1/ST	18	(intron 6 108)	btggcagccccacagcagg C/A cc g/a gattccccatcctgctct	6378
SULT1A1/ST	19	(intron 6 111)	gcagccccacagcagg c/a cc G/A gattccccatcctgctctct	6379
SULT1A1/ST	20	(intron 6 270)	ctccctgccaaaaggtgtgc C/T acccagggccacagtcattg	6380
SULT1A1/ST	21	(intron 6 488)	ttttacttttctgtaatcag C/T aatccagcctccactgagg	6381
SULT1A1/ST	22	(intron 6 509)	aatccagcctccactgagg A/G gccctctgctgctcagaacc	6382
SULT1A1/ST	23	(coding region 600 (Pro 201 Pro))	ccctctgctgctcagaacc C/G aaaagggagattcaaaagat	6383
SULT1A1/ST	24	(coding region 638 (His 213 Arg))	gatcctggagttttgtggggc A/G ctccctgccagaggagaccg	6384
SULT1A1/ST	25	(coding region 645 (Leu 215 Leu))	gagtttgtggggcactccct G/A ccagaggagaccgtggactt	6385
SULT1A1/ST	26	(coding region 902 (Gly 301 Ser))	gctgtgagaggggctcctgg G/A gtcactgcagagggagtggtg	6386
SULT1A1/ST	27	(coding region 973 (Trp 325 Arg))	taaaatatgaattgagggcc T/C gggacggtaggtcatgtctg	6387
SULT1A2/ST	1	(5' flanking region -547)	tgtttcttcttgggtctatg G/C atccatgctctgctccaccc	6388
SULT1A2/ST	2	(5' flanking region -425)	tgtgggttgactgggcccag G/A accctggcaccttcaagac	6389
SULT1A2/ST	3	(5' flanking region -358)	ctttccagggcctgctatc C/T ca g/t ctttctctccaatccc	6390
SULT1A2/ST	4	(5' flanking region -355)	tccagggcctgctatc c/t ca G/T ctttctctccaatccc	6391
SULT1A2/ST	5	(5' untranslated region -)	actcggggcgaggagggcac A/G aggccaggttcccaagagct	6392
SULT1A2/ST	6	(intron 1A 85)	ctgactggccttgtgagtg G/A ggcaagtcaactcagcctccc	6393
SULT1A2/ST	7	(coding region 20 (Ile 7 Thr))	catggagctgatccaggaca T/C etc t/c cgcccccaactggagt	6394
SULT1A2/ST	8	(coding region 24 (Ser 8 S))	gagctgatccaggaca t/c etc T/C cgcccccaactggagtacgt	6395
SULT1A2/ST	9	(intron 2 34)	gccaccacccctctccagg T/C ggcagtcctccacttggcca	6396
SULT1A2/ST	10	(intron 5 77)	cagcaacctgtgtgcccac T/C ccttgcctgcttctccagtg	6397
SULT1A2/ST	11	(intron 6 684)	actgggggtccaggggtcga G/C gagctggctctatgggtttt	6398
SULT1A2/ST	12	(coding region 704 (Asn 235 Thr))	gttcaaggagatgaagaaga A/C ccctatgaccaactacacca	6399
SULT1A2/ST	13	(3' untranslated region 89)	gctctgagctgtgagagggg T/C tcttggagtcactgcagagg	6400
SULT1A2/ST	14	(3' flanking region 98)	cttccctgctccagctcctc A/T acttgcctgtttggagagg	6401
SULT1A2/ST	15	(3' flanking region 817)	ccactgactcggggcttgcc A/C aggcgtccaggggtggcaaa	6402

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
SULT1A2/ST	16	(3' flanking region 1006)	cctotcccctggaggctgct T/C taccgctgtggggcgcat	6403
SULT1A2/ST	17	(3' flanking region 1464)	tcccgtagccaggcaagtt C/T ggtgaccagagagcagcccc	6404
(SULT1A2/S	18	(intron 4 1728)	tcagcttctcctcttgccaa A/Δ ccaagagatgagctgscctg	6405
SULT1A3/ST	1	(coding region 843 (Ala 281 Ala))	cgcttcgatgcggactatgc G/A gagaagatggcaggctgcag	6406
SULT1C1	1	(intron 3 2280)	gcaaatcttttggtattttta G/T tacagtcagggttttaccat	6407
SULT1C1	2	(intron 3 3742)	gcagatctcacttttctggca G/A attcctgaatttgcctccc	6408
SULT1C1	3	(intron 3 4453)	ttcatagggcttttccctca C/T ttgtttttgtaattttgtata	6409
SULT1C1	4	(intron 3 5234)	gaaaagagactagaggcagg A/G gagctttgcagttcttctaa	6410
SULT1C1	5	(intron 3 6175)	tggctggcaggagggtgagg G/C agtcctctcttctctgtgtcc	6411
SULT1C1	6	(intron 4 205)	acatgaaggcaggatccaga T/C tgaatgtttggagggaacta	6412
SULT1C1	7	(intron 4 408)	ggctcacgcctgtaatccca G/C cactttgggaggccgaggcg	6413
SULT1C1	8	(intron 4 429)	cactttgggaggccgaggcg G/C gtggatcacaaagtcaggag	6414
SULT1C1	9	(intron 3 2106-2115)	tgcagtggtctgtttgtttgg (T)8-11 gagacaaagtcgtgctgt	6415
SULT1C1	10	(intron 3 4199-4210)	atgcccgactaattttgtta (T)10-13 agagacaggatttcaccatg	6416
SULT1C2	1	(5' flanking region -110)	tcctgttaactcacagagaa C/T ggaagggtctggaacgggacc	6417
SULT1C2	2	(coding region 15 (Asp 5 G	acactaatggccttacacga C/G atggaggattttacatttga	6418
SULT1C2	3	(intron 1 297)	gtagactgttttattttatc A/C ttcccaatctaggcccttat	6419
SULT1C2	4	(intron 1 363)	gagtggtgtgagctagaaagg T/G gatcctgagctgtgatttggg	6420
SULT1C2	5	(intron 1 2300)	gggtactatcagcagccac C/T acctcagggaaggatgacttc	6421
SULT1C2	6	(intron 2 455)	aagacttggaaagcaataga T/G aaaaaaaatctgtagaaat	6422
SULT1C2	7	(intron 4 55)	caaatctccaaacacccta G/A aaggaaagaatcttttcttt	6423
SULT1C2	8	(intron 4 111)	ctgccttctttaaaggaa C/T tctcacttctcttcagggaat	6424
SULT1C2	9	(intron 5 1657)	ctttgtgtttactttgtttt T/C acttggtacaaaagtgtgtg	6425
SULT1C2	10	(intron 5 2082)	tctgctctagagatggagg C/A gtcccacagccacagtgatg	6426
SULT1C2	11	(intron 6 933)	agctactgaacctctccac A/G taactgtatttcaggggcag	6427
SULT2A1	1	(intron 2 478)	ggactgggctctgtacacac T/C tctgttactgtgtgtaaat	6428
SULT2A1	2	(intron 3 382)	caaaacctcttaataattct G/A tttctatctgtctcagaact	6429
SULT2A1	3	(intron 3 409)	tctgtctcagaactgattgc A/G tgactctaggatcgctatat	6430
SULT2A1	4	(intron 5 249)	agctggaaattacaggcaca C/T gccaccacaccagctaatt	6431
SULT2A1	5	(intron 5 395)	aggcatgagccacggcgccc G/A gccaatctacagctttaat	6432
SULT2A1	6	(3' flanking region 33)	ttcctgtttaaaggattacca G/C ggttggccaggc a/g cggtggt	6433
SULT2A1	7	(3' flanking region 46)	gttacca g/c ggttggccaggc A/G cggtgttccagccttaat	6434
SULT2A1	8	(3' flanking region 199)	ttagccaggcgcttggctc A/G tgtctgtaatcccagcactt	6435
SULT2B1	1	(intron 2 4162)	ttctcccctctctccaccat C/T cgcacacaggtgatctacat	6436
SULT2B1	2	(intron 3 879)	gaggcatccagctctgggg G/A ctggacctgggggtttgtgg	6437
SULT2B1	3	(intron 4 3882)	ttccacgctcctctcctggc C/T gagtgccctccctccgctga	6438
SULT2B1	4	(intron 5 1780)	cctgcagaaggggttccctt C/T catgtccacagcagtaatggc	6439
SULT2B1	5	(intron 5 1814)	taatggctgcagcatggagc G/A ttgtggggcattgagacag	6440
SULT2B1	6	(coding region 789 (Cys 263 Cys))	ccctcttctccagggtctg C/T ggcgactggaagaaccactt	6441
SULTX3	1	(intron 1 332)	cctgcttctccctttaccctg G/T ctggctgtgtgacctggac	6442
SULTX3	2	(intron 1 1167)	taggaatggcctaagcgtgtc G/A ttggctctgtgtggcactca	6443
SULTX3	3	(intron 1 2872)	cattctcactgatgcagacg G/A aagcttctgggctggggcgt	6444
SULTX3	4	(intron 1 6242)	cacccttggcttttaccagc A/G tggaaacattttacctgaat	6445
SULTX3	5	(intron 1 6601)	gcgtgggcttctggaggag C/T gagaggagagtgaggggccc	6446
SULTX3	6	(intron 1 6768)	agcttgaatgagccagact C/T tectgggacctgttgacccc	6447
SULTX3	7	(intron 1 6905)	agtactttgttttatctccc C/T catctccacaactttgccat	6448
SULTX3	8	(intron 1 7464)	gccaggatcccttgagagac G/A acatgaacacagccaggagc	6449
SULTX3	9	(intron 1 7833)	tgcttcgggctgggcttggc G/A ggggacagctgtgtccaggc	6450
SULTX3	10	(intron 1 8189)	caaatggggcccttaatgc C/T gcacaccagagcctcctttc	6451
SULTX3	11	(intron 1 8316)	ctctcacacaaggcgaggc C/G tcttccccttgaggcagagc	6452
SULTX3	12	(intron 1 8617)	agacagaggctggggccaag C/T cagggttgcggagcttccc	6453
SULTX3	13	(intron 1 8631)	gccaagccagggttgcggga G/T cttctggactggctcaggcc	6454
SULTX3	14	(intron 1 9493)	ttttctcttagagcttccc G/A tctgtctctgtgtcgagggc	6455
SULTX3	15	(intron 1 10306)	caggcggggagcctgaatgc C/T gcagtcgtgagggtggccag	6456
SULTX3	16	(intron 1 11987)	tcataaaataatgatcatcag T/C acactttttggaatttgag	6457
SULTX3	17	(intron 1 13085)	ctctgtgtcccgtgttgaga C/A aggccatgcccttagagctct	6458
SULTX3	18	(intron 1 13108)	gccatgccctagagctctgg G/A gagttccaccccagaacagc	6459
SULTX3	19	(intron 2 700)	gaaccatctgggagctgttc C/T gtactgccgtgccaggggcc	6460
SULTX3	20	(intron 2 818)	agccatagtagctagccagc G/A atcagcgctgggaggggagc	6461
SULTX3	21	(intron 2 1677)	actccacttcccctgaaccc C/T accccttcccttccctctg	6462
SULTX3	22	(intron 4 4954)	gcgtgccgaaggcggaggc C/T tgggatggctcaagacgtga	6463
SULTX3	23	(intron 5 3632)	ccagctgactcccacaccag C/T ggtcagagaaacttgtcttt	6464
SULTX3	24	(intron 5 3662)	acattgtcttttaagggttc C/T gaagtgtctgcaataaagaaa	6465
SULTX3	25	(intron 6 1874)	tctgatctcagagagctgac A/G atggaagaattctaaacga	6466
SULTX3	26	(intron 6 2133)	agaccgggtgctgcagttta T/G cccacagctcagccctccct	6467
SULTX3	27	(intron 6 2524)	ggaaggccagggtgctgctg T/C gatgccagagcagtgcaact	6468
SULTX3	28	(intron 6 2573)	agatcatactcgtcctggg A/G tgtttattaaacacctgcca	6469
SULTX3	29	(3' flanking region 12)	gttcccggcggttgcgtcgag C/G gtttctgctgtgggggtag	6470

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
SULTX3	30	(3' flanking region 445)	tccaaagcctgtcttccctga T/G ttccctgtggaaggagagtc	6471
SULTX3	31	(intron 1 6418)	ctctccctgttagtggtggg G/Δ cagctcttccagtgctcctg	6472
SULTX3	32	(intron 5 2458)	cccttaaaaggaagttcacc C/Δ ttctctgccttccaggctcc	6473
TPST1	1	(5' flanking region -298)	accgccaccatgccagct A/C attttttttgtatttttttt	6474
TPST1	2	(intron 1 3520)	agaaaaagcagattaatgtaa C/G agtgacgcttagacacaaag	6475
TPST1	3	(intron 1 3610)	ggcagaagagaatatagca A/G ctattaaacacaaataaatt	6476
TPST1	4	(intron 1 20828)	tattgtctgccacctggta A/G tctgtcctctgtataagtg	6477
TPST1	5	(intron 1 -6761)	aatacaatactattctgtta T/C aattctagaggccagaga	6478
TPST1	6	(intron 1 -544)	tagaacaagtgaattttta C/T gttcttagtggtttatgggt	6479
TPST1	7	(intron 1 -526)	tacgtttcttagtggtttatg G/T ttggcagttttcccccaaca	6480
TPST1	8	(intron 1 -234)	tcaagacatttaataatgca C/T atgtttcagctaaccctttt	6481
TPST1	9	(intron 1 -48)	ttatagtggttttaagcatg A/G ttctaaaaaatttaataa	6482
TPST1	10	(intron 2 -18944)	aaaacattagaactgggaag G/A ttaaaaaattcttagtcttt	6483
TPST1	11	(intron 2 -18687)	tatgtgcaccctaataacat A/G ttcccttaaaactagtacta	6484
TPST1	12	(intron 2 -18501)	ttggaaggttaacttaatgta A/G gtgcctgaaaacagggata	6485
TPST1	13	(intron 2 -159)	gaatggggatttccctcagt C/G ctgcccactggctgctcttg	6486
TPST1	14	(intron 2 -19)	acctgttgcccttaactcac G/A cctgctttgtttttccaggt	6487
TPST1	15	(intron 3 158)	tgctggggaagaagatcag C/G gtctgggacttggtgatttt	6488
TPST1	16	(intron 3 3779)	agcaggggcagctcaccctcc C/T ggcacacccatgtgttcacc	6489
TPST1	17	(intron 4 292)	ttgttattttcattatgaac C/T atgaataatttcagctgaaa	6490
TPST1	18	(3' untranslated region 15)	gttgctgtacatgttctaa T/G gttttgtagaacagctgtgc	6491
TPST1	19	(3' flanking region 264)	acgggtgctggcctgcatta C/T cattttgtagtgaagtttct	6492
TPST2	1	(intron 2 578)	tcacctatcactcactgc G/A aggatgccaggataacctccc	6493
TPST2	2	(intron 2 789)	cttaagccatctgtcaggtc A/G ttgctgtcttctgtcactt	6494
TPST2	3	(intron 3 2009)	cccaggctggagtgtagtgg T/C gtgatct c/t ggctcactgcaa	6495
TPST2	4	(intron 3 2017)	ggagtgtagtgg t/c gtgatct C/T ggctcactgcaaactccgcc	6496
TPST2	5	(intron 3 2035)	ctcggtcactgcacacctcc G/A cctcccggtttcaagcagtt	6497
TPST2	6	(intron 4 104)	aatgttcagtcctctcaattc C/T tggctcatctgattgttctt	6498
TPST2	7	(intron 4 379)	taataataataactattggt C/T cctttctgtcttataaaggt	6499
TPST2	8	(intron 4 588)	tactgcagcctgatacttct C/T ggcttaagccatcctctcac	6500
TPST2	9	(intron 4 626)	cacccaggtcctctgagtag C/T taggactgcaggtgcacgcc	6501
TPST2	10	(intron 4 718)	cccaggctggctcagaactc C/G tggccgtaaggatgccctt	6502
TPST2	11	(intron 4 873)	gttgatggccttatttata G/A ttccattacagctcttagt	6503
TPST2	12	(intron 4 949)	caaatatttgaataatggac C/G caggcctgaggaagagcttt	6504
TPST2	13	(intron 4 1033)	taagctcagcatttctgagc G/A tctgtctgattttaggaaata	6505
TPST2	14	(intron 4 1051)	gcgtgtgctgattttaggaa A/G taacacagttatcgtlattgaa	6506
TPST2	15	(intron 4 1356)	gattcaacgtacataaccagc C/T gacattgacaggtgaatggc	6507
TPST2	16	(intron 4 1707)	gtctccttaaaaggtggctc G/T ctgcccctggcttgcaccag	6508
TPST2	17	(intron 5 215)	aagaccagcctgaccaaacc G/A gtgaaccccgctcttacta	6509
TPST2	18	(intron 5 341)	tgggagggcagaggtcgagc G/A agctgagatcacgcccgttc	6510
TPST2	19	(intron 6 31)	ggacttcaactgggggttccc G/A ctgcttctgggtggccccc	6511
TPST2	20	(intron 6 273)	gtttgtctgacactggggac A/G gggcaggaagcaccactatg	6512
TPST2	21	(intron 6 693)	aaagggatttttttgaaact G/C gtaattcaagatttaagatt	6513
TPST2	22	(intron 6 1635)	tcttgggtacagagttggcc T/G tgaacaaacatgagtccttc	6514
TPST2	23	(3' untranslated region 11)	cttcccacttctcagatctc C/T gcaaatgacttcatggcaa	6515
CST	1	(intron 1b 6302)	agagctccccagagaggact A/G tgaggctgcatgatcatga	6516
CST	2	(intron 2a 1004)	gagtgagaccccatctctta C/T aaatttttttttaaaagta	6517
CST	3	(intron 2a 1395)	atgcctaagtttacagtagc T/C aggcaggaagggcacaacca	6518
CST	4	(intron 1d 473)	ccagagcctgaggttggtgc T/A ggggccccctccatggctgcc	6519
CST	5	(intron 2b 726)	ctatctctccagtgcccttc T/C gtccctgtctggaccctgct	6520
CST	6	(intron 2b 745)	ctgtccctgtctggaccctg C/A tggggggccacagagcaggc	6521
CST	7	(coding region 85 (Val 29 Met))	tcactagtttctctgctgctg G/A tgtactcctatgccgtgcc	6522
CST	8	(intron 3 308)	tcgtctgaggtcaggagttc G/A agaccagcctggccaacatg	6523
CST	9	(intron 3 853)	ttttgtctataaaatggca G/A tttcatgtggcccaagctga	6524
CST	10	(coding region 198 (Asn 66 Asn))	gaggcagtgatccggggccaa C/T ggctcggggggggagtgcca	6525
ST1B2	1	(intron 1 80)	acttgctcataaaatcatta C/T cattctaaataaagtttaata	6526
ST1B2	2	(intron 2 -352)	aacatttaaatagtcattta T/C agcaatgcacaggtataata	6527
ST1B2	3	(intron 2 -85)	attacataatgtcacaataat G/A tcttgaataaactggttgcca	6528
ST1B2	4	(intron 4 460)	gtacttgacattaaaaata T/C ctgatgttt a/g tatatccata	6529
ST1B2	5	(intron 4 470)	ttaaaaata t/c ctgatgttt A/G tatatccataaatagcta	6530
ST1B2	6	(intron 4 518)	tttaagattgtctcatatt C/G ttacttcttcttggttactaa	6531
ST1B2	7	(intron 4 616)	aatgtttatgaaaaatagact T/C ttatctggttttagtgccct	6532
ST1B2	8	(intron 5 53)	ctgcatcatgctgtaaaagg G/A ctgatattgtcttccaact	6533
ST1B2	9	(coding region 612 (Glu 204 Asp))	taatagaatccaaaggagga A/C atcaagaagatcattagatt	6534
ST1B2	10	(intron 6 582)	aatacattacttccatttaa G/A tagtctgttttattgtggctt	6535
ST1B2	11	(intron 6 3130)	agatgtaaaaattattcaa A/T ttttaaaagcctgaaaaatt	6536
ST1B2	12	(3' untranslated region 90)	tttaaaagtgtctaaatcaca C/A atctgaagaaataagagatt	6537

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ST1B2	13	(3' flanking region 50)	tcagatcccagttttgttcc T/G ttgattctgagtttccaaat	6538
ST1B2	14	(3' flanking region 328)	tttgaccacaggacactgtgt T/G ccactgctgtctaccgagtt	6539
ST1B2	15	(3' flanking region 446)	gtagttcagattttggaaat C/A ttttttctatcatcaccta	6540
CHST1	1	(intron 1 3900)	gccctgccccactcccaga C/G ttgcggccctccagccctt	6541
CHST1	2	(intron 1 6520)	cctccccagaggagctggg C/T acactggggccttggtgtg	6542
CHST1	3	(intron 1 7963)	aaaacattcatgggggatta G/C tgctggctacgtcagagta	6543
CHST1	4	(intron 1 9173)	gcgctgccacagatcaggcc G/A aggtgggggacagaaatgcc	6544
CHST1	5	(intron 1 9701)	cccagaattctgaatacaga A/G gcgatgacgggactacgagg	6545
CHST1	6	(intron 1 12132)	aacagatcccacaggaccaga C/A agcaaaagggaggaaatcgc	6546
CHST1	7	(intron 1 12465)	atgcagggaaggggctggc G/A caaaactgtcaactgagata	6547
CHST1	8	(intron 1 12561)	atgctccctgggtccactttc G/A ctttgagtttcaggtagctg	6548
CHST1	9	(intron 3 529)	ccatgggtctgcagggttct T/G catgctcaggggattgggtg	6549
CHST1	10	(intron 3 617)	agaggacagaggaagaggga C/A cactgggaactggggcgc	6550
CHST1	11	(intron 3 796)	aagaggcttcgcagctgtc C/T gcagggttaaatcctgggggtg	6551
CHST1	12	(intron 3 818)	cagggttaaatcctgggtg C/A aggaatgtttgttcagctcc	6552
CHST1	13	(3' flanking region 762)	ataactgggtacaggtttact G/C gtgtctacactggcagagaa	6553
CHST1	14	(intron 1 7874)	gttttccccttgcttgcct T/Δ cattttcatcactcatttt	6554
CHST1	15	(3' flanking region 335~3)	cacactgccacacctggcta (T)12-15 ggatttttagtagagcgggg	6555
CHST2	1	(5' flanking region -260)	agccggacagtcgccgggc G/A gtgatccggggccgcctccc	6556
CHST2	2	(5' flanking region -56)	gcgctggggaccagccggc C/T gcccgctcgcgagtcgggc	6557
CHST2	3	(3' flanking region 218)	aggagtgaacacacatcttg T/A attctaaggcagaaaccaa	6558
CHST2	4	(3' flanking region 383)	gcagagaccaatgttttgg T/G ctgaggtcgttcagaaaaa	6559
CHST2	5	(3' flanking region 952)	tactgaacatcttcagaa T/C gttatactatgagaagaat	6560
CHST3	1	(5' untranslated region -2)	tccagcgtgccgacggccc C/G gcagcgcctccatccctccg	6561
CHST3	2	(intron 1 96)	gcgtccagcgcgcgcgcca G/A actttggaggagaaaggggg	6562
CHST3	3	(intron 1 4467)	agagaagaatggggcagagc C/G ggagcagccagggaggtga	6563
CHST3	4	(intron 1 4853)	ggatgagcactgccagctg A/G tccctgccaccttccacag	6564
CHST3	5	(intron 1 4965)	tccactgcagaggggacaca G/C tgaccaggaggaagttggg	6565
CHST3	6	(intron 1 5046)	gggctgtccactcttctacc C/T ctggttccatcccagtcct	6566
CHST3	7	(intron 1 5300)	ccttttcttctctaaggcct A/G aagagatgacagaatgctgc	6567
CHST3	8	(intron 1 5354)	agccgctggactccacagcg G/A ggtgtgggtggccctggc	6568
CHST3	9	(intron 1 5428)	gacacgcttcagccctctgt C/G tctattgccccaaatctggc	6569
CHST3	10	(intron 1 6555)	gagtggggacactgctggaag G/C ttctggttctgctttgttc	6570
CHST3	11	(intron 1 6990)	aaacacactggggccacccc G/A tccccgactgtgactacac	6571
CHST3	12	(intron 1 7133)	ctgagggcctgtcctgcagg T/G ttgatgtgtctgaagagccc	6572
CHST3	13	(intron 1 7161)	gtctgaagaggcccccagaa T/C agaaatctagaacctgccag	6573
CHST3	14	(intron 1 7199)	cagtcacgaagcagtgctac C/T caccagaggatgaagaactg	6574
CHST3	15	(intron 1 7316)	cttgcatctgtgttagtg C/T tgggggtagcgtgccaggga	6575
CHST3	16	(intron 1 7967)	gacaggaaacccaccccgag T/G gatgtctggccctgtgacct	6576
CHST3	17	(intron 1 11412)	gcttgacactctgattcatt C/T tgcagtcactggctctttgt	6577
CHST3	18	(intron 1 11591)	ccctggaagggcctcactgc G/A gtgactcattaccagcatg	6578
CHST3	19	(intron 1 12541)	accacacagcatgaatggg G/C ccagccccagcctgccgct	6579
CHST3	20	(intron 1 12672)	gtagccacagctggggtgt G/C gggtcagggcacatggcaagg	6580
CHST3	21	(intron 1 14809)	ggatgtgtaggggttgggct C/T ggccttaagggatgggtgga	6581
CHST3	22	(intron 1 16161)	gatgctggtcaggcattgtc G/A ttgggatctttaaccacc	6582
CHST3	23	(intron 1 16385)	tatttagcatgtgggtttca A/C ctttctgttttttcaaaagg	6583
CHST3	24	(intron 1 33638)	gacttggggcacgtccttg G/C catgaactcttggtctatgtc	6584
CHST3	25	(intron 1 35145)	aggggaagccgaagcctact T/C gctggggcttgctggcctc	6585
CHST3	26	(intron 1 35340)	tgtgaagtgtttgccacagt T/C ggtggccatggttcgacccg	6586
CHST3	27	(intron 1 35436)	gccactcatgtatggagcaa T/C tgccttttttcttctctt	6587
CHST3	28	(intron 1 36150)	ccatagaagaggctgggct G/T aggaagccagggaagcagga	6588
CHST3	29	(intron 1 36194)	ggtgtggggaggccagcagg G/A gtgtgggctcagcggggag	6589
CHST3	30	(intron 1 37602)	ctggaaacagcaacttaaaaa A/T agaaatagtcctgggaagg	6590
CHST3	31	(intron 1 37725)	gggtagccagggcagctccc C/T gaccgcga c/g ctgccctttca	6591
CHST3	32	(intron 1 37734)	gggcagctccc c/t gaccgcga C/G ctgctttttaccctctccc	6592
CHST3	33	(intron 1 38208)	gccatttctagatgcagtgcc C/T gactttgggg t/c gcttgcat	6593
CHST3	34	(intron 2 255)	ctacagctgtgaaaggtag A/G caagatacttaacatttctg	6594
CHST3	35	(3' untranslated region 2)	acacctcagaggagcctgtg C/A ttaacattttagtagattatt	6595
CHST3	36	(3' untranslated region 2)	aggcctcatctgggtaggg C/G caagaggaaagtacagagt	6596
CHST3	37	(3' untranslated region 2)	ctggaattctccttagggc C/T ctgggaagagtagttgttaa	6597
CHST3	38	(3' untranslated region 2)	cttaacgcaggatgtgtcgg G/A tgttttgttctgggctttta	6598
CHST3	39	(3' untranslated region 2)	gcttgggtgtctttctgtttt C/T atggctgtgtttttgtctttt	6599
CHST3	40	(3' untranslated region 3)	ccgagggtcgtccagctctg C/T ttctgtgttctctggacatt	6600
CHST3	41	(3' untranslated region 3)	ctgtcagatcagggccattg T/C aaaccagagggtgcattt	6601
CHST3	42	(3' untranslated region 3)	gttcccatgtggaggctgg A/G ggggctgggactggggagg	6602
CHST3	43	(3' untranslated region 3)	ggccctgctaattgtggacag T/C agactttatccctctctt	6603
CHST3	44	(3' untranslated region 4)	ccagatgtgcatagaagcca G/A tctctgtcacatacaccgca	6604
CHST3	45	(3' untranslated region 4)	taaaagcaatttaggctttt G/A tcttctgtcacaatcatgcac	6605
CHST3	46	(3' untranslated region 6)	atttcatgtctgcaggttac G/A agacaccccttcac g/a gcata	6606
CHST3	47	(3' flanking region 281)	agacaggagtgttggggcag C/T ggtcagggggcctggggatg	6607

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
CHST3	48	(3' flanking region 997)	acctcttaaagtatttgagc C/T ggtgcctgtcatcccaacct	6608
CHST3	49	(intron 1 22595)	cgggagcaggaaaaaa A/ Δ gaataagaagaaaaggagct	6609
CHST3	50	(intron 1 35423-35424)	gctcatgctcacagccatc AT/ Δ gtatggagcaa t/c tgcctttt	6610
CHST4	1	(5' flanking region -1092)	atgaagccttbtgccatctc G/A ctgtgtcgtgccagcacctg	6611
CHST4	2	(5' flanking region -941)	ctgccagagagaacaggaa G/A ggaggaagagccacacaatt	6612
CHST4	3	(intron 1 -150)	caggaatgatattggagaag G/T actggtgccattgttggcac	6613
CHST5	1	(intron 1 -144)	ggcctcttaggtttcagcca A/C gacaggtgactcttagcacc	6614
CHST5	2	(intron 2 17)	caacgtaagagcgcttctca T/A tgtccagctcctttgtttct	6615
CHST5	3	(intron 2 139)	aatcccagcactttggagg C/A ggagatgtgcggatggatca	6616
CHST5	4	(intron 3 1829)	gactgtatgtctgtattca T/C ataggaacaaataattcatg	6617
CHST5	5	(intron 3 2037)	aaatgaacacacacacaa C/G tgcagagaagcaaaacaaag	6618
CHST5	6	(intron 3 2134)	aagcagctaaattgtgttcc G/A tacaggtgcaattaggcagg	6619
CHST5	7	(intron 3 2528)	atggtaaaagtgcctgggt G/A cagtatgtcagcatectgct	6620
CHST5	8	(intron 3 2674)	gcacttatcctagaagacc A/G tttctgaagactcagcagga	6621
CHST5	9	(intron 3 7039)	ctggctcccgccggccacc T/C gggaccgcagccacgtctga	6622
CHST5	10	(intron 3 7211)	gtagcccccaggacacccca T/G cctcaacatccattctggg	6623
CHST5	11	(intron 3 7294)	ggagcttccagtggttgg T/C acccccgactcttcgtccat	6624
CHST5	12	(intron 4 108)	gcagggctcctgactctgca G/A ggggcaatcacaggtgggag	6625
CHST5	13	(intron 4 402)	agcactggaaaaagtacagt T/C gcacttgtagcggaggtggg	6626
CHST5	14	(intron 4 547)	ctcctgtcccgcataggag C/G gaaggagcagaggtgagatc	6627
CHST5	15	(intron 4 1142)	gccccaggtctcatagctcc C/G cattggcagtgctgggattt	6628
CHST5	16	(intron 5 1187)	cactgggagcagtaattggggc A/G tgggatgggcatgagggccc	6629
HNK-1ST	1	(intron 1 139)	gtgttttggcgacttgaga C/T ctccctagttccgggagta	6630
HNK-1ST	2	(intron 1 1020)	acctgagcagaaaattctct T/C ctccgctgaaatgaaattg	6631
HNK-1ST	3	(intron 1 1091)	aagaatttgaacatcaca G/A gcaacttgagtttatattcg	6632
HNK-1ST	4	(intron 1 1971)	ctataactatttcaacata C/T gaaacaggcataattggatt	6633
HNK-1ST	5	(intron 1 2096)	atttagaatttatttacc A/C agaataccaaataaacctg	6634
HNK-1ST	6	(5' untranslated region -9)	ctatccagtgacaagaggaa C/A caagaacctcagttcagggg	6635
HNK-1ST	7	(intron 2 -530)	agtggcgaggagcgagaa G/A tcagttgttattcctttgct	6636
HNK-1ST	8	(intron 2 -466)	gctacatcttgtcagccagt C/T agaattttaaacacagccag	6637
HNK-1ST	9	(intron 2 -92)	acggaaatatttctgtctgat A/T ctactgactgaaatcacct	6638
HNK-1ST	10	(intron 3 152)	catggctccgttctctcat G/A ttacagaggtgtgagggagg	6639
HNK-1ST	11	(intron 3 312)	cacagtgcccttatgccttg C/T agcagggcgccctcagcgt	6640
HNK-1ST	12	(intron 3 1948)	tcctttgatgtatcaagttt T/C gtgctgaatgttttcagtg	6641
HNK-1ST	13	(intron 3 2140)	ttacacctggagaggagcac C/T gcagcggctccttaatactgc	6642
HNK-1ST	14	(coding region 187 (Leu 63 Leu))	agaagcacattcctgaggaa C/T tgaagtgggcacagccagg	6643
HNK-1ST	15	(intron 4 581)	cctgatcattccttagctgg G/A atgaggggtgcactctggaa	6644
HNK-1ST	16	(intron 4 615)	tctggaagccctctcacttc G/C taacccccattctggatcta	6645
HNK-1ST	17	(intron 5 7)	gattgttctaaatggtgtgt G/A tgggtctactgaatgtccac	6646
HNK-1ST	18	(intron 5 123)	acctgaaggagctggtggcc G/T tccagacaggcctgtttttg	6647
HNK-1ST	19	(intron 5 721)	ataattatgggctctgctta T/C gaaatttagcttcacagagg	6648
HNK-1ST	20	(intron 5 867)	tgctgcccacagagtcgggt G/A tcaactcctggccactgtttg	6649
HNK-1ST	21	(coding region 444 (Ile 148 Ile))	ccaggagcatttttcttccat T/C gaggagatccccgaaaacgt	6650
HNK-1ST	22	(intron 6 94)	ctgagttctgtacttggcag A/G ttgatcggaggaccacagag	6651
HNK-1ST	23	(intron 6 247)	catgaaggtgacatcatttt G/A ttaatagaattagcaggca	6652
HNK-1ST	24	(coding region 696 (Thr 232 Thr))	aggaggaaacggacagagac C/G cgggggatccagtttgaaga	6653
HNK-1ST	25	(coding region 870 (Ala 290 Ala))	gagaccctggaggacgatgc C/T ccatacatcttaaaagggc	6654
HNK-1ST	26	(3' untranslated region 11)	tcaaatatctttattagacc T/C ggggctaaccaggtgaagat	6655
HNK-1ST	27	(3' untranslated region 11)	ccacacccctccttttagga C/T gccgggggtctccacagcg	6656
HNK-1ST	28	(3' untranslated region 13)	ggaagcatcacacagcgta G/A gagccgttctcctcaggtgt	6657
HNK-1ST	29	(3' untranslated region 14)	tgaggttctcctggctagtc A/G ggggtggcttccaccatcact	6658
HNK-1ST	30	(3' untranslated region 15)	gcaagggggctgctgaaatc G/C cagagacttttcagcatca	6659
HNK-1ST	31	(3' untranslated region 16)	gggtggtgtggtgtccagg G/A tccatctttccagaatccat	6660
HNK-1ST	32	(3' untranslated region 18)	aggggagggctttttctacct G/A agaaggggagtgcttttgag	6661
HNK-1ST	33	(3' untranslated region 22)	tccagcagtgcggtcttctg G/T c/t aacaaggtaggccctgggtg	6662
HNK-1ST	34	(3' untranslated region 22)	ccagcagtcgggtctctg g/t C/T aacaaggtaggccctgggtg	6663
HNK-1ST	35	(3' flanking region 1016)	cacacgaaggtgtgactca C/T ggcctgcagggcaccaggt	6664
HNK-1ST	36	(3' flanking region 1152)	gcactgttgcctcatctgga A/C tctccagaagcagggaaacag	6665
HNK-1ST	37	(3' flanking region 1291)	gccagagaccctcagcaggat A/G gtgcagttacagggctgagc	6666
STE	1	(5' flanking region -605)	caggtttcttaaaataataat C/T gaaaggtgagtgatgtttac	6667
STE	2	(5' flanking region -536)	taaaattttcaggtctgctt A/G agagttaaaggcaaaagatt	6668
STE	3	(5' flanking region -231)	ccttcttccccaccctga C/T ggcagacttgggaatttgaa	6669
STE	4	(5' untranslated region -6)	tgacgotttaagatctgctt G/A gtatttgaagagataaaac	6670
STE	5	(intron 1 69)	aaatatagaatgaaaattat G/A tattacaagctcttaaaaa	6671
STE	6	(intron 1 311)	caatgagaaaataaagcaag C/G agggtagaaggaggtagaat	6672
STE	7	(intron 1 655)	tctaagaaagtagggactat G/A agaaccctatgtatctata	6673

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
STE	8	(intron 1 671)	ctatgagaacccctatgtat C/T tatatccaccatagttattct	6674
STE	9	(intron 1 772)	aaaaggcaggttggaagatg C/A aggggggagtagtcagaaaa	6675
STE	10	(intron 1 1715)	taaccattcttgcttaacctt A/G tcatttttagccaagtcatt	6676
STE	11	(intron 1 1928)	aaatgatacatatttcaggaa A/G tcaaaaatctctgacttaga	6677
STE	12	(intron 1 1953)	aaatctctgacttagatacc C/T ggcaataataatcaaatgta	6678
STE	13	(intron 1 2087)	aattttgaagaattgaag T/G tctgtggtttttattatca	6679
STE	14	(intron 1 2323)	taggtatgtaggagggtccc G/C ttatatacatagtgtttaat	6680
STE	15	(intron 2 165)	tctattccatgaccacaatt T/G ttacctgttaacttgaatagt	6681
STE	16	(intron 2 1707)	cctaggaccacaacatgagac A/G taatataccatcagtaaaat	6682
STE	17	(intron 3 850)	gggtgccattccctcaagaa T/G ttatactttgtgttacacac	6683
STE	18	(intron 4 1653)	agtaacaggcttagtagataa T/C ataataactgaggccaacg	6684
STE	19	(intron 4 1899)	tacatgaacttagagaatca A/G gtatagtcacacacccaaca	6685
STE	20	(intron 4 1930)	cacaccaacaataaaattac A/G cagaatgataaaagaatttg	6686
STE	21	(intron 5 666)	ttctgatcatgtagtaacaa T/C tataaagaaaaataaatgt	6687
STE	22	(intron 5 982)	aggcaaaacagaaacctttt A/C ctcacacaacattatattat	6688
STE	23	(intron 7 369)	agattttattctctctctctt T/C ttgagtgaagaaataagtt	6689
STE	24	(intron 7 447)	cacctttcaagggttaagtgg C/A aaaaaatagaaattcaata	6690
STE	25	(intron 7 672)	aatcttctctcttgaacat A/T ctgtcagtgagagtcagggg	6691
STE	26	(intron 7 856)	tggtacagaggacttaaaac A/G gttgtctgtctgtgcaaacgg	6692
STE	27	(3' flanking region 218)	cagcctcccaagtagctagg A/G ctacagacatgtgcaaacat	6693
NQO1	1	(intron 1 80)	aggagggttgtaggggttgg C/A ctgaattttgttctcttgact	6694
NQO2	1	(5' flanking region -434)	ttctgttggtgaccacggacc C/G tcattctgttaacgggatac	6695
NQO2	2	(5' flanking region -406)	gtaacgggataaccagccag A/G gatggggagcgggagcgca	6696
NQO2	3	(5' untranslated region -1)	tctgtcgggtcctactctggg A/C gtgcgctggtcggaagtga	6697
NQO2	4	(intron 1 1919)	tcactcaaatagagctgagt T/C agtcaactcagctcttgacc	6698
NQO2	5	(intron 1 2004)	acaaactcacatgccaccag C/G catatgatgtaaacatgtaa	6699
NQO2	6	(intron 1 3391)	aaagcagagggctgtgcagg C/T gccctgtcccttaggctagg	6700
NQO2	7	(intron 1 3456)	caaaggcctcatcctcaggg C/A ggccaactctctgttttag	6701
NQO2	8	(intron 1 3595)	actgccagcttttaggttca T/C tctgttaagtgttgctggtg	6702
NQO2	9	(intron 1 3596)	ctgccagcttttaggttcat T/C cttgtaagtgttgctggtg	6703
NQO2	10	(intron 1 3598)	gccagcttttaggttcatc T/C tgttaagtgttgctggtgca	6704
NQO2	11	(intron 1 3651)	coctgcgctttgaagggtg A/G atgtgacctctcccaattc	6705
NQO2	12	(intron 1 6036)	tggtgtggtggttcaactgat C/T cccagcctctctgctgac	6706
NQO2	13	(intron 2 14)	atggcaggttaagtattcact A/G ttgtggagtaagacttttt	6707
NQO2	14	(intron 2 192)	gccacgtggaagtgtataaa C/T tatctggaaattatctgttt	6708
NQO2	15	(intron 2 635)	caccctgttttagcacctagc A/C ccattcctggcctctgcca	6709
NQO2	16	(intron 2 685)	agtagcacccctccccacc G/A gctgtgacaaacaaaatgt	6710
NQO2	17	(coding region 139 (Phe 47 Leu))	ctgatttgtatgccatgaac T/C ttgagccgagggccacagac	6711
NQO2	18	(intron 3 36)	aatgctctatttataaaaaa T/C atctttatgtttttacttt	6712
NQO2	19	(intron 3 728)	aacgtgggataaaccacca T/C ctagtgcacaaaagcaggtg	6713
NQO2	20	(intron 4 1577)	tgctctgtcacaccccttcc C/T gacaccagccctttctttac	6714
NQO2	21	(intron 4 1832)	tcggccggccacgtggagcc C/T gcttctcctctgcacccac	6715
NQO2	22	(intron 4 2583)	tggtgttacgcacagctcct C/T gtccccctcctgctgcca	6716
NQO2	23	(coding region 330 (Pro 110 Pro))	ctgtactggttcagcgtgcc A/G gccatcctgaagggtggat	6717
NQO2	24	(coding region 405 (Ser 135 Ser))	atcccaggattctcagatc C/T gggttgctccaggtatgtgc	6718
NQO2	25	(intron 5 21)	gtatgtgctcttggaagga A/T tcactatggatagttggagg	6719
NQO2	26	(intron 5 253)	atggcaaaacaggagtgagg T/C caggtgtcaggtgacggggg	6720
NQO2	27	(intron 6 2435)	cccccttaaatcatttaac T/C gaattggtatgtaacaggtgt	6721
PIG3	1	(5' flanking region -47)	gggaaggaggaaagaaaga G/A ggggaggtggttctctgta	6722
PIG3	2	(intron 2 243)	taacaccggagcccgagcag A/C agtcccagcttcttagaatt	6723
PIG3	3	(3' flanking region 282)	agcaggccccagccctgcc G/A ctactcactgggccccacc	6724
PIG3	4	(5' untranslated region -9)	tccgagagatacagcggcc (CCTGY) 16 cagacaatatgttagcgtc	6725
PIG3	5	(3' flanking region 625-62)	ctcctcaggccccgccccctt (T) ccattactcacttgggtccc	6726
PIG3	5	(3' flanking region 625-62)	ctcctcaggccccgccccctt ccattactcacttgggtccc	6727
PIG3	6	(3' flanking region 770)	tcacctgggtcccgccctac C/Δ tgtcataacctgtctcaagc	6728
NDUFA1	1	(5' flanking region -1437)	agggtcaaaaatcctgatta T/A acctaccttgaaagcttttaa	6729
NDUFA1	2	(intron 2 3071)	aataaaagtacatggcatat C/A tttagtgggaacagacttgt	6730
NDUFA1	3	(3' flanking region 1218)	aactccatgtgtataaagca A/G caccacagatgacacttcca	6731
NDUFA1	4	(3' flanking region 1411)	ggattgtgccatcccttgat C/T ggcaatgaccttttactttt	6732
NDUFA1	5	(3' flanking region 1411)	ggattgtgccatcccttgat C/G ggcaatgaccttttactttt	6733
NDUFA2	1	(intron 2 1087)	aacatacaaaaattagccgg A/G t a/g tgggtggcgggacactgta	6734
NDUFA2	2	(intron 2 1089)	catacaaaaattagccgg a/g t A/G tgggtggcgggacactgta	6735
NDUFA2	3	(intron 2 1356)	tccctgaacaaacacattg T/C ggccatccagaaatgaccaa	6736
NDUFA2	4	(3' flanking region 467)	cacagcctcatgggtcagcc C/T actccagaggtgtgacttccc	6737
NDUFA2	5	(3' flanking region 744)	ggaagcaaggggcccctggcca C/T agccgctggcagtaagcagg	6738
NDUFA2	6	(3' flanking region 838-83)	tatagttctacaaagaatgaa (ACAC) aaagatcataacaatagcta	6739
NDUFA2	6	(3' flanking region 838-83)	tatagttctacaaagaatgaa aaagatcataacaatagcta	6740

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
NDUFA3	1	(intron 2 2656)	tccttgcctgccctccctgc G/A cactttatcttccctttgcc	6741
NDUFA3	2	(coding region 241(Leu 81	agggcccccagcctggagtg C/G tgaagaaactgtgagcacct	6742
NDUFA3	3	(3' flanking region 1019)	tccttaactgcactggcacc A/G gctctggagcccccagtcctc	6743
NDUFA5	1	(intron 3 2155)	agactctagcatgtgtacgt G/C aacataagggttcccttagaaa	6744
NDUFA5	2	(intron 3 2493)	ggcatattgtctagttttctc G/T gctcaatttcacatctat	6745
NDUFA5	3	(intron 3 2712)	acaaattttgaactgtttcac C/T taacacaggctttttctgaa	6746
NDUFA5	4	(3' flanking region 1296)	aggtatctaaaaggattgc A/C atttggtcattgtgtctttc	6747
			aagtcagttttgtgtctgt (GATTGTGGTATCCAG)	
NDUFA5	5	(intron 3 30-31)	tgtaacatttaacaaaaaa	6748
			aagtcagttttgtgtctgt	
NDUFA5	5	(intron 3 30-31)	tgtaacatttaacaaaaaa	6749
NDUFA5	6	(intron 3 427-428)	attaagtagcagttataaa AG/Δ tctagactgctgattcatc	6750
NDUFA5	7	(intron 3 4733-4734)	tataggaatttttaaaata TA/Δ ggatattgaaacattcagtt	6751
NDUFA6	1	(5' flanking region -1148)	tttataatttatatatgtta C/T gtgctttctttgtatagct	6752
NDUFA6	2	(5' flanking region -363)	actaccaaggagcgcgcgg G/A cagccggatagcaggacgt	6753
NDUFA6	3	(coding region 26 (Ala 9 V	ggggagcggcgtccgcgaag C/T tacttctaccgccagcacct	6754
NDUFA6	4	(intron 1 1318)	attcagcagtttgaaacat A/G atgtttgctcggcagaatac	6755
NDUFA6	5	(intron 2 562)	agttaaagaatctgaaagt G/C tcagaaatgatttaccctga	6756
NDUFA6	6	(5' flanking region -861)	ctgtaaaaatgggagtgctga (T) ggtacctacctgacctatga	6757
NDUFA6	6	(5' flanking region -861)	ctgtaaaaatgggagtgctga ggtacctacctgacctatga	6758
NDUFA6	7	(intron 1 1251-1278)	tgtggggagtgactgtagca (GT) 12-14 ttoggggtgtgtcattcaaa	6759
NDUFA7	1	(5' flanking region -731)	accacccaaggctctatcaa A/G ggggtgtcctctttgcaccc	6760
NDUFA7	2	(5' flanking region -434)	aaaggaaccatcagaaccc C/T gtgatgaaatgagaatcgcc	6761
NDUFA7	3	(5' flanking region -395)	gctcccgattccggctggc A/G ggggttagggcagggtagag	6762
NDUFA7	4	(5' flanking region -100)	agaggagtcacgtgcttcgg G/A gagagcctttataggacgtt	6763
NDUFA7	5	(intron 1 92)	tcaactccctcctaagccgg G/A acccttcgctctcccgaat	6764
NDUFA7	6	(intron 1 133)	ctccctgggaaccccagct A/C gt c/g accccttcagcccgga	6765
NDUFA7	7	(intron 1 136)	cctgggaaccccagct a/c gt C/G accccttcagcccgga	6766
NDUFA7	8	(intron 2 89)	tccttttagaccctgaaacg G/C agggctgacatcctgccacc	6767
		(coding region 196		
NDUFA7	9	(Pro 66 Ala)	gccgcgggaatctgtgccc C/G cttccatcatcatgtcgtcg	6768
NDUFA7	10	(intron 3 4203)	gcctccacccctggggcgcc T/G cctccatcaccccccctcc	6769
NDUFA7	11	(intron 3 4604)	gggccttgtgtacgtggag A/G ccaaaagtgggaaggagga	6770
		(5' flanking region		
NDUFA7	12	(-1353)-(-1360))	aggggtccagggtccctgct CAGAGGCT/Δ aacactggccgaagagaa	6771
		(5' flanking region		
NDUFA7	13	(-1233)-(-1234))	agccctgactccaccactct CT/Δ gaaacttctttgctaataaa	6772
NDUFA7	14	(intron 2 4142-4143)	cattttgtgactgaggtgac AG/Δ gggcccaacagcggggccatg	6773
NDUFA8	1	(intron 1 -75)	tttgtgttctctattctgac C/T cgcattgaggttaagctgaga	6774
NDUFA8	2	(intron 2 790)	caaacctagacaaagtgtgc C/T ctttatccagaagtgcagcag	6775
NDUFA8	3	(intron 2 900)	ttcaggagataaaaagctct G/A attgctcaggcctgagatgg	6776
NDUFA8	4	(intron 2 3837)	gaagttgtctgttaagttag A/G taagaatgttactcacata	6777
NDUFA8	5	(intron 2 3942)	tcattgttttgcaaaagat G/T cccctaaccagcttctttt	6778
NDUFA8	6	(intron 3 -66)	gaggagacaccaggagggc A/G ttgatggttacagattctct	6779
NDUFA8	7	(3' untranslated region 52	tttattcttgaccacagtaa A/G gatgggtcctgtggccacac	6780
NDUFA8	8	(3' flanking region 367)	gtcatacaaggaggagcctcc A/G ggatagaagtgcaaaactt	6781
NDUFA8	9	(3' flanking region 777)	attcttttttctactactagg C/T tgtttctctccatctgact	6782
NDUFA8	10	(3' flanking region 1053)	aaagaaaaagcactgtgtga T/A ctgcatggccgcttctgca	6783
NDUFA8	11	(3' flanking region 1190)	gattctctaatgaaaaataa G/T acttttttttgcattttttt	6784
NDUFA8	12	(intron 2 449-453)	tcattgtgcattgatacttaa GTAAA/Δ aaaaaactaagctgtgtaat	6785
NDUFA8	13	(intron 2 455-459)	tgcatgatacttaagtaaaa AAAA/Δ ctaagctgtgtaattgtagg	6786
NDUFA8	14	(intron 2 707-708)	tcatttttgaaagactctca (A) ccttgctgtacaaaaatgg	6787
NDUFA8	14	(intron 2 707-708)	tcatttttgaaagactctca ccttgctgtacaaaaatgg	6788
NDUFA9	1	(5' flanking region -807)	gatggctctttgtagaacaa T/G gcagattctcaaaagtgacc	6789
NDUFA9	2	(5' flanking region -769)	accacagttaaagaaaaaat T/C acaagccattgcgctagaga	6790
NDUFA9	3	(5' flanking region -353)	cacaccctattttggtttct C/G ttctccacttttccctcgt	6791
NDUFA9	4	(5' flanking region -322)	ttccctctgttcttctgtccc C/T cttttctctctcctgggcc	6792
NDUFA9	5	(intron 1 447)	attcatatgagcacaatgga A/G atgataatattacaatacca	6793
NDUFA9	6	(intron 1 1039)	ggcttgatgttcagcctgag G/A caagaattaggagtggttag	6794
NDUFA9	7	(intron 1 4010)	aatgtatccaaaagagattc T/G cacttcctgccatgaagaa	6795
NDUFA9	8	(intron 3 49)	gacaaatataaattactaag G/A tcatttttaggagtgatagg	6796
NDUFA9	9	(intron 3 107)	aattttctcccagaatggac C/T aaaggcatcctctgttccca	6797
NDUFA9	10	(intron 3 1183)	attcttggttaattatcaac A/G gattattgttaatcccttta	6798
NDUFA9	11	(intron 3 1395)	attctagttctttgtccct C/T aagttttgtgttcaccttgt	6799
NDUFA9	12	(intron 3 2363)	agaaaatagtcattgaatggc C/T ccaactaacactagtcttta	6800
NDUFA9	13	(intron 3 2608)	gtcatttgattacctgagta A/C agtgactgtttacctgtttg	6801
NDUFA9	14	(intron 4 561)	attttataaattctttgatg A/C cttgggggtcttattcaact	6802
NDUFA9	15	(intron 4 860)	attgtgtagtagtaatgacag C/T agagctgtcaacttttttaa	6803
NDUFA9	16	(intron 4 879)	gcagagctgtcaactttttt A/T aaaaaataatttttagcttaa	6804
NDUFA9	17	(intron 4 893)	ttttttaaaaaataattttt A/G gcttaaaaaataaaaaatt	6805

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
NDUFA9	18	(intron 4 1090)	atcattgctgttttaaaagtt T/C aagtagtgtgaatttcagta	6806
NDUFA9	19	(intron 4 1188)	aaccaatcctttttttttt A/T tcttcagaaaactttgattt	6807
NDUFA9	20	(intron 5 161)	gggtgtgtgtgatgttttga C/T gttttgattgattgccttct	6808
NDUFA9	21	(intron 5 373)	ctttctcacccttgcaactg C/T agtgggtttgtgccactctt	6809
NDUFA9	22	(intron 5 457)	gccagggaagatgcctattc A/C cacagtgttatgtctccttt	6810
NDUFA9	23	(intron 5 3113)	gatttttctccttcttcaat G/A taagcttcccttaaaataaa	6811
NDUFA9	24	(intron 5 3339)	tctaaactcaaaacagggtt G/A tttggttattgtttaggctg	6812
NDUFA9	25	(intron 6 414)	tatagttttgccttttccag G/C atattacatatatggttaga	6813
NDUFA9	26	(intron 6 518)	ctttcatttcttttcatagc T/C tgatagctcatttctttata	6814
NDUFA9	27	(intron 7 974)	ggattatgcgtactctggaaa A/G tacttggtatagcgggtgatta	6815
NDUFA9	28	(intron 8 368)	acattaattttgatggagta T/G cacaatgcctccagaggctg	6816
NDUFA9	29	(intron 8 954)	gcatgcaatcagttatatag T/C ctgataagaattacaattc	6817
NDUFA9	30	(intron 8 1253)	tcctcttgaattgttagata G/T gtatctacacatttctcatc	6818
NDUFA9	31	(intron 8 11608)	gaaaagatagatgtataaat G/A accaaaaattcgtgaagaaa	6819
NDUFA9	32	(intron 8 11930)	ctacaaatatattctaaatg C/T gtaatcattgataagtagaaa	6820
NDUFA9	33	(intron 9 1998)	tggttttcaagccttttaac G/A gctgtggaaccctgtgctca	6821
NDUFA9	34	(intron 9 2238)	ccagctactctggaggctga A/G gttggaggatcacttgagcc	6822
NDUFA9	35	(intron 9 2885)	acagcggtctgtcttctctgc A/G gttctcataggctagcttac	6823
NDUFA9	36	(intron 10 801)	tacactaaagtgtctctttac G/A tttatacttgagaaagtgtt	6824
NDUFA9	37	(intron 10 910)	tgcagactttcaggtgggta G/C gatgagggattgtctgtgct	6825
NDUFA9	38	(intron 10 1180)	aaaactgagtcagaacgccc G/A tgctcagaaaacagggcgct	6826
NDUFA9	39	(3' flanking region 554)	gtgccagcacttaggaatta T/G gaccttctaataagattcttt	6827
NDUFA9	40	(5' flanking region (-1129) - (-1128))	taaacagtaggggcaagata (TC) gagtggaaacagccaagatt	6828
NDUFA9	40	(5' flanking region (-1129) - (-1128))	taaacagtaggggcaagata gagtggaaacagccaagatt	6829
NDUFA9	41	(5' flanking region -341)	tggtttct c/g tctccacttt T/Δ cccctgttcttctgtccc c/	6830
NDUFA9	42	(intron 4 594)	attcaactttttatcccccc T/Δ aatgattaacatagtgatt	6831
NDUFA9	43	(intron 10 356-375)	taacttctcttaacgtcct GAGAACTGTTGACAGTT/Δ	6832
NDUFA9	44	(intron 10 379-381)	cttctcttttcttttaacct	6833
NDUFA9	44	(intron 10 379-381)	gaaactgttgacagtttctt CCT/Δ tctttcttttaacctactcca	6833
NDUFA9	45	(intron 10 384-387)	tggtgacagtttcttctctt TTT/Δ ttttaacctactccagtcagg	6834
NDUFA9	46	(intron 10 436-437)	ccattttctcccttaaaattg (TTCTTTTAAATTG) ctcttttcaaggt	6835
NDUFA9	46	(intron 10 436-437)	ccattttctcccttaaaattg ctcttttcaaggt	6836
NDUFA9	47	(intron 10 495-496)	gccacatccaatggtcagtt (TTCAGGCCTT) ctccagacctcagtc	6837
NDUFA9	47	(intron 10 495-496)	gccacatccaatggtcagtt ctccagacctcagtc	6838
NDUFA9	48	(intron 10 519-520)	gacctcatgtcatgtgctg (GGCCTG) tgcatttgcttctagggagg	6839
NDUFA9	48	(intron 10 519-520)	gacctcatgtcatgtgctg tgcatttgcttctagggagg	6840
NDUFA9	49	(intron 10 558-559)	gatgcaaaaataaaaataaaa (A) tactataccaataccacatc	6841
NDUFA9	49	(intron 10 558-559)	gatgcaaaaataaaaataaaa tactataccaataccacatc	6842
NDUFA10	1	(5' flanking region -1734)	tgccacttgaactgtttact T/C tctgttaaccatttaccctt	6843
NDUFA10	2	(5' flanking region -1492)	aaaacatccacgcaaacagg T/C tgtgagaagttacgtctg	6844
NDUFA10	3	(intron 3 370)	aagactgtgcatgtgccaatg C/A agacagagatgtggatgcca	6845
NDUFA10	4	(intron 3 2485)	ttgttattttcttttctctg G/A aatgcagtgatcagttgaca	6846
NDUFA10	5	(intron 4 236)	ctgtgaaagcagattggagc C/T ctggacctcaaacacagca	6847
NDUFA10	6	(intron 4 1742)	tgtcgccatctgtctgagtg C/T tgcgtgaagtctgaggactgg	6848
NDUFA10	7	(intron 4 2090)	ggctgggggaaagcagatca T/C gttgctaaaggacaggtgg	6849
NDUFA10	8	(intron 4 3054)	cagctgattatactactgaa A/C cgggataaatg c/t agcttgat	6850
NDUFA10	9	(intron 4 3066)	ctactgaa a/c cgggataaatg C/T agcttgatgattttcagctg	6851
NDUFA10	10	(intron 4 3377)	gtcacagtttaaatgctgct G/A ttttactctgtgtaagtagc	6852
NDUFA10	11	(intron 5 46)	aagcatctctattttgaatg T/C agatcagcactaaaagccct	6853
NDUFA10	12	(intron 8 1465)	gcaacgcccagtttctgtgta C/T aggcctcataatccagctgc	6854
NDUFA10	13	(intron 8 1809)	cctggaggcacaaggtggc C/A ggggcactcaacttccctct	6855
NDUFA10	14	(intron 8 11226)	gttgtgtgactgtgtggggc A/G tctcaccctctcgggctgag	6856
NDUFA10	15	(intron 8 11319)	atcttgcccttccctctctg G/A tctgttccaggcttgaacct	6857
NDUFA10	16	(intron 8 11386)	ccataatcctagcttgaacc C/T tcttttttccctgctgaccc	6858
NDUFA10	17	(intron 8 13361)	ccaggccactgattgttttc G/A cattttctagcattttctta	6859
NDUFA10	18	(intron 9 183)	ttctgtgtggaagctgat G/A aagtcctcagatgacagccc	6860
NDUFA10	19	(intron 9 8028)	gaggacattccacagaact G/A tgactattagagcagaaggt	6861
NDUFA10	20	(intron 9 10742)	ctggaggagaggggtggagc C/G agtgcagccagcactgggtt	6862
NDUFA10	21	(intron 9 13908)	cacattgttatgtaaccaag C/T ct g/t gaattgcagtgtaaga	6863
NDUFA10	22	(intron 9 13911)	attgttatgtaaccaag c/t ct G/T gaattgcagtgtaagaact	6864
NDUFA10	23	(intron 9 14064)	tcttgactattagaaccct A/G tcagataaattttaaaacag	6865
NDUFA10	24	(intron 9 14184)	tggtttgtgtgggaacagc G/A agagatacagaaccgaggt	6866
NDUFA10	25	(intron 9 16487)	cttgaagctgatcgttccct C/A cttgaagctgatcgttccct	6867
NDUFA10	26	(intron 9 16779)	gccagacgtgactgcttttag G/A ttctctcatgacattcagacc	6868
NDUFA10	27	(intron 9 17663)	ttccaaatcaccacagaact T/G tgcagtattttgaagctcct	6869
NDUFA10	28	(5' flanking region (-1668) - (-1659))	gtaaaattgttttaactaga (C) 9-11 ttcctaaaccaaggtataaa	6870

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
NDUFA10	29	(5' flanking region (-1355) ~ (-1334))	ctgtatccattggaaggcac (A) 15-21 tgcaaggaaacaaggcaaa	6871
NDUFA10	30	(intron 1 46-61)	tggcggggtggcagggtggc GGGGTGGCGGGGTGGG/ Δ gacagttcc	6872
NDUFA10	31	(intron 4 2486)	ctcactggaacttttttttt T/ Δ aatttaatttttaaaatttt	6873
NDUFA10	32	(intron 7 1600-1601)	cacttccattctgactgtta (A) cgggtgtgattcttctcgcca	6874
NDUFA10	32	(intron 7 1600-1601)	cacttccattctgactgtta cgggtgtgattcttctcgcca	6875
NDUFA10	33	(intron 9 1054)	gcgctgtcgttttctcctt A/ Δ tctgtcctgtacacgtgtg	6876
NDUFA10	34	(intron 9 8161-8172)	tttctcgtctttctggagac (T) 10-12 aatgttgaaaatatgtgtt	6877
NDUFA10	35	(intron 9 8646-8647)	aattccccattgtcttctct (TT) ctgtagacattttaaacctta	6878
NDUFA10	35	(intron 9 8646-8647)	aattccccattgtcttctct ctgtagacattttaaacctta	6879
NDUFA10	36	(intron 9 16503-16523)	ccct c/a ctggaagctgatcgt TCCTTCCTGAAGCTGATCGT/ Δ gtccaagatagttgctagga	6880
NDUFA10	37	(intron 9 17905-17936)	caaatatagtatacatgta (CA) 12-18 tccttcatgaaactctttc	6881
NDUFAB1	1	(intron 1 8451)	cagcacctctgtagaggcctc G/A ggatgctgaagatgccatga	6882
NDUFAB1	2	(intron 1 8495)	gacacagcgattctgcagac G/A ctgagacaattttatggcag	6883
NDUFB3	1	(5' flanking region -1439)	ttaaaagtgtacttttttct G/A cc g/a ggcacggtggctcacgc	6884
NDUFB3	2	(5' flanking region -1436)	aaagttgacttttttct g/a cc G/A ggcacggtggctcacgcctg	6885
NDUFB5	1	(5' flanking region -213)	ggcggatgaaactctctac A/C aagaaggcccaaacggccg	6886
NDUFB5	2	(intron 1 6288)	ggggatgttgattacctagg T/C cagtaagtaagaaggcat	6887
NDUFB5	3	(intron 1 -1581)	cttctgggccactgtatcct A/G tttctttctcctgtttaccct	6888
NDUFB5	4	(intron 1 -1487)	ccctcttagacgctatatag T/G tctagcataggatctgcaca	6889
NDUFB5	5	(intron 2 556)	ttgtctggacctctgccac G/A gtatataaagctctgaatca	6890
NDUFB5	6	(intron 3 467)	ggcgccatcgcaactccagcc C/T gggcaacagagtgcagactct	6891
NDUFB5	7	(intron 3 497)	agtgcagactctgtccccc C/G caaaaaaaactataatcct	6892
NDUFB5	8	(coding region 397 (Tyr 133 His))	atgatagtcctgaaagata T/C atgaagaacaatggccgtc	6893
NDUFB5	9	(intron 1 213-215)	attagcattttctaaaacgtt GTT/ Δ attcaccatcccaattaatg	6894
NDUFB7	1	(intron 1 68)	cctgaacacctggcaccacca G/A ggctggcaccacaggctgg	6895
NDUFB7	2	(intron 2 266)	gggctctcttaggggctgtt T/C gatggggacagggcagtg	6896
NDUFB7	3	(intron 1 4480-4481)	agttctgaggctgagagaga (GA) ggccacgcgcggccagtg	6897
NDUFB7	3	(intron 1 4480-4481)	agttctgaggctgagagaga ggccacgcgcggccagtg	6898
NDUFS1	1	(5' flanking region -3)	tcttagggggtcgtcgtgtt C/G cagacagtttagcagacag	6899
NDUFS1	2	(intron 1 445)	gtgttagcaatggctcacgc T/C tctgtttgtgtccttgttt	6900
NDUFS1	3	(intron 1 470)	tttgttgccttgtttgttt G/T gtccattgaccacgttggac	6901
NDUFS1	4	(intron 1 502)	acgttggacagcattttttt A/G ttcttttaactaacgggaaa	6902
NDUFS1	5	(intron 1 557)	ttttgaaaagttagccagg A/G ttgcattgcaataacaaaa	6903
NDUFS1	6	(intron 1 5218)	tatctcagaatatctcagga A/G catttagtagacagctatgc	6904
NDUFS1	7	(intron 3 1371)	aagccctaaaatagatagtg T/G caatgggaatgaaaacaga	6905
NDUFS1	8	(intron 5 414)	ttttgaaacgaggtctcact A/G tgtgtccaggtcgggttg	6906
NDUFS1	9	(intron 10 812)	gagtgcggtggcgcgatctc G/A atctcggtgcactgcagcct	6907
NDUFS1	10	(intron 11 233)	ggaggcccaaggcaggcagat C/T gcctaagtgcaggagtttga	6908
NDUFS1	11	(intron 11 283)	ggccaacatggcgaaacccc G/A tctctactaaaaatacaaaa	6909
NDUFS1	12	(intron 11 585)	ctgtatgtcttaatttttaa G/T taaatttgcattttatatat	6910
NDUFS1	13	(coding region 1251 (Arg 417 Arg))	gcaccactgttttaatgctag A/G attcgaagaggttggtaat	6911
NDUFS1	14	(intron 13 5159)	attacttttagaaaacgtgt T/C tttagctgatactcaggcata	6912
NDUFS1	15	(intron 14 250)	aaaaattgttatattagtta C/T accttggttcaaaaattgca	6913
NDUFS1	16	(intron 14 550)	gataaagtctcactatgttg C/T ccaggttgatctcacaactcc	6914
NDUFS1	17	(intron 14 2429)	ctgaaaatacaaaaattagc C/T ggggtgtggtggcagtgccct	6915
NDUFS1	18	(intron 14 2530)	ttacagttagcgagatcac G/T ccactgcgctccagcctggg	6916
NDUFS1	19	(intron 14 2659)	acacatttaattttttacat T/C gaaaaactgcagttatggt	6917
NDUFS1	20	(intron 16 150)	agaaaacatgtattcagaaa C/T aggaattcaaggttacagtg	6918
NDUFS1	21	(intron 18 279)	cactgtgtagcaatttatgg T/C gaattttccaaagtggcaaa	6919
NDUFS1	22	(3' flanking region 182)	tctaggataaattataataa T/A aataatcatagtaacaatgg	6920
NDUFS1	23	(intron 12 3226)	aaatgtattgtcgtgtctt T/ Δ aacattttgtaaatagtaaat	6921
NDUFS3	1	(5' flanking region -194)	tctgccacaaggagctagga C/T cagctcacctcagcatttc	6922
NDUFS3	2	(intron 1 46)	cggggtcaggcgagcgcg T/C gccagtgacagagagctcct	6923
NDUFS3	3	(intron 6 -439)	aaagctgtgtcaaatgtact G/A ctttagatctggactgtgaa	6924
NDUFS3	4	(intron 6 -280)	gggtgggtgagcagtcagttc G/A gagctcctgatgtgggagtg	6925
NDUFS4	1	(5' flanking region -439)	aactgaatacagccctgtcc T/A gagggttgcaaaagtgaatc	6926
NDUFS4	2	(intron 1 1829)	gaaaaaaaatcttaatgccca G/T ggaagacgttttttaatac	6927
NDUFS4	3	(intron 1 2057)	attaatgggaaaaatctacat C/G taaaattcattttatgttaa	6928
NDUFS4	4	(intron 1 -521)	ttcatttttaactaattttat T/G tctccattttgtgtaatggg	6929
NDUFS4	5	(intron 3 -1259)	ataaaaattatgatattatta G/A tactaatatagccagccata	6930
NDUFS4	6	(intron 3 -1174)	aatatatataattataggaa T/C ctacagtagtcaaacatggt	6931
NDUFS4	7	(intron 4 10682)	cacaatataaggcacaacctt A/C ctaccaagcactaacaagt	6932
NDUFS4	8	(intron 4 12299)	tttactatatagatatatgg A/T atagactatagagtatctct	6933
NDUFS4	9	(intron 4 12560)	accaaaataaggtattatgca G/A gctcatctttttatataaga	6934
NDUFS4	10	(intron 4 18801)	ggaagacttgctttgccag T/C gtatccgaaacctctgttat	6935
NDUFS4	11	(intron 4 19888)	tcgcacagctgagaagagca A/G ggggctgtgttttcagttacc	6936

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
NDUFS4	12	(intron 4 20178)	agaaaagatgagtataattc G/A tetaacttaccattcttaa	6937
NDUFS4	13	(intron 4 23016)	ctactctgtgaaagtaagg T/A atgttgaaacaagtaaat	6938
NDUFS4	14	(intron 4 23124)	actttcttggagatggagt T/A ccagcagttgggaatgta	6939
NDUFS4	15	(intron 1 766)	tgtgatgatttttttttt T/Δ ggctgtattaaccttccatt	6940
NDUFS4	16	(intron 1 1261)	tttcttctcttttttttt T/Δ gagatacattctcactctga	6941
NDUFS4	17	(intron 4 19744-19745)	ctcatcatttaggtgctggt (T) agttgggtttgtggcaaatc	6942
NDUFS4	17	(intron 4 19744-19745)	ctcatcatttaggtgctggt agttgggtttgtggcaaatc	6943
NDUFS5	1	(intron 1 388)	ccaaacatagccagcacttc C/T ggctgtaactccgggctgtt	6944
NDUFS5	2	(intron 1 -13082)	agtgaagcagagattgcacca G/A tgcattccagcctgggcaac	6945
NDUFS5	3	(intron 1 -12905)	gttttcaacaaggactcca G/T agtagtagagaagtctctgt	6946
NDUFS5	4	(intron 1 -12564)	attttcatcacacctcaact T/G aaggtataacagccttaaga	6947
NDUFS5	5	(intron 1 -12561)	ttcatcacacctcaactaa G/A gtataacagccttaagaatg	6948
NDUFS5	6	(intron 1 -10561)	aaacaatgtggtatagtgagg C/G ggggtgtgagcaggtgtcat	6949
NDUFS5	7	(intron 1 -9065)	cctgatgctcctgggtccag G/A gtacaccttttccctttaga	6950
NDUFS5	8	(intron 1 -8871)	tcaccacgtgtctgtagata T/C aggacccgagaccttcgctt	6951
NDUFS5	9	(intron 1 -7312)	aaatccitggcttctagaa G/T ggctactgatggtatataat	6952
NDUFS5	10	(intron 1 -6827)	aaactctgcctccccgattc A/G cgccattctctgctcagc	6953
NDUFS5	11	(intron 1 -6725)	agtagagacgggttttacc G/A tgttagccagcatggtctcg	6954
NDUFS5	12	(intron 1 -6631)	aggcgtgagccactgcgcc G/A gcctagaccttctcttata	6955
NDUFS5	13	(intron 1 -6531)	cccaacagctcccaatgtaa A/G acagatctatttaattctg	6956
NDUFS5	14	(intron 1 -6346)	gcaacagatcttgacctata T/C cccataggggtacagctgagg	6957
NDUFS5	15	(intron 1 -6327)	atcccataggggtacagctga G/C gactttaacagaaaggag	6958
NDUFS5	16	(intron 1 -6122)	tagccttgcttttactctac T/C gttcctcccaaatcacacc	6959
NDUFS5	17	(intron 1 -2512)	acaaactcttaatgcgaatt T/C tgcagatcaaagtgggctta	6960
NDUFS5	18	(intron 1 -1945)	tttaactctctttaaatttc G/A caatttcacaaactagggtta	6961
NDUFS5	19	(intron 2 75)	ttttttttttttttttgagac G/A aagtctcactcttgcctcc	6962
NDUFS5	20	(intron 2 148)	ctgtagcctctgctcctccag G/A ttcaggcgattcgcgtacct	6963
NDUFS5	21	(3' flanking region 150)	cagattcaagtggttctcct G/C cctcagcctcccaagtagct	6964
NDUFS5	22	(intron 1 (-10682)~(-10681)	attataaacactaaacaaac AT/Δ gtgtggtctcttttagagggg	6965
NDUFS5	23	(intron 1 -10267)	caagtactacctgaaaaa A/Δ gaagagatgaacaaatcac	6966
NDUFS5	24	(intron 1 -2069)	accagacagagtttccctta C/Δ ttgttttctgtggcaaga	6967
NDUFS6	1	(intron 1 26)	ggccgctgggtacaggtgc A/C ccttctccagccgcacctc	6968
NDUFS6	2	(intron 2 1076)	ggatcatggtggtggagagg G/A gcttgtgtctggtgggtttg	6969
NDUFS6	3	(intron 2 1260)	cagttgtgcagtaagtgggtg T/C atagggtaagtgtctttct	6970
NDUFS6	4	(intron 2 1413)	caaaggagctcatggcattg C/T gaatgggacatttcttccgt	6971
NDUFS6	5	(intron 2 1568)	tggagaaggagggtttctc T/C tagtgggtgagcgtatggt	6972
NDUFS6	6	(intron 2 1692)	gaccgtggtgacggaggttt C/T ctgggcatcgatgggtggt	6973
NDUFS6	7	(intron 2 6488)	tagcttaataattattggc A/G ttcattgttcagaatgcctga	6974
NDUFS6	8	(intron 2 6563)	tttaaccttttattttaa G/A tccatgaatggggtcggtat	6975
NDUFS6	9	(intron 2 6740)	aaagatttaacctacatat C/T tttatgcccaatcatttgat	6976
NDUFS6	10	(intron 2 6832)	gcgagggactcattttacag A/T ggttggaacttctactgtgt	6977
NDUFS6	11	(intron 2 7054)	ttcactgcccagagcttgcc G/A tgtgaaccggagccgggct	6978
NDUFS6	12	(intron 2 7186)	ggtcagggtcacccttgagc T/C gcgcacactaaatgacggga	6979
NDUFS6	13	(intron 2 7225)	gagggacatcccgcgtcagc G/A ccagtgctcagggcgtcagca	6980
NDUFS6	14	(intron 2 7810)	cttccactctggggcgggga C/T gctgtagaaggagcacaag	6981
NDUFS6	15	(intron 2 11080)	gtactgttcagtgctttct C/T ctttggatttcatgtaaatc	6982
NDUFS6	16	(intron 2 11657)	gggacagaaacgatgtggtg G/A gagaagagggcgtggcagag	6983
NDUFS6	17	(intron 3 208)	cgaaaacccctttcaactg T/C gaagtgtggggcgcatggt	6984
NDUFS6	18	(intron 3 1031)	ctagagtgaggactgggcacc C/T ggcattgcccctctctgggt	6985
NDUFS6	19	(3' flanking region 270)	gcttcagagagccaaggtgg G/C tcttgaggtgcatagtgaag	6986
NDUFS8	1	(5' untranslated region -4	agtgtagcctcgcctcccg A/C ttgactggcctgcttggcaa	6987
NDUFS8	2	(intron 1 163)	aggtgcagcggggagccggc T/C ctcagggcgcagcgcgcc	6988
NDUFS8	3	(intron 3 123)	tctctgagcctgtttccact T/C ttaaaatgattatggtgatg	6989
NDUFS8	4	(intron 5 -505)	aggcaaggcaggccgggac G/A gtggctcacgcttgtaatcc	6990
NDUFS8	5	(3' flanking region 491)	ggccctgagctggcctgcgt C/A cagccacatcctcttccctg	6991
NDUFS8	6	(3' flanking region 693)	ttcacttcatgttcagtgag G/A aaaccagctccgagaggtga	6992
NDUFS8	7	(3' flanking region 1267)	ttttccagacgttaaccgcc G/A tcagagcgtggcagtgagcc	6993
NDUFS8	8	(3' flanking region 1362)	cgctgggttcttcccttac C/T gtggtctcccaggcatttac	6994
NDUFS8	9	(3' flanking region 1449)	tgtcagaacaggcctatggc G/A cccaaccacaagtcctccaa	6995
NDUFS8	10	(3' flanking region 1572)	cagccccacaggcctgtgct C/A gctgtgtgggcttagggat	6996
NDUFS8	11	(3' flanking region 783-78	cagagaccttgaccccccc (C) atctaccatcatttccaaaa	6997
NDUFS8	11	(3' flanking region 783-78	cagagaccttgaccccccc atctaccatcatttccaaaa	6998
NDUFV1	1	(intron 3 670)	ctgggtggagtggggtggca T/C ggagttgaagaccagtcct	6999
NDUFV1	2	(intron 6 160)	tgtgcccggcccagccctga C/G catgcattcccttggggacc	7000
NDUFV1	3	(intron 9 27)	accacccttctgcgtgacac G/A gaggtgtgggtggcatcaagg	7001
NDUFV1	4	(3' flanking region 1111)	tgtaggctgaggtcagcccc A/C atccagtcacaaagccacc	7002
NDUFV1	5	(3' flanking region 1658)	gaatgcggaagtgcctctgtg G/A gcacccaccatgctccgggc	7003
NDUFV1	6	(3' flanking region 1713)	gatctggggcgagggttaca C/T ggggctggcgtgggtgaag	7004
NDUFV1	7	(intron 4 214)	tgggtgtaatttttttttt T/Δ gcttcaaaaatagatattt	7005
NDUFV1	8	(3' flanking region 772-7	tgaactcggggttcagggtc TTC/Δ ctgtgaacactggttttgaa	7006

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
NDUFV2	1	(intron 1 526)	ggaaatgctggcctaataaa C/T ggtatcaaaactaactctgaa	7007
NDUFV2	2	(intron 1 6689)	tcgttggatggtagtattgt T/G tgaacaacagaagaattca	7008
NDUFV2	3	(intron 1 14767)	ccaaatgcatgccagcagag C/T gtggcaggaaggtacacaag	7009
NDUFV2	4	(coding region (Ala29Val))	aaggaatttgcataagacag T/Ctatgcacaaatggagctggag	7010
NDUFV2	5	(intron 2 -289)	cagaagatcttactctctaa T/G gaagctggataaacacttttt	7011
NDUFV2	6	(intron 2 -168)	tttacttttggtatcact T/C atcaaatgtgtgttagaca	7012
NDUFV2	7	(intron 4 677)	aaaccacatactatttgatt C/A tgatgagaatcacataacca	7013
NDUFV2	8	(intron 4 2295)	tatgattcaactttcaaaag A/T gtattgtgatatgaaataga	7014
NDUFV2	9	(intron 5 102)	caacttctgccatcttattg G/A atctgtacttacctagtaat	7015
NDUFV2	10	(intron 7 5466)	tggttaagggctttaagata A/C caaatgctcagctttcagga	7016
NDUFV2	11	(intron 1 13562-13563)	tactcttaaaattaactctt (CTT) ttattataagtatacagct	7017
NDUFV2	11	(intron 1 13562-13563)	tactcttaaaattaactctt ttattataagtatacagct	7018
NDUFV3	1	(5' flanking region -222)	cgccgcgccccgccacagc G/A cccagggccccgcaggccac	7019
NDUFV3	2	(5' flanking region -111)	tgcccccagggaggcactt A/G gccctactggggatgcgcgc	7020
NDUFV3	3	(intron 1 137)	ttggccgcctgaccccgctc C/T ctggcccgagactgacccgc	7021
NDUFV3	4	(intron 2 152)	tatacaagacacaagatcta T/C aacagatttttagaccaaca	7022
NDUFV3	5	(intron 2 6304)	ttcacagatgaagggttcc G/A aaattttgtcaagaagac	7023
NDUFV3	6	(intron 2 6433)	tcgcctctgcttctcctc T/G tccagctcctctgattctga	7024
NDUFV3	7	(intron 2 6563)	cctttgaaacagagccccc C/T gaggtaagtagatcagcaaaa	7025
NDUFV3	8	(intron 2 9619)	actatcttctgtgcgcatgc G/A cagagccaccttgacagagc	7026
NDUFV3	9	(intron 2 9858)	aggatgcccagctctttaa G/A agacatcgtttttgcctaac	7027
NDUFV3	10	(intron 2 11673)	cttggtaggtgaagcctgt A/G tgtgagcccaagtcattcata	7028
GGT1	1	intron 1 + 85	ttatccagtaaggtgctcc G/A tcacctcttttctcgtggg	7029
GGT1	2	exon 3 + 68	gagcgccaggtccggatggt G/T gtgggagctgctgggggcac	7030
TGM1	1	exon 2 + 179	tgccgaatgcggcagatga C/T gactggggacttgaacctc	7031
TGM1	2	intron 9 + 1594	acttaccactctgtctctc C/T tgccaggcctctctctgca	7032
TGM1	3	intron 9 + 1933	ccgcacatctgtacctgcc C/G ccactctcagcagcagcagc	7033
TGM1	4	intron 10 + 54	tcagtcagtggtttctctgt C/T ccaacttccagcgtgactga	7034
TGM1	5	intron 10 + 420	aggaggccgggagtcaggcc A/G cctcagaccctctggctca	7035
TGM1	6	intron 12 + 101	gggagtcctctgggggaagcc T/G catgtagggaagcagggcctc	7036
TGM1	7	intron 13 + 72	ggataaggacatcagaggtg G/A gcgctaagccagcagcagc	7037
TGM1	8	intron 14 + 1671	atctcttaccacacccccca C/G catggtggggaggttctca	7038
TGM1	9	intron 14 + 1691	ccatggtggggaggttctc G/A tccaaagggatccgcagagc	7039
TGM1	10	intron 14 + 2983	tcctgtcctcctcctctcag G/A gagctcagaaacaccttcaa	7040
TGM1	11	intron 14 + 3158	ggaaacccctcagaaccagg T/C tccaagccaaatgctttgcc	7041
TGM1	12	intron 14 + 3816	cagaatacaaaagtgggatg G/C gaggcaaggagtcocgttag	7042
TGM1	13	exon 15 + 233	ctcaggtggagcttagccc T/C gtgccaggagcaatgggact	7043
TGM1	14	exon 15 + 369	ggagtcagcttctcacttga C/A tgggggaacagatgctaata	7044
CYP1A1	1	5'flanking - 1061	cgcccccagactcctcctccc C/G tcgcgtgactgcgagcccc	7045
CYP1A1	2	5'flanking - 1035	tgactgcgagcccccgccc G/A gggccgggaatgggtcggt	7046
CYP1A1	3	5'flanking - 1020	gcgcggggccggggaatggg T/G cggctgggtgggtgcgcggg	7047
CYP1A1	4	5'flanking - 947	cgccctcctcgggccaggtgg G/A gcggggagcgggcgcctgac	7048
CYP1A1	5	intron 1 + (1326-1334)	cattcattgagaattgagcc (A)8-9 ccttggcctgagttctctg	7049
CYP1A1	6	intron 1 + 1357	ctggcctggatttctctgac T/C aaagagctcaatctagctg	7050
CYP1A1	7	intron 1 + 1590	ccactcttcaaaaggagta C/T atgtgacagcagctggaaat	7051
CYP1A1	8	exon 2 + 160	gaatccaccagggccatggg G/A ctggcctctgattgggcaca	7052
CYP1A1	9	3'flanking + (710-720)	caccgcgagatttccaggtc (T)10-12 gagacggagtctcactgtgt	7053
CYP1A1	10	3'flanking + 834	gcctcagctcccaagtagc C/T gggactacagggcctgcca	7054
CYP1A2	1	intron 1 + 103	gcctgggctaggtgtaggg T/G cctgagttccgggctttgt	7055
CYP1A2	2	intron 2 + 371	cttccctgtgttcaactaa C/T ctttccctcttttgaattg	7056
CYP1A2	3	intron 4 + 44	atagccaggagaagccttga G/A acccaggtgtttgttcagt	7057
CYP1A2	4	intron 4 + 206	aagagtgcacatggggtataa G/C aggggataattcatggggca	7058
CYP1A2	5	intron 5 + (623-648)	tgccccaggtgcctgctgc (T)22-25 catagaaaatagaaaaacat	7059
CYP1A2	6	intron 6 + 81	tcctgtctaggaactgttta T/C ataataaggaggggacct	7060
CYP1A2	7	exon 7 + 181	ctggccatctctgtacagca A/T ctggagttcagcgtgccgc	7061
CYP1A2	8	exon 7 + 295	cggctgcgcttctccatcaa C/T tgaagaagacaccaccattc	7062
CYP1B1	1	5'flanking - 3669	tgatctctgtgaagcatcac G/A gttatctctctctgcacatg	7063
CYP1B1	2	5'flanking - 3149	tgacagcacttaccaccta G/C ttctctgtattttttgagta	7064
CYP1B1	3	5'flanking - 1222	gggggaagccacccccgcc G/A agcgctccggcttccctta	7065
CYP1B1	4	5'flanking - 376	ttccgggaagcaagctcaag T/C cgcggagagggaaggagggt	7066
CYP1B1	5	5'flanking - 265	ctggggacaccgtgcggcct C/T gattggaggtggtgtgatg	7067
CYP1B1	6	intron 1 + 129	tgccccagcgtttgtcccca G/A attgcaggaaacggttacgcg	7068
CYP1B1	7	intron 1 + 379	tgagtgtcacgcttctctc C/T tctgtccccagcatggggac	7069
CYP1B1	8	exon 3 + (799-800)	agcttctggtgagattttttt (T) gagtcaaaagacttaaggggc	7070
CYP1B1	8	exon 3 + (799-800)	agcttctggtgagattttttt gagtcaaaagacttaaggggc	7071
CYP1B1	9	exon 3 + 1284	agtagtgggggttccatga G/T ttatcatgaatttttaagta	7072
CYP1B1	10	exon 3 + 1398	tcagcaaaagaaaaaaa A/Δ gccagccaaagctttaaatta	7073
CYP1B1	11	exon 3 + 1468	ttctcataggttaaaaaaaa A/Δ gtcaccaaagtagtgtgaaat	7074
CYP1B1	12	exon 3 + 1564	ttgaataatatatgccttgt G/A taattattgaaattgaaaaa	7075
CYP1B1	13	exon 3 + 1762	ctgaaattctattataata C/Δ agaattctgttttgaaaaata	7076

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
CYP1B1	14	3' flanking + (2216-2226)	agccagcctcttcttcttctt (T) 10-12 aaaatttattcctatttctt	7077
CYP1B1	15	3' flanking + 2230	tttttctttttttttttttaa A/Δ tttattcctatttcttcttaca	7078
CYP3A4	1	intron 2 + (754-763)	cacaaaatgagttgtgtggg (T) 9-11 acacaaaggcggaatcacat	7079
CYP3A4	2	intron 7 + 258	accactaatcaactttctgc C/T tctatggatttgctattct	7080
CYP3A4	3	intron 7 + 894	tgctgatctcactgctgtag C/T ggtgctccttatgcatagac	7081
CYP3A4	4	exon 9 + (32-33)	ttccttcagctgatgattga (A) ctctcagaattcaaaagaaa	7082
CYP3A4	4	exon 9 + (32-33)	ttccttcagctgatgattga ctctcagaattcaaaagaaa	7083
CYP3A4	5	intron 10 + 12	cccaataaggtgagtggtg G/A tacatggagaaggaggagg	7084
CYP3A4	6	intron 10 + 459	agacatgtgactttttttt T/Δ gaaaggttaacaatcactttc	7085
CYP3A4	7	intron 10 + 608	agccgtctcgaatgtctccc C/T acttcataactcctccacac	7086
CYP3A4	8	intron 12 + 2467	ttttttgcccattactccat A/G gagatcagaatatcactctg	7087
CYP3A5	1	exon 1 + 69	ggaagactcacagaaacacag T/C tgaagaaggaaagtggcgat	7088
CYP3A5	2	intron 1 + (955-956)	tggtgggtagtgagggtccca (A) cctgtcccattaaacttctac	7089
CYP3A5	2	intron 1 + (955-956)	tggtgggtagtgagggtccca cctgtcccattaaacttctac	7090
CYP3A5	3	intron 1 + 1126	acatttttaaatgaattgat A/G tggtttaaatctcattcattt	7091
CYP3A5	4	intron 1 + 1145	tatggtttaaatctcattcat T/G ttttaaacagaaatttttgg	7092
CYP3A5	5	intron 1 + 1543	ttcatgggtcctggcccccac C/A gtggagggtcactcaaggggc	7093
CYP3A5	6	intron 1 + 2366	cttatcttataatgcatact G/A caccatttgctatcaacagg	7094
CYP3A5	7	intron 4 + 1813	tggttcttaattttactcttc G/A tgttctctcatccttgaaat	7095
CYP3A5	8	intron 4 + 1887	aatgacatgaacaaggtgtg A/T ttgtgaagcaagggaatttt	7096
CYP3A5	9	intron 4 + 3384	gagtgtctcgtattttgct C/T aacaagaaaagtctattgt	7097
CYP3A5	10	intron 4 + 3415	agtcatttgcctcacttttca T/C tgaacaactcttctcctcc	7098
CYP3A5	11	intron 4 + 3760	aagataacacactggaagtc G/A cacaccaccataaaactgaa	7099
CYP3A5	12	intron 4 + 3885	acaattcacttccactgtgcca C/T tgaatagcgtctctctgct	7100
CYP3A5	13	intron 4 + 5061	tacctacttttcaaaaaaaa A/Δ tcaccacatcatggcatccc	7101
CYP3A5	14	intron 4 + 5316	ccagatggctgggtctctccc A/T ctcccaccccccgcacacat	7102
CYP3A5	15	intron 9 + 77	gttctgaaaaatgtgcaggaa G/T tattccagggaagtggagaat	7103
CYP3A5	16	intron 9 + 1791	aaattttttatgggaaaaag C/T ctaccccatatttacttaca	7104
CYP3A5	17	intron 12 + 1408	atttaataaaaaaa A/Δ cagagtcacacaagaatttg	7105
CYP3A5	18	3' flanking + 542	tggagaaaaattcatagtt T/C cattctgctctctttgaaga	7106
CYP3A5	19	3' flanking + 737	atgaacactgaataaaaaat T/G gtcaattgtcagttgattg	7107
CYP3A5	20	3' flanking + 804	ttttccttttttattcttttc A/C ttttccctctctttctgaa	7108
CYP3A7	1	5' flanking - 1680	cccaagggaacatgtggtcc C/A ggcacatacctggcacaaca	7109
CYP3A7	2	5' flanking - 1191	tagaaaaatcctccactgttc A/C aaaaggaagccatttgcttt	7110
CYP3A7	3	intron 1 + 1173	ccccatttcaaatcacact G/A cttagcaggttatctctaaac	7111
CYP3A7	4	intron 1 + 1597	tttttctgttagcctcttca T/C tgaacacaaagcagcatta	7112
CYP3A7	5	intron 3 + 762	tccagtgtctgctattccc T/C tcttcttttttcttccctt	7113
CYP3A7	6	intron 7 + (1060 - 1069)	atggtttctgtttctgttgg (T) 9-10 ctacagaagtcttccattc	7114
CYP3A7	7	intron 11 + (592 - 594)	tgaacaaaggtaggaggag AAG/Δ gaggagaattgaaaaacaa	7115
CYP3A7	8	intron 12 + 911	ccccctccattaaacatct C/T tctcattttattccatttaa	7116
CYP3A7	9	intron 12 + 1137	gtctgtctgcagggaata T/Δ attcatgctctttgaaatt	7117
CYP3A7	10	intron 12 + 2147	tattgtcagtaattttttt T/Δ actttgatgctatactttct	7118
CYP3A7	11	exon 13 + 218	ttcatccaatgtgctcata A/C ataatacagggtattctgtacg	7119
CYP3A43	1	intron 1 + 3579	tcatgtctcactttttttt T/Δ ctcaaaatgatcagtcacac	7120
CYP3A43	2	intron 2 + 2427	tagaggaatctttttttt T/Δ cctttttttctgctgccag	7121
CYP3A43	3	intron 3 + 3034	tttttatatagctagggaga T/C tgaataatacaagtttctt	7122
CYP3A43	4	intron 3 + 3433	agtcagaataactttttt T/Δ cataaaggaccagatagt	7123
CYP3A43	5	intron 3 + 3504	catgactcagtttccaacca T/C aacttttctattttggcatag	7124
CYP3A43	6	intron 4 + 2767	tagtgacttttgaaaaaaa A/Δ tagtaataagcaaaagact	7125
CYP3A43	7	exon 5 + 22	aaaacttaaggcacttttca G/A aaatcccattggacctaaag	7126
CYP3A43	8	intron 12 + (1585-1584)	tactttgagccctcattctc (A) ccaagtcacttcagtgtag	7127
CYP3A43	8	intron 12 + (1585-1584)	tactttgagccctcattctc ccaagtcacttcagtgtag	7128
CYP4B1	1	5' flanking - 333	gaaacattcacagtgcttgt A/T tgagaagacagtggtatta	7129
CYP4B1	2	5' flanking - 18	gagcagctgaaggcaggtca G/T atgaaggctagtggtgga	7130
CYP4B1	3	intron 1 + 341	tcacaaacctctggatagta C/T atagaagtaggcaatccatt	7131
CYP4B1	4	intron 1 + 542	cctatgggtggtcaggagc C/T gtgacaccttccagggttca	7132
CYP4B1	5	intron 1 + 2856	gaggactttgcacatagtag G/A tgctcagctatattgttggc	7133
CYP4B1	6	intron 1 + (2923-2938)	caacaaattggtgtgtgtg (GT) 7-8 agaatgccagctcccagatc	7134
CYP4B1	7	intron 1 + 6086	tttggaaatcaagactggg G/T cagcatgctagtgtgtgtgac	7135
CYP4B1	8	intron 1 + 6598	ttttgggtgtgtgggagagg G/A cccatagtagggagacagct	7136
CYP4B1	9	intron 1 + 6660	acctaaagggtgtccactctg A/G aggagagcagtcctaggggg	7137
CYP4B1	10	intron 1 + 7242	ccctgggtctcccttaactca T/C gctggactgttccctttggt	7138
CYP4B1	11	intron 2 + 107	gcctgtgtactaagctctgc C/G agctgaggttccaccctac	7139
CYP4B1	12	intron 3 + 361	atggtgtgtgtgttaggacca C/T ggctggctcaccagaggtgt	7140
CYP4B1	13	intron 4 - 492	aaaggctttcacatctaaaa C/A gtgtctctctcattttctgtc	7141
CYP4B1	14	intron 4 - 315	ggattacttacatatacacc A/G tgggggggagctcaccacct	7142
CYP4B1	15	intron 4 - 157	ctaccacacctatcctgata T/C tccagcaggtaggaggcag	7143
CYP4B1	16	exon 5 + 22	acaagtgggaagagaaagct C/T gggagggttaagctccttgac	7144
CYP4B1	17	intron 5 + 125	cccaggagccttagcttgc G/A gggagacaggacctgtcat	7145
CYP4B1	18	intron 5 + (287-289)	tgtctaaagccaatccctct CCT/Δ accctctgcttagcagggac	7146

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
CYP4B1	19	intron 6 + 54	gectgggttctctctctctgg C/T cctctatgccccctcccat	7147
CYP4B1	20	intron 7 + (99-100)	agctcttaagcatttcccc (TC) ttctctcagcaaatataacc	7148
CYP4B1	20	intron 7 + (99-100)	agctcttaagcatttcccc ttctctcagcaaatataacc	7149
CYP4B1	21	exon 8 + 114	tcctgggttctctactgcat G/A gccctgtaccctgagcacca	7150
CYP4B1	22	exon 8 + 139	tgtaccctgagcaccagcat C/T gttgtagagaggaggtccgc	7151
CYP4B1	23	intron 8 + 247	agaaagtgtcaacaagagg C/T tgatatgtgtgtgtact	7152
CYP4B1	24	intron 8 + 366	tgtgggggtgaacagagctg A/G gacagctgggagagccagtt	7153
CYP4B1	25	intron 8 + 650	cccttgcctgtgtgtgagaca C/A cctgcctttctctctgggct	7154
CYP4B1	26	intron 8 + 844	tcatatgtgagaatcccc C/A ccacggggtatccagacaca	7155
CYP4B1	27	intron 8 + 1767	tcacattccaagaatgttct G/T gttgtgtgtgtgtgtgtgt	7156
CYP4B1	28	exon 9 + 53	tgtgcacgaaggagagcttc C/T gccctaccacacctgtgcc	7157
CYP4B1	29	intron 9 + 652	agtcggatgtgtgtcatgaac G/T ctctgtcactggcagtggtc	7158
CYP4B1	30	intron 9 + 774	cctgggtcaccaacctctgtt C/T tgcccacaggaagcctgac	7159
CYP4B1	31	intron 10 + 33	tgggctgggagatcagacag G/T ggggggactgggaggtca	7160
CYP4B1	32	exon 12 + 224	ccagatggctcaggctgtga C/A ctccctgggaccacccctcc	7161
CYP4B1	33	exon 12 + 270	ctgggtgtggaggagttggg G/A cccctgccttcaggaggt	7162
CYP4B1	34	3'flanking + 129	ctgtgtctcagctcagct G/A gtgctccagcattcagggt	7163
CYP4F2	1	intron 1 + (145-146)	ccaagccctggcaacctca CA/Δ gtgattcaggctgggcttt	7164
CYP4F2	2	intron 1 + 193	tttaacagctctctctctct C/T ttccctattctaagtgtta	7165
CYP4F2	3	intron 1 + 324	ccctgtctcactctcggcac T/C gccctcctcctcctctccac	7166
CYP4F2	4	intron 1 + 367	tcctctggaggtccctgggccc G/C ttctctgggctcaggatct	7167
CYP4F2	5	intron 1 + 402	ggatctcaccgtccctccgc T/C ctgcccctcaggatgtccca	7168
CYP4F2	6	exon 2 + 35	gcctgtcctggctgggcttc T/G gggcagtgagcatccct	7169
CYP4F2	7	exon 2 + 166	cggtgtttcccaaccccc A/G agacggaaactggttttgggg	7170
CYP4F2	8	intron 2 + 125	ggcagagaagcagagaggc A/G tcttactcattctctgctt	7171
CYP4F2	9	intron 2 + 440	gggcccgtctccactctccac T/C acacccgaaggcacctttct	7172
CYP4F2	10	exon 3 + 48	gttctgactcagctgtgtggc C/T acctacccagggcctttaa	7173
CYP4F2	11	intron 3 + 701	agactccacccagcttggg T/A cctttctctgacctctgtg	7174
CYP4F2	12	intron 3 + 742	cttccactcgttggcagggc G/A aggctgagcagggggaatgg	7175
CYP4F2	13	intron 3 + 1020	gccttagctttctccatgtc G/A cttttctctcaagggtggc	7176
CYP4F2	14	intron 3 + 1039	cgcttttctctcaagggtgg C/A cttttctctcatgatgtcaac	7177
CYP4F2	15	intron 3 + 1040	gccttttctctcaagggtgg C/G ttttctctcatgatgtcaacg	7178
CYP4F2	16	intron 3 + 1920	ccactgtctaacctctgtt G/C ctgtttgtctcatgtctggg	7179
CYP4F2	17	intron 3 + 1945	ttgtctcatgtctgggctgtg T/A ctctacaatggctgttatat	7180
CYP4F2	18	intron 3 + 2621	agcattctgtagaatgtga G/A ctgtgctcaggggttgagg	7181
CYP4F2	19	intron 3 + 2665	tgttgatcgtgtaggaggc A/G tgtcaaggcatgctggaacc	7182
CYP4F2	20	intron 6 + 194	gggtttgaactggtgggtgt G/T gtcagagctctgtaggggac	7183
CYP4F2	21	intron 7 + 67	tgtgaaatgtcagatgaaag G/A atttgaactgtattgaagg	7184
CYP4F2	22	intron 7 + 2811	ttccaaggggaattgccatt T/G aattctctctgaactcaggt	7185
CYP4F2	23	intron 7 + (3096-3097)	gggggtgggggttggggggg (G) ttactgcctctctccagga	7186
CYP4F2	23	intron 7 + (3096-3097)	gggggtgggggttggggggg ttactgcctctctccagga	7187
CYP4F2	24	intron 8 + 145	gggtcgtgtctaccttcgggt G/A ctgaagcagccagagacc	7188
CYP4F2	25	exon 9 + 44	ctctcctgggtcctgtacca C/T cttgcaagcaccaggaata	7189
CYP4F2	26	exon 11 + 48	gaaccatcacaccagct G/A tgtggccggaccctgaggtg	7190
CYP4F2	27	intron 12 + 108	tgttccaagttccagctctc C/T ttccctcaactcctctggag	7191
CYP4F2	28	intron 12 + 285	gcatggggatccaggcacgg A/T taccctctctctattctctc	7192
CYP4F2	29	exon 13 + 238	aagtgaagcctagaattacc C/A taagacctgttccacagtc	7193
CYP4F2	30	exon 13 + 342	tgtgcgtgaatgttcatggc G/A gccctattccagtagccaa	7194
CYP4F2	31	exon 13 + 563	tagtgtactgtctctttata T/C gaaatttccagacagggcca	7195
CYP4F2	32	exon 13 + 707	aaatgttccggacccatagata G/C tgacgaaggtagcacgacac	7196
CYP4F3	1	intron 2 + 258	cattaatgcacctctgcggg G/T ctcttgggcaggggttggg	7197
CYP4F3	2	intron 2 + 916	ttaggacatgtctctgagtc C/T acactgtctcccaaaacct	7198
CYP4F3	3	intron 2 + 3417	atccaggtctcacacagtg C/T acttctctcttggcttttag	7199
CYP4F3	4	intron 2 + 4090	gagagcatgaattgggtcct G/A tgtctttctctccagattca	7200
CYP4F3	5	intron 3 + 89	tgtgtgcctccagcgggtc G/A cgtgcccatgtgcagacagg	7201
CYP4F3	6	intron 3 + 243	tcaagtctgtgtacggcta C/T gtcttgtcacctgtatattt	7202
CYP4F3	7	intron 3 + 502	aggtctgggacccagggctcc G/C taagtgaactgtctgagaca	7203
CYP4F3	8	intron 3 + 755	ttttgtggccatgtcaggac A/T tgtgaacacatgtcagtgct	7204
CYP4F3	9	intron 3 + 855	gggacagacaggggtgtcta G/A gtccctgtgaaggcattctg	7205
CYP4F3	10	intron 3 + 970	cctgacatagctcctacgtg C/T catgttaggcaggtgtcattg	7206
CYP4F3	11	intron 6 + 122	gaggagttgtttacactgat C/T gttgaaggactggtatgat	7207
CYP4F3	12	exon 7 + 159	gggtcacgacttcacagat C/A cgtcatccaggagcggcgcc	7208
CYP4F3	13	intron 7 + 2107	caggttgccagtgatttttt T/A ctcaagaagtgtttcatcaag	7209
CYP4F3	14	intron 7 + 2255	gaccaagaagggtctaggag T/A gcaagatgggcttgggttct	7210
CYP4F3	15	intron 8 + 132	cctcaatgcaaggttctgt A/C caccctcgggtgctgaagca	7211
CYP4F3	16	exon 9 + 59	taccaccttgaagacacc G/A gaataccaggagcgtgtgct	7212
CYP4F3	17	intron 9 + 13	attgaatggtgagtgagggt G/A ctgggtccctgttctgagc	7213
CYP4F3	18	intron 9 + 36	gggtccctgttctgagcct G/C tctcattggctctgttcccc	7214
CYP4F3	19	intron 9 + 167	accatcctgactgtctggg C/G aaaggttataggcccttagg	7215
CYP4F3	20	intron 9 + 369	tcctaatctcacccttcc G/A tccagtcaggagattataa	7216

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
CYP4F3	21	intron 9 + 458	tcattcatccatccagtcct T/C gttcagcaaaactctcata	7217
CYP4F3	22	intron 10 + 46	ctcctgggttaggaagagggg A/C ccctcaggcagggagcattg	7218
CYP4F3	23	intron 10 + 63	gggccccctcaggcagggagc C/A ttgtcctgactgcccccttc	7219
CYP4F3	24	intron 11 + 14	ccctgaggtgctggggccccc C/G tctctgtttttgtccattcc	7220
CYP4F3	25	intron 11 + 84	gatcaggagaatccaacatc G/A cctccctccaagacacacac	7221
CYP4F3	26	intron 11 + 113	caagacacacaccactgtct T/C tccaaggctggcgactggg	7222
CYP4F3	27	intron 11 + 164	cggcaacccttctgtgtctc T/G cctccaggctctatgaccct	7223
CYP4F3	28	intron 11 + 165	ggcaacccttctgtgtctcg T/C ctcaggctctatgaccctt	7224
CYP4F3	29	intron 12 + 156	gaaaaggccccacagagtagg G/A ttgggttggtcctagaagga	7225
CYP4F3	30	intron 12 + 253	gagctcgggttaggtctcgag T/G atatgcaagccacatgggg	7226
CYP4F3	31	intron 12 + 346	tggtgtgtccaggccaggtt A/C cgggttgatggggccagga	7227
CYP4F8	1	5'flanking - 61	accatgtttacccatcattg G/T tcttgagctccccagcccc	7228
CYP4F8	2	exon 1 + 67	gtggcagcatccccgtggct G/T cctctgtgtgtgtgtggggc	7229
CYP4F8	3	intron 1 + 707	tacgcagcaggtattcacca T/G tatttccacattatccactg	7230
CYP4F8	4	intron 1 + 857	acacccccctaccctcacatc G/A tgacacagctggggcagaag	7231
CYP4F8	5	intron 1 + 907	tgccatctccaccctcccc G/A tgcaggggcatcttctttat	7232
CYP4F8	6	intron 2 + 668	tgtggcacttccaccatag T/C tcatggccctctgtgtccag	7233
CYP4F8	7	intron 2 + 818	gccacagagaccatgtgtca G/A gcccacaaatgtgtgtagac	7234
CYP4F8	8	intron 2 + 1079	tatgcttgggtgtgtgcagaa C/T atgttgagcatgttaggagc	7235
CYP4F8	9	intron 2 + 1194	cgggtccccctttatgcccc C/A accctcccttcttctctgtgc	7236
CYP4F8	10	intron 5 + 45	aacatggggtgaggtggggg G/T gtgggtgtggggagagcaaa	7237
CYP4F8	11	exon 8 + (19-20)	ggccatgacaccacggccag (GCCAG) tggcctctcctgggtcttgt	7238
CYP4F8	11	exon 8 + (19-20)	ggccatgacaccacggccag tggcctctcctgggtcttgt	7239
CYP4F8	12	intron 8 + 222	tttatttccccactaacttg C/G tatgcaagcttagtaaaate	7240
CYP4F8	13	intron 8 + 334	cttgagagaattaacgcgcaaa A/T accgcaatgacttttgacc	7241
CYP4F8	14	intron 8 + 1999	ttctaagtacatttattctc T/C tgccttttagctatgatctag	7242
CYP4F8	15	intron 8 + 4184	caggagggccgtgtatgtctc C/T ctggataattgttgggtgtt	7243
CYP4F8	16	exon 9 + 119	acgtgggtgtctccagacagc C/T gagtcatcccaaggtgccc	7244
CYP4F8	17	intron 11 + 282	gggttgggggttccggggcct G/C gtctctggcagtggggccc	7245
CYP4F8	18	intron 11 + 340	tcagctcagaccccttccacct C/T gggcccccaggaaactgcacg	7246
CYP4F8	19	3'flanking + 35	atcacctacacctttgcaccaa T/C taccttttcagatttccggt	7247
CYP4F8	20	3'flanking + 83	ctgtgttggccctctgtgct G/C agtcccgcgatggccagta	7248
CYP4F8	21	3'flanking + 90	ggccccctgtgctcagtcctc A/G cggatggccagtagggggcg	7249
CYP27A1	1	intron 1 + 295	aggagggagctgtcttggga A/G gagagtgccagagggcaaatg	7250
CYP27A1	2	intron 1 + 17503	cagtgcataaagcctctgat C/T ctccttagaggaaggaggac	7251
CYP27B1	1	intron 6 + 173	cagccccctagcctcatcttg C/T tgcctccattttgtgctttg	7252
CYP27B1	2	intron 8 + 113	atataagacctggtagaatag A/C atcttctgaaatatgataag	7253
CYP27B1	3	3'flanking + 1081	taccctggaaatcagtgatga G/C aattctgccccatccgtactc	7254
AADAC	1	exon 1 + 29	attaaagtacactattccagg C/T atactatgtaggtttacttt	7255
AADAC	2	intron 1 + 138	gctgtggcctttgacaatgt G/A ttacttagaaatgtgtgttg	7256
AADAC	3	intron 1 + 142	tggcctttgacaatgtgtta C/T ttgaaatgtgtttgtttt	7257
AADAC	4	intron 1 + 1033	ttccagcagagacacaca A/G gtaaaacacccccagctaca	7258
AADAC	5	intron 1 + 1253	tttttttccctcatatttgc T/C gtctgtgctacacatgtga	7259
AADAC	6	intron 1 + 1366	ctctgttagccttttaatta A/G ttaattcattcatttactta	7260
AADAC	7	intron 1 + 1369	tgttagccttttaattaatt A/C attcattcatttacttacct	7261
AADAC	8	intron 1 + 2501	ggttacagaaagatgggtg C/A ttggccaaaaaatgatatgg	7262
AADAC	9	intron 2 + 46	tgctactgaggtagttcgca A/G acattttactaaagtcttcag	7263
AADAC	10	intron 2 + 1971	aaatgagagtttaagtaggag A/C atttctctttattttttgtgc	7264
AADAC	11	intron 2 + 1988	gagaattttctttttttttt A/G tgcaggagaaataataacaa	7265
AADAC	12	intron 2 + 2341	agggtgcctttctattgtcc C/T atgcagacttaggtgatcct	7266
AADAC	13	intron 2 + 2546	gtctgacacagaaggatcaa T/A ggcaaaatgtgcaagacaaa	7267
AADAC	14	intron 2 + 2609	taggaggttccactgggaaac T/C tgaatttccactgagtcatga	7268
AADAC	15	intron 2 + 2663	tataaatacagtggttaatt T/C gtctctcgatttttaaggta	7269
AADAC	16	intron 4 + 605	tgtgtcagtaaaatattata T/C taagttaggtgaatgagatca	7270
AADAC	17	intron 4 + 621	tatattaagttaggtgaatga G/T atcatgtaatgtgagacta	7271
AADAC	18	intron 4 + 679	ttagagattcagacgaattc A/G tataatcttcgatgggtgat	7272
AADAC	19	intron 4 + 1680	gttaaaatgtggataaaatc C/T acaatttgcacaaatatttgg	7273
AADAC	20	intron 4 + 1748	atttagaagttctatcacatc T/C tttatagtatattacacact	7274
AADAC	21	intron 4 + 1771	tatagtatattacacacttc G/A aaaaacacaaattattttt	7275
AADAC	22	exon 5 + 238	caagctcatctctcaaaattt A/G ttaattggaggttccctgctc	7276
AADAC	23	exon 5 + 678	ttagaaattgtgtctttctta A/G aatggctcagtttaagttcca	7277
AADAC	24	3'flanking + 208	aatgtcaaaaaaaataaa A/Δ tcaactgtgttactttgggga	7278
CES1	1	5'flanking - 983	tatttcccttagccagcggtg T/C cacagtggttttagtgatt	7279
CES1	2	5'flanking - 814	tcacattgctcttgacatcac A/C cctactgctctccacccta	7280
CES1	3	5'flanking - 248	agtcctgcaaggggtgacacc G/Δ ttatgccacaagcagttggg	7281
CES1	4	intron 1 + 22	tgagtctctctgaagtcaaa T/Δ atgcggggcacttttgaaa	7282
CES1	5	intron 1 + 30	tctgaagtcaaatatgcggg G/T cactttttgaaatcctgtgt	7283
CES1	6	intron 1 + 1662	aagggaatccctgagctgag C/A atgaccagcccagtggtttc	7284
CES1	7	intron 1 + 1726	cctccctgaagtcctcagca A/C tcttagctgggttctcggcc	7285
CES1	8	intron 1 + 2716	tgcttccaaggaagttcatc T/G cagtattattttgaattagc	7286

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
CES1	9	intron 1 + (2747-2749)	tgttaattagcaacaacaaca AAA/Δ gaaaagaagctaaatattga	7287
CES1	10	intron 1 + 3288	ttatttggccattaaagaaa A/Δ ctcaagcgcttagcctggca	7288
CES1	11	intron 1 + 3691	gagaatattgggacacccctt T/G ttctctctctcatccagcat	7289
CES1	12	intron 1 + 3819	tccttcttgcaattattttt A/G gctggatgtttttatgcctc	7290
CES1	13	intron 1 + 3880	aaccagctcaatgggttagg G/A aggacattgatcgtcatccc	7291
CES1	14	intron 2 + 74	gagtcaggcagctcccctga T/C gggctgatcctttgctctgg	7292
CES1	15	intron 2 + 552	atggaagggtgtgtccattca C/A cctggccaagctgggaagaa	7293
CES1	16	intron 2 + 885	cagtatttttagatggtaaaag T/C attatgatgtaatatattgt	7294
CES1	17	intron 2 + 2001	ttggcatgtcagggtgctcaa G/A actcatgtagaaatcactcc	7295
CES1	18	intron 3 + 2119	cgctgagtgcatagaatagtc T/C aggccttgagggtgatgggag	7296
CES1	19	intron 4 + 127	taaggcatccaagccccttc G/A taattggacactacctaccc	7297
CES1	20	intron 4 + 347	tctgtcatgacacttagcag T/G cagcccagcagggtgaaggtt	7298
CES1	21	intron 4 + (1984-1985)	gtggctcctgaaggtcctgca (C) tgacatctctgctccccacc	7299
CES1	21	intron 4 + (1984-1985)	gtggctcctgaaggtcctgca tgacatctctgctccccacc	7300
CES1	22	intron 5 + 766	gaggtgggagaggggtcagc T/C cactactggattcctcagtc	7301
CES1	23	intron 5 + 825	ggagtagatctagcctggaa T/G agcgagtgagtcactgaccc	7302
CES1	24	intron 5 + 828	gtagatctagcctggaatag C/T gagtgtgactgaccccccac	7303
CES1	25	intron 5 + 868	ctcctgagcatgaactctcc T/A cccctccactctgctgtcag	7304
CES1	26	intron 7 + 68	actctctcatttcagctgtc C/G tcttcccagggagaggttct	7305
CES1	27	intron 7 + 681	cctccaaatcaacaatcca A/G ttatcgctgtctgctagtt	7306
CES1	28	intron 7 + 885	aggaactatccaaagagaaa T/C acattcatatactctgcagg	7307
CES1	29	intron 7 + 2151	gtcgtgttaactgaaatct C/G aggagttgatggcttcaggc	7308
CES1	30	intron 7 + 2470	atatagatatagcaattcac G/A gagtgtgctggggaagaaact	7309
CES1	31	intron 8 + 128	cgtgttttctgttctgagggcc A/C gagaggggttagtgactcacc	7310
CES1	32	intron 8 + 2618	cctgatggcaacacatgagt T/C gggctctctctaatctgtga	7311
CES1	33	intron 8 + 2665	aaaaattattcatcaaaggt G/A aaactcaaatgaagacatg	7312
CES1	34	intron 8 + 3785	ccatggcgcatggccatgcc G/A gtctatgtgtactggctcacc	7313
CES1	35	intron 8 + 3791	cgcatggccatggcgttcta T/C ggtactgtgtcaccctcag	7314
CES1	36	intron 10 + 222	gtgggctggagaagctgcat C/T gctcaccgggggtgtgtgt	7315
CES1	37	intron 10 + 230	gagaagctgcatcgctcacc A/C ggggctgtgtgtcacttttt	7316
CES1	38	intron 11 + 1177	ctagcaggtggcctgacaca C/G ctttgacaggaaggggag	7317
CES1	39	intron 11 + 1311	gccctatgtctctgctgtga A/G ctatatatagagttcccatc	7318
CES1	40	intron 11 + 2025	ttctcatttgggatgctaag A/G ttaaaaattagcataaact	7319
CES1	41	intron 11 + 2029	catttgggatgctaagatta A/C aaattagcataaacttcca	7320
CES1	42	intron 11 + 2317	cattcacaaaagctctttct T/C ctatgtgtgtgtctgtgatt	7321
CES1	43	intron 11 + 3887	caaatatttggctctaattc C/T gcttccacctcagacagcta	7322
CES1	44	intron 12 + 2311	gcgcctctgggcatctcact G/A tgcattgcttaggcgcttgc	7323
CES1	45	intron 12 + 2331	gtgcatgcttaggcgctctg C/G ggctctgtgtttttcagaa	7324
CES1	46	3'flanking + 71	aacggtgatgaaaggagcga T/C gtgagaagggaaggtgtgt	7325
CES1	47	3'flanking + 362	ttgcatggcacttactgacc G/A ttgcacaggcctgcaacacc	7326
CES1	48	3'flanking + 581	atttctggattctgttagta C/T gtgaaagctctaagcatg	7327
CES1	49	3'flanking + 1348	aaatctgctgctgggagaga G/C agcaaaagcatcagatcaac	7328
CES2	1	intron 1 + (1303-1321)	caacaagacttgtctctacc (A)17-19 gtcaagcatgggtggcagaca	7329
CES2	2	exon 5 + 60	ggaccaagtggtgctcactac G/A ctgggtccagcagaatateg	7330
CES2	3	exon 12 + 256	agcctgctgtgcccacacac A/G cccactaaggagaagaagt	7331
CES2	4	3'flanking + (155-172)	acacagtgagacccctctc (A)16-18 gagagagtggtgtgattagaa	7332
CES2	5	3'flanking + (173-178)	tcaaaaaaaaaaaaaaaaaa (GA)4-6 gtgtgtgattagaagctaaa	7333
CES2	6	3'flanking + 377	gggtcaagggtgagcagaacac C/G tgaggacaggagtttgagac	7334
GZMA	1	5'flanking -424	cctcagcttgcaacttggcct A/G ctaattcttatataaccacaa	7335
GZMA	2	5'flanking -134	agcctgcctgtggcagtgga G/C ccatcatccaccattctcac	7336
GZMA	3	intron 1 + 1947	gacataagggttctctctatc A/T gcatgtatggtttgcttgt	7337
GZMA	4	intron 2 + 958	gactgcgtgaccaggtagaa C/T tagcctcagcatggaagggt	7338
GZMA	5	intron 2 + 1525	gttggtgttagtttatactag G/A ttatgaatgatagccttaat	7339
GZMA	6	exon 4 + 105	tgccaaagttgcaggggtggg C/G aggaactcacaatagtgcac	7340
GZMA	7	intron 4 + 696	atagagccttacctgaagaa A/G ggtgtgcagtatgcatgggt	7341
GZMA	8	intron 4 + 1141	ctgttcaggaggatcccg G/A ttccaacatgggtctttatt	7342
GZMB	1	5'flanking - 961	tgtttagcaaatgttttactg T/C gagcctgttatgtgtgagc	7343
GZMB	2	5'flanking - 263	ggctgataccacatcctaca A/G ttccattcatagggcttgggt	7344
GZMB	3	exon 2 + 109	gtgcgggtggctctctgatac A/G agacgacttcgtgctgacag	7345
GZMB	4	intron 2 + (242-243)	tgggggcactactttggcata (A) gaatacaaaactgaagcaatt	7346
GZMB	4	intron 2 + (242-243)	tgggggcactactttggcata gaatacaaaactgaagcaatt	7347
GZMB	5	intron 4 + 131	atttctctctggaagagaa G/A aggggactgactgagctgg	7348
GZMB	6	intron 4 + 182	gggctctgcaaaacttacc G/A gaggttatggttgatgggtg	7349
GZMB	7	3'flanking + 54	attctcaggcaccacatctg C/T gctatgcaggccaatgacac	7350
GZMB	8	3'flanking + 184	tcacacaccagtttctccagg G/T cctgcctctctgccaaggct	7351
GZMB	9	3'flanking + 256	ccactttgttctctggggctt T/A gggtaaaactcttacctcct	7352
GZMB	10	3'flanking + 406	ctgagctcaaggctcagctc G/A tctctcagcctcttggctgc	7353
ESD	1	5'flanking - 333	gtcttgggacagaggagttg G/A gggagttgaaattaggccct	7354
ESD	2	intron 1 + 603	gtcatttctgatggggtcat C/T agggaaatgggattgagcgc	7355
ESD	3	intron 1 + 698	tgtgtgtgtagaagcagcatt C/T taagcactacgtgaattaac	7356

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ESD	4	intron 1 + 1864	gctttcatgcaggattgac G/C tagtgggatgtattaggaag	7357
ESD	5	intron 1 + 2389	ttttgggaacacctgtctag G/A ttgttaagagccagtggaat	7358
ESD	6	intron 2 + 22	taaaactgttttattgttta T/C atgttactctgaacattgaa	7359
ESD	7	intron 2 + 589	taaaattagtagtctctctct G/A taagtctcattatttaagata	7360
ESD	8	intron 2 + 1499	tagaaaaatgtgtatcacac C/T gtaagtgttcagtaattgtta	7361
ESD	9	intron 3 + 92	ctttatctagatattatagt C/A cctcatcttacttttaaaact	7362
ESD	10	intron 3 + 422	gtaaaagagattaacacaca C/T gcacacatacatatacctat	7363
ESD	11	intron 3 + 581	agaaaaacctgagaaatgaca C/T aatttatttaaagccatagt	7364
ESD	12	intron 3 + 2270	gccagtaattacatgtagcc G/A tttacatcaaattagctaat	7365
ESD	13	intron 3 + 2951	taatgaaagtaaatgtttca A/G cttccctaacaaaagtgtga	7366
ESD	14	intron 3 + 3003	aaatgtcagaaaattttttgt G/A ccgtcagtcacacaagaa	7367
ESD	15	intron 3 + 3097	aaggagcatcacagaaaactt G/C ccatgatggggcctttgtgg	7368
ESD	16	intron 4 + 2616	tctaagtgtccagctatta A/G tgggtgcacatcttcattgtcc	7369
ESD	17	intron 5 + 392	tcttttttctctctgtttta C/T atcaaccatacagcttaaca	7370
ESD	18	intron 7 + 107	ttagtattggaactaaactt T/C tctagtgttgagaactttgg	7371
ESD	19	intron 8 + 1091	aaattctaaactaattaaagg G/T ttcactcttttagtaactaga	7372
ESD	20	intron 8 + 1652	tataaagtgtgtggttaatga A/G tatatatgaataagaatatt	7373
ESD	21	intron 8 + 2048	agaaggaaaaagggccattt G/C ttaagaatccctgagatag	7374
ESD	22	intron 9 + (1523-1526)	ctgccacacaaagtctgaaaa (TC)2-3 aagtttgttataaaaaacagc	7375
ESD	23	intron 9 + 2468	atagaaggagaggctatact A/G cctccttaagtctcaggacc	7376
ESD	24	intron 9 + 3362	actaaggataaaaaatagtc G/A tactcagtcacattggaact	7377
ESD	25	intron 9 + 5292	aggccttaatgacataattt C/T cctcacataaagatacaaca	7378
ESD	26	intron 9 + 5298	taatgacatatttcccctca A/C ataaagatacaaatgcttt	7379
ESD	27	3'flanking + 798	tatggtaactgaagaaaatg A/G cattaagtctcctaaagtatt	7380
CEL	1	5'flanking - (611-617)	tggatcaaggcaataaattt (A)6-7 ggaattatttgaagaaaaa	7381
CEL	2	intron 1 + 20098	atctctaccaaggtaccaat T/G ccttaagggaagtgttaatt	7382
CEL	3	intron 1 + (20911-20924)	taatgacatttaacttagc (A)13-15 ctgaatatgactaaaactga	7383
CEL	4	intron 1 + 22374	ttaagtttaaatgtaaacagc A/G cctttgcacactattcagtg	7384
CEL	5	intron 1 + (22460-22469)	ttaatttttagtttaggttg (T)9-10 ctctttttttttatcacatg	7385
CEL	6	intron 1 + 24205	agaatttgagtcattcttg T/G gtgccttctgactacatcct	7386
CEL	7	intron 1 + (24404-24417)	gcaagttttaactgaattac (A)11-14 gcagatgataatcattctat	7387
CEL	8	intron 1 + 26983	tagattttgatgagtttgag T/G tttttttttttttttccaa	7388
CEL	9	intron 1 + (26983-26999)	tagattttgatgagtttgag (T)14-17 ccaaaaggggtgggggtgtgt	7389
CEL	10	intron 1 + (32166-32174)	tcaactttgtcgtgtaaccag (A)8-9 gaaaagccactatttaatac	7390
CEL	11	intron 1 + 37217	aaatttgaatgaatgtta T/G ataaaaatctgtaacaatta	7391
CEL	12	intron 1 + 37685	taattcaaattggattaatca T/A tgataatttctattttttaa	7392
CEL	13	intron 1 + 38032	caggcctaataaatgaaatg T/C tcactactgttgccaacacc	7393
CEL	14	intron 1 + 38133	attcgggagtcctgtctgccc A/C ttgtgataaacatccagct	7394
CEL	15	intron 1 + 38169	cagctcatcttctactctt A/T gtgttgggggtttttgtcccc	7395
CEL	16	intron 1 + 38544	gtttctgtcaactctccaga T/C ataaaaatcaaatgctcttcc	7396
CEL	17	intron 1 + (38642-38643)	caatttcttcacaatacctg (G) attgctgccaggcagcaata	7397
CEL	17	intron 1 + (38642-38643)	caatttcttcacaatacctg attgctgccaggcagcaata	7398
CEL	18	intron 1 + 48429	gaaagagaaactgtgtcccc A/C gaaactgtgtgaagtatgcc	7399
CEL	19	intron 1 + 49038	ttgaaactgcactgacacta A/G tttaaattttacaagtaatt	7400
CEL	20	intron 1 + 49040	gaaactgcactgacactaat T/G taaattttacaagtaatttt	7401
CEL	21	intron 1 + 49256	acatgagaaaaagaatggag C/A taagtttaaaaacagaatga	7402
CEL	22	intron 1 + 49386	aatagttctcagtagatatt C/A ttttacctatatttagtata	7403
CEL	23	intron 1 + 50786	tactttgtctcaccatgac G/A tattcttcccttaaacagat	7404
CEL	24	intron 1 + 50977	ctccagccagagaggacaga T/C agctgagtttctgtttggct	7405
CEL	25	intron 1 + 51150	agcaccattggactgtttttg C/G agtctcctcttttattatgc	7406
CEL	26	intron 1 + 52333	tcagtcaaaacttaaggctc A/C gagatctattaatgcttatg	7407
CEL	27	intron 1 + 52589	gtgtcagcatctgttagata C/A gggagggtgttgaaagaaaa	7408
CEL	28	intron 1 + 55838	tctcgcaggtaaatgaggat G/A gaatacttttaatacaaatc	7409
CEL	29	intron 1 + 56028	ataagtttggaaaaatttgt G/C taaaaatacactaaatatttc	7410
CEL	30	intron 1 + 58738	tggtggagaaataggttata G/A tgctgtgcaaaactgtcccat	7411
CEL	31	intron 1 + 59358	cagaaattgtacttttaaaat A/G cgaactgcaagcactgcagt	7412
CEL	32	intron 1 + 59359	agaaattgtacttttaaaata C/T gaactgcaagcactgcagt	7413
CEL	33	intron 1 + 59464	accagaaaggagcatgtcc C/G ttgtcatttgtgtgaaac	7414
CEL	34	intron 1 + 61340	aaaaaaaacttcaaaatact C/G caatatccaaagtgtgtaca	7415
CEL	35	intron 1 + 62739	cagtcttttaggcacaaagag A/G caaagagtcttctcatctct	7416
CEL	36	intron 1 + (64764-64779)	ctgggtgtgtttctcataaag (T)14-17 aatgtgggatagtggtataa	7417
CEL	37	intron 1 + 65243	tttcaggcttctgtgacagaa T/C agtattatgataaaagctat	7418
CEL	38	intron 1 + 65269	tatgataaaagctatttaata T/A ttagggaagattcctctgact	7419
CEL	39	intron 1 + 65325	aattagaaaaagcaagttttg G/C ggggggggttgcaaaacaaa	7420
CEL	40	intron 1 + (65326-65334)	attagaaaaagcaagttttg (G)7-9 tgcaaaacaaaaagaaaaa	7421
CEL	41	intron 1 + 65524	cacacccataaacaccagtt A/C gttgcctctcctgagccatg	7422
CEL	42	intron 1 + 65869	cagagtaacattcgggctcc A/T actgtcctttcttatagaga	7423
CEL	43	intron 1 + 65910	aaggctgtctcctgtctgtt G/C tggatccaaggcctgtgaa	7424
CEL	44	intron 1 + 66000	gctgtgtttgcatgcctcac C/A gagcatattcactgtcctat	7425
CEL	45	intron 1 + (66226-66235)	tctgtttttgaaaaacaag (A)9-10 tctctccctgcctttggaaa	7426

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
CEL	46	intron 1 + 81816	aatgtttgcttactttccac A/G tatttccagaagccctgac	7427
CEL	47	intron 1 + 83480	tatgactgtcaggaagaaaa T/C tagaattatctttgtctct	7428
CEL	48	intron 1 + 83732	gggggtttgaatctatggag T/C catttccctctttttaaata	7429
CEL	49	intron 1 + 85507	ctggaagaaattttgtgtc A/T ctgcattattttaaattgttag	7430
CEL	50	intron 1 + 87299	caatggctattatattctcc G/A tgtgtgaagacagtcaagaa	7431
CEL	51	intron 1 + 87426	caacaggataatcccagaat G/C ctctgtctgccccttggctct	7432
CEL	52	intron 1 + 87670	tattttgttctcatattca T/C gacatgacacacacataa	7433
CEL	53	intron 1 - (77494-77503)	ttgggttctgttttttcttt (A) 9-10 caactctgtcaacaggggcc	7434
CEL	54	intron 1 - 77368	agctcaggggagagaacact G/C gggggaggcaagaaagcggs	7435
CEL	55	intron 1 - (75135-75129)	tggcggtctggcccaagggt (G) 6-7 tgggactctctgacgcctc	7436
CEL	56	intron 1 - 74785	gctgccacaggaagctgggg G/C ctgttgcctctcttctctgt	7437
CEL	57	intron 1 - 74755	tcttctctgtgtccatgaa A/G cctcaggctctcagggtgcag	7438
CEL	58	intron 1 - 73099	ccccgggtctctctctggc C/T tcttcttgcgcgcctgct	7439
CEL	59	intron 1 - 72559	agcagcagctgggcccgtcc G/A tgcaggagtgaggtgggca	7440
CEL	60	intron 1 - 70098	acaggaggaaacagcaaaa T/C ctcaacactgtttgatctcat	7441
CEL	61	intron 1 - 69440	gttggccatgagagaaaaa C/T aggaaggtattggaaaatga	7442
CEL	62	intron 1 - 65270	attctgcactgctgggaag G/A ctgtggttgggcttctctggc	7443
CEL	63	intron 1 - 64434	ccacattagggttggaatg C/T aacatctgtaattattttca	7444
CEL	64	intron 1 - 63966	agatcagacatccccaccc C/T atcgcttagagaactgagcc	7445
CEL	65	intron 1 - 63916	gctgtcaccatgacctgac C/T ttcagggtgctgacccagtc	7446
CEL	66	intron 1 - 60392	tctggggctccaggatgca C/T gtggaaatccctgggagcag	7447
CEL	67	intron 1 - 60321	aattacttgaacccattcc A/T tcccaccccaaccccttttc	7448
CEL	68	intron 1 - 60318	tacttgaacccattccatc C/T caaccccaacccctttctctc	7449
CEL	69	intron 1 - 56852	tgtctcaagccctccccctg C/A gccacgacgaccccatctc	7450
CEL	70	intron 1 - 56133	gctggctcgtggatgtcta C/T ggggcttgcctggcaccccc	7451
CEL	71	intron 1 - 55964	ccccagcgcctccagcccg G/A cctgagacttatcactgcc	7452
CEL	72	intron 1 - 52016	tcttggaactagggtgggg G/A ggcactgccaagtggccagg	7453
CEL	73	intron 1 - 51998	gggggcaactgccaagtggcca G/A gggaggggactgcggggcac	7454
CEL	74	intron 1 - 51578	gtgggatcgacttgcatttt G/C gggggagaagcatccctggt	7455
CEL	75	intron 1 - 39557	ggccacgacatggcttcca T/C gaggtcttaagctccccaag	7456
CEL	76	intron 1 - 39490	gcccttttctccaggtgttc A/C tgggcaactgaggtcaccag	7457
CEL	77	intron 1 - (31332-31340)	tccggactctcattggctc (A) 8-9 ctgctcggccctcggtatc	7458
CEL	78	intron 1 - 19634	ttatttcagggtggccatc C/T tagctgctcaggagctgt	7459
CEL	79	intron 1 - 6589	gacgggtgatcgagggaact T/C gctgtcccccagtgcttggg	7460
CEL	80	intron 1 - (3340-3345)	gctggcagtgctggcctgtg (C) 4-6 tcaatgtggtcgggttggg	7461
CEL	81	intron 3 + 35	tgccggactggccctcgccg G/A gggcgggtgagggcggtgc	7462
CEL	82	intron 6 + 157	gtggggagcggccttggtga C/T gggatttctgggtcccgtag	7463
CEL	83	exon 9 + 137	aacatggagcggccacatctt C/T gccagcatcgacatgcctgc	7464
CEL	84	intron 9 + 41	tcaggggcgaccctgcccgg A/G gggccgcccgggaaagcactg	7465
CEL	85	intron 9 + 151	gggggtgagtatgcacacacc T/C tctgttggcacaggctgag	7466
CEL	86	exon 10 + 82	acgacctttgatgtctacac C/T gagtctctgggcccaggaccc	7467
CEL	87	exon 12 + 583	ccccgggtgactcgggggc C/A cccccgtgacccccacggg	7468
CEL	88	exon 12 + 759	gttttagcgtcccatgagcc T/C tggatbcaagaggccacaag	7469
IL17	1	5'flanking + 832	cctgagaagggaactattctc A/G aggacctgagttccaaagttca	7470
IL17	2	5'flanking + 692	tgcccccttttctccatct C/T ctacacctttgtccagtcctc	7471
IL17	3	5'flanking + 76	ccctgaacccactgcgacac G/A ccacgttaagtaccacagaa	7472
IL17	4	intron 1 + 18	gtggtgagtctcactaac G/A tgcgatgctcttctgtgattt	7473
IL17	5	intron 1 + 126	ctgtatatgtaggataggaa A/G tgaagcttttggtaggtatt	7474
IL17	6	intron 1 + 762	ctgagaacaatggtgcagga G/A gatatttctacctagaaaaat	7475
IL17	7	intron 2 + 594	tattttgatcatattgacttc A/T tacaataagtcctctgttct	7476
IL17	8	exon 3 + 1487	agctgatggggcagaacgaa C/T ttttaagtatgaaaaagttc	7477
IL17	9	3'flanking + 657	ccctgaatcttttctctct G/T cctctccctcattctcaaca	7478
UCLH3	1	5'flanking - 1034	ataatgtgaagaagaaaaaa A/G agacactgctactgggctcc	7479
UCLH3	2	5'flanking - 490	cactcctgcaccccgacaaa G/C gaacaacagcaccgtgctgc	7480
UCLH3	3	5'flanking - 480	ccccgacaaacgaacacag T/C accgtgctgcacggcgctct	7481
UCLH3	4	5'flanking - 295	atgcgtagaaacgcgagcgct T/C ggcaaggctcggtcgggaag	7482
UCLH3	5	5'flanking - (25-11)	tggggcgaagcggcgccggc GCGAAGGCGCGCGC/Δ tgtcagagctg	7483
UCLH3	6	intron 2 + 28	aggtgtctgtctcgctcgggac T/C tcggagctttttctgtctgc	7484
UCLH3	7	intron 2 + (5639-5640)	aattttttattataataata (ATA) tataagtagaagaattatat	7485
UCLH3	7	intron 2 + (5639-5640)	aattttttattataataata tataagtagaagaattatat	7486
UCLH3	8	intron 2 + 7862	aggtggattccaccaccca G/A gctaactgcttaacatttttag	7487
UCLH3	9	intron 2 + (7936-7947)	tgatcatttcaaacacaggg (T) 11-12 aattgtaaaaagtagacatt	7488
UCLH3	10	intron 2 + (7975-7988)	aaagtaggacatttttaata (T) 12-14 gaagacgtgaggtgaaag	7489
UCLH3	11	intron 2 + 8117	cctgactctggcaatctgg A/C gtcaggatcttaacaatat	7490
UCLH3	12	intron 2 + 8361	ttgttagctttggctgacat G/A gagttagatttgcagtgaaat	7491
UCLH3	13	intron 2 + 9800	taagatatagtgtgacttt C/T taatatgatttttgttctct	7492
UCLH3	14	intron 2 + (10738-10747)	taccaactaatgttccattg (T) 9-10 ctttctttctttaccagtt	7493
UCLH3	15	intron 3 + 11	tacagaaaaggtaattgtta A/T gtaaaatagaagtttctgg	7494
UCLH3	16	intron 3 + (662-675)	cttaataacagttttttcaa (TA) 6-7 aggaatcttcttctgtatt	7495
UCLH3	17	intron 3 + 866	tcaagctcatatatttttagt T/C ttttttctagaatgatata	7496

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
UCHL3	18	intron 3 + (944-945)	tacatacgtatatacgtatata (TGTATACGTATACATACGTATACATATATACATACGTATATA) cgtaacgtatatacgtatatac	7497
UCHL3	18	intron 3 + (944-945)	tacatacgtatatacgtatata cgtaacgtatatacgtatatac	7498
UCHL3	19	intron 3 + 5052	aggcagtcagctatagagcc T/C acatctttgatgcttattat	7499
UCHL3	20	intron 3 + 5282	acctctattaagtttttgca T/C acctcttcagactttccaat	7500
UCHL3	21	intron 6 + 2191	tttctagggtttctctagtg C/T gttagagcagtgattctcaag	7501
UCHL3	22	intron 6 + 8264	tctgcaagtcacaaatgtgaag G/C caagaagaaaaatccaaaa	7502
UCHL3	23	intron 6 + (8741-8744)	atgtgagtaaacacacattt ATTT/Δ ttcatttccctaaacttttga	7503
UCHL3	24	intron 6 + 9411	tcctctgttttagaactctact T/G ggccttttttgcccagccag	7504
UCHL3	25	intron 6 + 9459	tgtagtgagcagtaaatagtg T/A taaagtttcatcttccattag	7505
UCHL3	26	intron 6 + 9772	gaaacaatacagtgatcatg T/C ggttcaagatgtagagtcga	7506
UCHL3	27	intron 6 + 10158	ttattttaaaggaaaattct C/T agaccgaacttaccagttca	7507
UCHL3	28	intron 6 + 10839	tttactaaaaaatctacaga A/C atccatttagaatttaattta	7508
UCHL3	29	intron 6 + 12493	agtcacaaatagttgacagtt A/G atgggcagtgaccttgcaa	7509
UCHL3	30	intron 6 + (20435-20437)	cttttttaattagtagtctct CCT/Δ cgccatctctacacagcct	7510
UCHL3	31	intron 6 + 21202	ttgatctgatcttctctgccc C/T attcagtttctcaagatctt	7511
UCHL3	32	intron 6 + 21295	caaatattatgatttctctt T/C ataggctaattgatctctga	7512
UCHL3	33	intron 6 + 21639	taagaacaattaaagtcac C/T ggcaagcattcttctctcc	7513
UCHL3	34	intron 6 + 21778	tcattttctgtcagtagtca A/G caaactcacatctcttctta	7514
UCHL3	35	intron 6 + 23299	cttttagattaaaggtgcaa T/C gatgcacaaattttgagtcac	7515
UCHL3	36	intron 6 + 23498	tattcagttctctgactcca A/G ttgtactacttttaccteta	7516
UCHL3	37	intron 6 + 23790	ttagccttaaaaaattggac A/T ctcttctgattattgataaa	7517
UCHL3	38	intron 6 + 23894	actcattatcagctgtcttca A/C atattttaagaaaatagtct	7518
UCHL3	39	intron 6 + (24729-24732)	agtccttaatttcaaatgtt TGT/Δ aagcatcaaaagcaagagaaa	7519
UCHL3	40	intron 6 + (25083-25084)	catgtattcatttcattcag (A) taagtagcaatgtgcatat	7520
UCHL3	40	intron 6 + (25083-25084)	catgtattcatttcattcag taagtagcaatgtgcatat	7521
UCHL3	41	intron 6 + 25084	catgtattcatttcattcag C/T aagtagcaatgtgcatata	7522
UCHL3	42	intron 7 + 1342	gaagaagtcattatttttggt G/A gtatataaatggaccctcagg	7523
UCHL3	43	intron 7 + 1387	ttttgaagatgtgcttctgct G/A attgagtcctacaaaatctgc	7524
UCHL3	44	intron 7 + 1760	actcggttttactagttaga T/G agctgtcttggctcagagggc	7525
UCHL3	45	intron 7 + 2096	taggtacattacaagatgg G/A cagttgctgattcattgcaa	7526
UCHL3	46	intron 7 + 2873	ttaattgtattaattctctac T/G ctaataaattgttaaggttaa	7527
UCHL3	47	intron 7 + 7554	ctctcgagcctcatggatcc T/A tctgcaagcgtatgcattac	7528
UCHL3	48	intron 8 + 207	ctctatgaacaaatgtaaaa T/A ttgaaaaggcaagaatagta	7529
UCHL3	49	intron 8 + 252	aagacttgctcattatattcc C/G agatttccatcaaatccagga	7530
UCHL3	50	intron 8 + (883-892)	tttactactgaaaaatcatac (T) 9-10 cctccataggatgccataga	7531
DDOST	1	intron2 629	attctgtttaagaagttcttta T/C attaaagaatattgtctctct	7532
DDOST	2	intron2 3125	gagaatataaggagcttctgc G/A tatgcctgaaagtcagtcag	7533
DDOST	3	intron2 3920	attactcattttaaataataa A/G tggattactgagcactgtct	7534
DDOST	4	intron3 189	actgctgtccaggggtccat C/T tggggctgagccagctgga	7535
DDOST	5	intron6 185	ctgtctcttctgttcgggagg C/T gtggcagcttttcccttact	7536
DDOST	6	exon8 37	aactatgaactagctgtggc C/T ctctcccgtgggtgttcaa	7537
DDOST	7	intron9 37	tctgcccagaatgctgccc A/Δ aaaaacggccccagggctca	7538
DDOST	8	intron2 + 1299	atctctctgatgactgggctt C/T ggtgcagtaactggtgtttg	7539
DDOST	9	intron2 + 1581	gatactgttgggtgggagaaa T/C gacagagagtgtaaaacagt	7540
DDOST	10	intron2 + 2822	gtttctcaacaggtgcatcc T/G tgcgctttcagactggataa	7541
DDOST	11	intron2 + 3392	cagaaggcgtggagggcctgc C/T gcgcctccctctgttctgc	7542
DDOST	12	intron5 + 495	attgcttgaaccagggaggc G/A gaggttgcaatgagccaagg	7543
DDOST	13	intron6 + 226	ggaactgcttgggtccacagc C/T tgcgtttgttccagtatcc	7544
DDOST	14	intron8 + 303	aagagaaataggtcattagg A/T tgaatttgttaggcaagaga	7545
DDOST	15	3' flanking + 40	cacagcgtggagacggggca G/A ggaggggggttattaggatt	7546
NTR	1	5' flanking - 535	cacgatctgtctccgatcc C/T tgttaactctagactttctg	7547
NTR	2	5' flanking - 15	gtaaatccccggcaaaaaacc A/G gcagcgccttgcaagccac	7548
NTR	3	5' flanking - 748	agcatggcgcgaggaggagg G/T gtgggaggggtcgaggaggac	7549
NTR	4	5' flanking - 690	tgaataatttaaagggggccc T/C gcctgcggagcggggcgga	7550
NTR	5	intron6 + 605	tcttgccatataacttagtg G/A ggggtctacatcaggggttt	7551
NTR	6	intron6 + 748	agcctccagcctctctctctc C/T ggggggttatctcaggcatct	7552
NTR	7	intron6 + 987	gggtctggctctggggtatccc C/T gtgcgtcatgtagctacct	7553
NTR	8	intron6 + 1882	tggcctcaagcaatctctccc G/A cctcggcctccaaaagtgt	7554
NTR	9	intron6 + 2222	gaatgtttatgtagaacaga G/A agactgtatctgcgggtcttc	7555
NTR	10	intron12 + 166	tatctggtaccgaggagct C/G tggcctcgtcccaaggggcc	7556
NTR	11	intron13 + 69	atccaggtccacgcctgccc C/T gtcttgattgttttaattctg	7557
NTR	12	intron14 + 8	agccccgcctcgggttaaggc C/T tgggaccctgcccgggtgtg	7558
NTR	13	intron16 - 113	gccacgcgcgcctctgcccct T/C atatttttcttaacccttcc	7559
NTR	14	intron21 + 34	agagccggcgccggccagagc A/G tgctgggagatgtagtccgg	7560
NTR	15	intron21 + 128	gaagaaatcgtgcccttgag G/A gtttcaaaccttaagtagga	7561
NTR	16	intron21 + 151	ttcaaaccttaagtaggacc C/G aggtgcagagcattctgggg	7562
NTR	17	intron21 + 651	ccactgtactccagccggga C/T gacagagctagaacctgttt	7563

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
NTE	18	intron21 + 737	tggaaaatagtctgtggatt G/T ttgttttaggactctgggcac	7564
NTE	19	intron21 + 1752	acagctgggtctaggctgtta G/C tggagaaactgggaagcaac	7565
NTE	20	intron21 + 1788	gaagcaacagctgggtcaaaa A/Δ gtactttttctttcttggc	7566
NTE	21	intron21 + 1907	cactgcaacctctgctctccc A/G ggttcaagtgtattctctgc	7567
NTE	22	intron21 + 2065	ctgcctcggttttatgttcag G/T tccccattagacagaggaa	7568
NTE	23	intron21 + 2336	agtctgggagcacaggagca G/A gaatttcagataaggaggaa	7569
NTE	24	intron23 + 41	tggggagggtgggtgggtggg G/C ctggagcctcaattctttc	7570
NTE	25	intron23 + 71	caaattctttcagacctgag T/C tcaagtctctcgcttccaac	7571
NTE	26	intron23 + 81	cagacctgagttcaagttct C/T ggcttccaaccacggagcct	7572
NTE	27	intron24 + 150	gtggggcggtggtgacctc A/C gccgtcgttattccgcagct	7573
NTE	28	intron29 + 37	gctgcagcaaccgctgacg T/C cactgggggttgggggatg	7574
NTE	29	intron29 + 370	cgtcccaggtcagcgagccc G/A tggggccggctgggctccg	7575
NTE	30	intron30 + 56	acctcccgcaccacacacac G/A cacacgcgtgggcacacaca	7576
NTE	31	intron30 + 358	aaaaatacaaaaaattaacc A/G ggctgggtgggtgtgctgt	7577
NTE	32	intron30 + 372	ttaccaggtggtgggggtg T/C gcctgtaatcccagctactc	7578
NTE	33	intron30 + 430	aaatcactgaacctgggag G/T tggaggttgagtgagctga	7579
NTE	34	intron30 + 655	gtgtgcacaccagctatata T/C gcaaatgctttctctcaggg	7580
NTE	35	intron30 + 659	gcacaccagctatataatgca A/C atgctttctctcagggcgag	7581
NTE	36	intron30 + 760	tgaatatgggcatattgcaa C/T gcatgccagctgtgccgtt	7582
NTE	37	intron30 + 835	gcacacagctagataggatg T/C ggcacctctgaccaggttaa	7583
NTE	38	intron31 + 40	tgggtgcctgcataggtggtc T/C ggctaaagctttgctacttaa	7584
NTE	39	intron31 + 41	gggtgcctgcataggtggctc G/A gctaagctttgctacttaa	7585
NTE	40	intron31 + 1329	gtctgtcaaggcgaggacag G/A ggatgtgtaggcgagtggtc	7586
NTE	41	intron35 + 31	aatggcttctctgtctgtttc G/A gactggggagccacacctctg	7587
L1CAM	1	intron 1 + 767	tttgacttctctacatgggt G/A actgtgtgagtcactctgtt	7588
L1CAM	2	intron 1 + 862	gcattgggtcatgtgtatgt G/C tgagtggggctgaatgtaag	7589
L1CAM	3	intron 1 + 1332	cagggatgaaggagcagagc C/T gctgagaggccacacaggtg	7590
L1CAM	4	intron 4 + 502	tttccctgggggttttccctt T/C gcattccatctccctgagc	7591
L1CAM	5	intron 18 + 147	agcgacgttatgaaattccc C/A acacttccattttctataat	7592
L1CAM	6	intron 24 + 221	ctccttagccccccagaggg C/T cccaactttaagagcatact	7593
AANAT	1	5'flanking-542	aggggtgcaggatgggtgt G/T agctggaggcgaggggtag	7594
AANAT	2	5'flanking-263	ccccccacataagaggtggg C/G ttgtccaagactccgagggga	7595
AANAT	3	intron3 39	cgccccagctccaggaggccc T/A ctgaagacagaggtcagcca	7596
AANAT	4	exon4 150	cagccggcgctgcgcggggc C/T gcgctcatgtgcgaggacgc	7597
ARD1	1	intron1 + 317	ccgtcggtctgctcggcccc C/G ctcccctggggctggggcagg	7598
ARD1	2	intron6 + 322	gctcctcagcactcgtctcac G/A ccaggagaccacacactctc	7599
ARD1	3	intron6 + 1095	aaggctccatcctgagacaa A/C aagtcagtgtagacctgcc	7600
ARD1	4	intron6 + 1179	aggaggaagacctgtatccc A/G gggacacctctccacctcc	7601
ARD1	5	intron7 + 159	cctccaggctgctaggcaga C/T ggctcctctctaaagccagc	7602
ARD1	6	intron7 + 295	tgaccagccctgccacccca G/T gagccttgggcagaaacctg	7603
ARD1	7	intron7 + 416	actaccatggaggccccccac G/A acagagcgctgccccctgac	7604
NAT1	1	3'UTR 215	aataataataataataataa A/T aaatgtatttttaagatggc	7605
NAT2	1	exon2 867	cgtgcccaaacctggtgatg G/A atcccttactatttagaata	7606
NAT2	2	3'flank 521	ccatccatacttttggcaca G/A agaaggaacatgagctttat	7607
NAT2	3	3'flank 573	gatttgaatcctgtggaca C/T ggggtgaattacttttaaaa	7608
NAT2	4	3'flank 918	attttctgtttgtgaaattcc A/G gtatcagggtatagtttaa	7609
NAT2	5	3'flank 979	actattctccctctctcgact C/T gtgatgactataataatctt	7610
NAT2	6	3'flank 1958	tacctattgaagtaagccta C/T gtcatatccacctatttgtt	7611
NAT2	7	3'flank 2034	ccactgattccagagcttag T/G tcatataagaagacagtgct	7612
NAT2	8	3'flank 2201	cagattactggaggctact G/A ttgtctcaccatgcaaatg	7613
NAT2	9	3'flank 2818	gggatatttgtctcctttct C/G cccagtgcatgttggaaacc	7614
NAT2	10	3'flank 3237	atatatatccaattaaaaa A/Δ caaaataaatttccgaaact	7615
NAT2	11	3'flank 3386	caacaagagatttttttaa G/A ctttttaaaacaccagacag	7616
NAT2	12	3'flank 3660	cagcactattcgcaatagca A/G agatgtggaatcaatctaaa	7617
NAT2	13	3'flank 3973	agcagaaaaataaataatg C/T gtactaggcttactacctgc	7618
NAT2	14	3'flank 4029	caaaacaaacccccatgaca T/C gagtttatctatatacaaaa	7619
NAT2	15	3'flank 4118	ataagattaatatctgcata C/A aaatctttgtttacagcttg	7620
NAT2	16	3'flank 4146	tgtttacagctgtttatata C/T tgaattatgtctgtccccc	7621
NAT2	17	3'flank 4279	ttaatctgataggattgggtg G/C ctttataagaaaaagaaaag	7622
NAT2	18	3'flank 4323	ttgctctctccccagtgag T/G taccaggaagggccatgtg	7623
NAT2	19	3'flank 4446	tcaattggctttatctgcga T/C tctggaatcaggcaatactc	7624
NAT2	20	3'flank 4462	gcgattctggaaatcaggcaa T/C actccatttcataaaacaga	7625
NAT2	21	exon2 + 288	atgttaggagggtattttta C/T atccctccagtttaacaaata	7626
NAT2	22	5'flank - 2053	ctggattgcacattttta T/C ccaggtgtcaggttttccaac	7627
NAT2	23	5'flank - 1299	gaatccagctgcgggaggt A/G taacagtgaaacccaagacac	7628
NAT2	24	5'flank - 1145	ctgtagaacacaaagatatt C/T ggaggcagtttgtacatgcc	7629
NAT2	25	5'flank - 1036	ccttccacagagtcctccag T/A tcatgtggcagcatgccaga	7630
NAT2	26	5'flank - 94	aaagatttgctaagagattc G/A cagaggcaacctgaggccct	7631
NAT2	27	5'flank - 643	atgtttatatattttatata T/C attaatgtaaaaaaatatt	7632
ABCB2	1	5'flanking - 673	agctaagagtcaaagcacc G/C ctttttccaccagctcgcg	7633

Table 1

GENE	NO	LOCATION	SEQ.	SEQ ID NO.
ABCB2	2	5'flanking - 646	ccaccagcctcgctgcctg T/G tcccttcacggacactctag	7634
ABCB2	3	5'flanking - 563	ttgcaagcgcctggctgctac A/C ggcgacctccctgcgctccc	7635
ABCB2	4	5'flanking - 236	gctttgcgcgcggcgctaac G/T tgtgtagggcagatctgccc	7636
ABCB2	5	Intron3 + 408	aaggaaactgagggccaagac C/T ctaaatgctgaaactgcaca	7637
ABCB2	6	Exon4 + 153	ccctcaccatgggtcacctg A/G tcaccotgcctctgcttttc	7638
ABCB2	7	Intron4 + 289	gtatttcttttagcatccaag G/T ggcatagctgtgtctcttttc	7639
ABCB2	8	Intron4 + 291	atttcttttagcatccaaggg C/G catagctgtgtctctttctc	7640
ABCB2	9	Intron5 - 63	ttccttcagggttaatgactg C/T gggtctttgtgtccctcca	7641
ABCB2	10	Intron7 - 185	gtctctgcctctgtctttgc C/T gcttctcttatctctactec	7642
ABCB2	11	3'flanking + 71	agcgcaacttttcagctgcgg G/A tgtctctctttttatctec	7643
ABCB2	12	3'flanking + 129	aactgcatcaccttttcct T/C aagctttttaattcctatga	7644
ABCB2	13	3'flanking + 459	cattcagggaggccaggtc G/A tgtgacgtgcacagttgctg	7645
ABCB3	1	intron3+8	tctctttggcaggtagtg G/A tgggcagctgggtccatttg	7646
ABCB3	2	intron4+104	cttcaccgtatgccaggac C/T tggggatgcttttctcttgt	7647
ABCB3	3	intron10+219	gcagcagtggtgtccctcc A/G tgggcagcccgctcaggtcc	7648
ABCB3	4	intron11+(317-319)	atgggtgccaggtggatgtg GTG/Δ tccatctcattctgtcttt	7649
ABCB3	5	exon12+19	agctgcaggactggaattcc T/C gtggggatcgacagtgctg	7650
ABCB3	6	exon12+(356-357)	aggtgggggtgggtgggtg GG/TGGTGGGGTGA ggcgtgtctgtgctc	7651
GSTM3	1	5'flanking - 144	ccaacgccggcattagtcg G/T cctgcgcacggccctgtgga	7652
GSTM3	2	intron 7 + 165	agcctaactctataccctg A/G aggcactgtctacaaaaaa	7653
GSTM3	3	intron 7 + 257	ctgttggtgactgggtgggtc T/G ttataagattggtgtatatt	7654
GSTM3	4	exon 8 + 91	cccagtggggcaacaagcct A/G tatgctgagcaggaggcaga	7655
GSTM4	1	intron 4 + 67	ttggctggattgggtgcta T/C gctcagagtgagctctgtgt	7656
GSTM4	2	intron 7 + 77	gatgcttcccagtcctgga T/G ctgcataaagaataactgc	7657
GSTM4	3	intron 7 + 80	gctttcccagtcctggatct G/A cataaagaataacttgatt	7658
ALDH7	1	intron1+464	catgaatgactctgggaaag A/G atcattcttagcaatggact	7659
ALDH7	2	intron1+2269	aaatggaatccaacagcaa G/C agacctccccctcacgggtca	7660
ALDH7	3	intron2+1349	actgagcttctgcccacggc C/T gcctgccggcctcatgaga	7661
ALDH7	4	intron2+1820	tccgtgtggaaggcaccttc C/G cccagcctcagtggttagga	7662
ALDH7	5	intron2+2046	aacctcaggcgtgcctcag C/G caggagagccagcctggcccc	7663
ALDH7	6	intron2+2939	aagcacgcactgaacatgga G/A tgagtgaagtgaacgaatgaa	7664
ALDH7	7	intron3+7	tgcccaagaacctggtgagc C/T gccgggctgaggcgggcag	7665
ALDH7	8	intron4+36	gccccctccggtcaccttc T/C ccgctcagagcctcagggcc	7666
ALDH7	9	intron6+(116-117)	attctctctctctctctct CT/Δ ggaccaggctgggagcagtc	7667
ALDH7	10	intron6+263	cagaccdctacagtgaacc T/C gctgccccccaggctcttag	7668
HMG17L1	1	3'untranslated + 864	ctttctgatttttgatagtc G/C gttgaagaaggagtttgaa	7669

In some embodiments, a drug-metabolizing enzyme is at least one of the following:
epoxide hydrolase, methyltransferase, N-acetyltransferase, sulfotransferase, quinone
oxidoreductase, glutathione S-transferase, UDP-glycosyltransferase, aldehyde
dehydrogenase, alcohol dehydrogenase, esterase, NDUF, cytochrome P450 (CYP) and
5 ATP-binding cassette.

The present invention relates to a method for detecting a genetic polymorphism in
a test subject using the genetic polymorphism data related to a drug metabolizing
enzyme. The present invention analyzes the effectiveness, safety and strength of drugs
metabolized by a drug metabolizing enzyme. The relationship between a disease and the
10 drug to be evaluated is based on the results of the analysis. The genetic polymorphism
data for the drug metabolizing enzyme is different for each patient with a given disease.
Therefore, the effectiveness and safety of a specific drug depends on drug metabolism in
the presence of certain genetic polymorphism data and the side effects in the presence of
certain genetic polymorphism data. As a result, a physician can determine whether a
15 certain drug should be used by a certain patient and can tailor drugs for use by a certain
patient based on the genetic polymorphism data (so-called "made-to-order" treatments).

"Drug metabolizing enzymes" refer to a group of enzymes that catalyze *in vivo*
structural changes in exogenous materials including drugs. When used for clinical
purposes, the group of metabolizing enzymes includes some endogenous materials.
20 Because drug-metabolizing enzymes absorb, metabolize and secrete drugs, the
polymorphism of an enzyme depends on the amount of enzyme expressed (transcription
and translation) and the amount of activity. As a result, there are blood serum
concentrations of both unchanged materials and metabolites.

Drug metabolizing enzymes expressed by the genes that are targeted for genetic
25 polymorphism analysis in the present invention include, but are not limited to the
following classes of enzymes:

- Epoxide hydrolases
- Methyltransferases
- N-acetyltransferases
- 30 Sulfotransferases

Quinone oxidoreductases
 Glutathione S-transferases
 UDP-glycosyltransferases
 Aldehyde dehydrogenases
 5 Alcohol dehydrogenases
 Esterases
 Ubiquinone dehydrogenases : NDUF
 Cytochrome P450s (CYPs)
 ATP-binding cassettes
 10 ATP-binding cassettes / Transporters

Examples and descriptions of these enzymes are provided below.

(1) Epoxide hydrolases are enzymes that hydrolyze epoxide using a trans-
 cleavage mechanism to produce 1,2-glycol. Examples include microsomal epoxide
 15 hydrolase 1 and cytoplasmic epoxide hydrolase 2.

(2) Methyltransferases are enzymes that catalyze transmethylation in amino
 groups, hydroxyl groups and thiol groups. Examples include the following.

Catechol-O-methyltransferase
 20 Vitamin-N-methyltransferase
 Phenylethanolamine-N-methyltransferase
 Phosphatidylethanolamine-N-methyltransferase
 Nicotinamide-N-methyltransferase
 Acetylserotonin-O-methyltransferase
 25 Thiopurine S-methyltransferase

(3) N-acetyltransferases are enzymes that catalyze transacetylation in amino
 groups, sulfonamide groups and hydrazine groups. Examples include the following.

Arylamine-N-acetyltransferase 1, 2
 30 Arylalkylamine-N-acetyltransferase

N-acetyltransferase homologues of *saccharomyces cerevisiae*

LI intracellular adhesion molecules

(4) Sulfotransferases are enzymes that contribute to sulfate conjugation and catalyzes trans-sulfonylation in phenols, steroids, arylamines and biliary acid. Examples include the following.

Sulfotransferase 1A1, 1A2, 1A3, 1C1, 1C2, 2A1, 2B1

Thyroid hormone sulfotransferase

Tyrosyl protein sulfotransferase 1, 2

Sulfotransferase-opening protein 3

Estrogen sulfotransferase

Cerebroside sulfotransferase

HNK-sulfotransferase 1

Carbohydrate sulfotransferase 2, 4, 5

Carbohydrate sulfotransferase 1, 3

(5) Quinone oxidoreductases are enzymes that catalyze the reduction of quinones such as o-quinone and p-quinone. Examples include the following.

NAD(P)H: Quinone oxidoreductase 1

NRH: Quinone oxidoreductase 2

Quinone oxidoreductase homologues

p53-induced gene 3 (PIG3) of a quinone oxide transferase homologue

(6) Glutathione S-transferases are enzymes that catalyze the conjugation of glutathione. Examples include the following.

Glutathione S-transferase Mu1, Mu2, Mu3, Mu4, Mu5

Glutathione S-transferase Z (zeta)

Glutathione S-transferase P (pi)

Glutathione S-transferase 1 T1 (zeta)

Glutathione S-transferase 1 Theta 1, Theta 2

Microsomal Glutathione S-transferase 1
 Microsomal Glutathione S-transferase 1-1
 Microsomal Glutathione S-transferase 2, 3
 Microsomal Glutathione S-transferase Ha Subunit 1, 2
 5 Microsomal Glutathione S-transferase A3, A4
 Glutathione S-transferase A1, A4
 Glutathione S-transferase M1, M2, M3, M4

(7) UDP-glycosyltransferases are enzymes that catalyze the contribution of
 10 glucuronic acid to functional groups such as hydroxyl groups, carboxyl groups, amino
 groups and thiol groups after their introduction in the 1st drug metabolism route.

Examples include the following.

UDP-glycosyltransferase 1
 UDP-glycosyltransferase 1 Family Polypeptide A1
 15 UDP-glycosyltransferase 2 Family Polypeptide A1, B7, B10, B4, B11, B15, B17
 UDP-glycosyltransferase 8
 Dolichyl-diP-oligosaccharide protein glycosyl transferase

(8) Aldehyde dehydrogenases are enzyme that converts aldehydes into
 20 carboxylic acids. Examples include Aldehyde dehydrogenase 1 through 10.

Aldehyde dehydrogenase 1 family member A1, A2, A3
 Aldehyde dehydrogenase 1 family member B1
 Formyltetrahydroforate dehydrogenase
 Aldehyde dehydrogenase 2
 25 Aldehyde dehydrogenase 3 family member A1, A2
 Aldehyde dehydrogenase 3 family member B1, B2
 Aldehyde dehydrogenase 5 family member A1
 Aldehyde dehydrogenase 6 family member A1
 Aldehyde dehydrogenase 8 family member A1
 30 Aldehyde dehydrogenase 9 family member A1

(9) Alcohol dehydrogenases are enzymes that convert alcohols into aldehydes or ketones. Examples include the following.

Alcohol dehydrogenase 1 through 7

5 Hydroxy-CoA-dehydrogenase

Short-chain alcohol dehydrogenase family genes

(10) Esterases are enzymes that hydrolyze some esters. Examples include the following.

10 Arylacetoamide deacetylase

Granzyme A

Granzyme B

Interleukin 17

Ubiquitin carboxyl-terminal esterase L1, 3

15 Carboxyl esterase 1

Lipase A

Esterase D-formylglutathione hydrolase

Carboxylester lipase

Dolichyl-diphosphooligosaccharide-protein glycosyltransferase (DDOST)

20 Neuropathy target esterase

(11) Ubiquinone dehydrogenases (NDUF) are enzymes that support energy metabolism, *e.g.*, as in the mitochondrial respiratory chain. Examples include NADH ubiquinone dehydrogenase 1a Subunit 1 through 10.

25 NADH-dehydrogenase (ubiquinone)1 α -subcomplex 1 through 3 and 5 through 10

NADH-dehydrogenase (ubiquinone)1 α / β -subcomplex 1

NADH-dehydrogenase (ubiquinone)1 β -subcomplex 3, 5, 7

NADH-dehydrogenase (ubiquinone) Fe-S protein 1, 3, 4, 5, 6, 8

NADH-dehydrogenase (ubiquinone) flavoprotein 1 through 3

30

(12) Cytochrome P450s (CYPs) are enzymes that regulate 1st drug metabolism and introduce oxygen atoms to the drug. Examples include Cytochrome P450 (CYP) 1A1, CYP 1A2, CYP1B1, CYP 2A6, CYP 2B6, CYP 2C8, CYP 2C18, CYP 2C9, CYP 2C19, CYP 2E1, CYP 2D6, CYP 2E1, CYP 2F1, CYP 3A3, CYP 3A4, CYP 3A5, CYP 3A7, CYP 3A43, CYP 4A11, CYP 4B1, CYP 4F2, CYP 4F3, CYP 4F8, CYP 11B1, CYP 11B2, CYP 17, CYP 19, CYP 21A2, CYP 21A1, CYP 27B1 and CYP 27.

(13) ATP-binding cassettes absorb the drug and adjust the interstitial concentration with a transporter. Examples include the following.

- ATP-Binding Cassette Subfamily A Members 1 through 6, 8
- ATP-Binding Cassette Subfamily A Members 1, 4, 7, 8
- ATP-Binding Cassette Subfamily B Members 1 through 11
- ATP-Binding Cassette Subfamily B Members 1, 4, 7, 8, 9, 10, 11
- ATP-Binding Cassette Subfamily C Members 1 through 6, 8 through 10
- ATP-Binding Cassette Subfamily C Members 1, 2, 3, 4, 5, 7, 8, 9
- ATP-Binding Cassette Subfamily D Members 1 through 4
- ATP-Binding Cassette Subfamily D Members 1, 3, 4
- ATP-Binding Cassette Subfamily E Members 1
- ATP-Binding Cassette Subfamily F Members 1 through 3
- ATP-Binding Cassette Subfamily F Member 1
- ATP-Binding Cassette Subfamily G Members 1
- ATP-Binding Cassette Subfamily G Members 1, 2, 4, 8
- Organic anion transporters 1, 2, 3
- Organic anion transporter polypeptides 1, 2, 8
- Transporter 1 ATP-binding cassette subfamily B
- Transporter 2 ATP-binding cassette subfamily B
- SLC22A4 solute carrier family 22 (organic cation transporter) member 4
- SLC22A5 solute carrier family 22 (organic cation transporter) member 5
- SLC22A1 solute carrier family 22 (organic cation transporter) member 1
- SLC22A2 solute carrier family 22 (organic cation transporter) member 2

SLC10A2 solute carrier family 10 (sodium/bile acid cotransporter family)
member 2
SLC15A1 solute carrier family 15 (oligopeptide transporter) member 1

5 (14) Other enzymes include gamma glutamyl transferase 1, transglutaminase 1
and dihydropyrimidine dihydrogenase.

Genetic polymorphism data relating to DMEs can be obtained using any general
genetic polymorphism detection method. Examples include, but are not limited to, PCR
10 or other amplification methods, hybridization methods using an allele-specific
oligonucleotide matrix (e.g., TAQMAN PCR method, INVADER assay method), primer
extension reaction methods, sequencing methods, MALDI-TOF/MS methods and the
DNA chip methods (e.g., microarrays). Examples of detection methods that are
applicable to analysis of the DME associated polymorphisms of the present invention
15 include but are not limited to those listed below.

1. Direct sequencing Assays

In some embodiments of the present invention, variant sequences are detected
using a direct sequencing technique. In these assays, DNA samples are first isolated from
20 a subject using any suitable method. In some embodiments, the region of interest is
cloned into a suitable vector and amplified by growth in a host cell (e.g., a bacteria). In
other embodiments, DNA in the region of interest is amplified using PCR.

Following amplification, DNA in the region of interest (e.g., the region containing
the SNP or mutation of interest) is sequenced using any suitable method, including but
25 not limited to manual sequencing using radioactive marker nucleotides, or automated
sequencing. The results of the sequencing are displayed using any suitable method. The
sequence is examined and the presence or absence of a given SNP or mutation is
determined.

2. PCR Assay

In some embodiments of the present invention, variant sequences are detected using a PCR-based assay. In some embodiments, the PCR assay comprises the use of oligonucleotide primers that hybridize only to the variant or wild type allele (*e.g.*, to the region of polymorphism or mutation). Both sets of primers are used to amplify a sample of DNA. If only the mutant primers result in a PCR product, then the patient has the mutant allele. If only the wild-type primers result in a PCR product, then the patient has the wild type allele.

3. Fragment Length Polymorphism Assays

In some embodiments of the present invention, variant sequences are detected using a fragment length polymorphism assay. In a fragment length polymorphism assay, a unique DNA banding pattern based on cleaving the DNA at a series of positions is generated using an enzyme (*e.g.*, a restriction enzyme or a CLEAVASE I [Third Wave Technologies, Madison, WI] enzyme). DNA fragments from a sample containing a SNP or a mutation will have a different banding pattern than wild type.

a. RFLP Assay

In some embodiments of the present invention, variant sequences are detected using a restriction fragment length polymorphism assay (RFLP). The region of interest is first isolated using PCR. The PCR products are then cleaved with restriction enzymes known to give a unique length fragment for a given polymorphism. The restriction-enzyme digested PCR products are generally separated by gel electrophoresis and may be visualized by ethidium bromide staining. The length of the fragments is compared to molecular weight markers and fragments generated from wild-type and mutant controls.

b. CFLP Assay

In other embodiments, variant sequences are detected using a CLEAVASE fragment length polymorphism assay (CFLP; Third Wave Technologies, Madison, WI; *See e.g.*, U.S. Patent Nos. 5,843,654; 5,843,669; 5,719,208; and 5,888,780; each of which

SEQ ID NO:4590 n represents ct or deletion (Location 21).

(Northern) is isolated from a subject. The DNA or RNA is then cleaved with a series of restriction enzymes that cleave infrequently in the genome and not near any of the markers being assayed. The DNA or RNA is then separated (*e.g.*, on an agarose gel) and transferred to a membrane. A labeled (*e.g.*, by incorporating a radionucleotide) probe or probes specific for the SNP or mutation being detected is allowed to contact the membrane under a condition or low, medium, or high stringency conditions. Unbound probe is removed and the presence of binding is detected by visualizing the labeled probe.

b. Detection of Hybridization Using "DNA Chip" Assays

In some embodiments of the present invention, variant sequences are detected using a DNA chip hybridization assay. In this assay, a series of oligonucleotide probes are affixed to a solid support. The oligonucleotide probes are designed to be unique to a given SNP or mutation. The DNA sample of interest is contacted with the DNA "chip" and hybridization is detected.

In some embodiments, the DNA chip assay is a GeneChip (Affymetrix, Santa Clara, CA; *See e.g.*, U.S. Patent Nos. 6,045,996; 5,925,525; and 5,858,659; each of which is herein incorporated by reference) assay. The GeneChip technology uses miniaturized, high-density arrays of oligonucleotide probes affixed to a "chip." Probe arrays are manufactured by Affymetrix's light-directed chemical synthesis process, which combines solid-phase chemical synthesis with photolithographic fabrication techniques employed in the semiconductor industry. Using a series of photolithographic masks to define chip exposure sites, followed by specific chemical synthesis steps, the process constructs high-density arrays of oligonucleotides, with each probe in a predefined position in the array. Multiple probe arrays are synthesized simultaneously on a large glass wafer. The wafers are then diced, and individual probe arrays are packaged in injection-molded plastic cartridges, which protect them from the environment and serve as chambers for hybridization.

The nucleic acid to be analyzed is isolated, amplified by PCR, and labeled with a fluorescent reporter group. The labeled DNA is then incubated with the array using a

fluidics station. The array is then inserted into the scanner, where patterns of hybridization are detected. The hybridization data are collected as light emitted from the fluorescent reporter groups already incorporated into the target, which is bound to the probe array. Probes that perfectly match the target generally produce stronger signals than those that have mismatches. Since the sequence and position of each probe on the array are known, by complementarity, the identity of the target nucleic acid applied to the probe array can be determined.

In other embodiments, a DNA microchip containing electronically captured probes (Nanogen, San Diego, CA) is utilized (*See e.g.*, U.S. Patent Nos. 6,017,696; 6,068,818; and 6,051,380; each of which are herein incorporated by reference). Through the use of microelectronics, Nanogen's technology enables the active movement and concentration of charged molecules to and from designated test sites on its semiconductor microchip. DNA capture probes unique to a given SNP or mutation are electronically placed at, or "addressed" to, specific sites on the microchip. Since DNA has a strong negative charge, it can be electronically moved to an area of positive charge.

First, a test site or a row of test sites on the microchip is electronically activated with a positive charge. Next, a solution containing the DNA probes is introduced onto the microchip. The negatively charged probes rapidly move to the positively charged sites, where they concentrate and are chemically bound to a site on the microchip. The microchip is then washed and another solution of distinct DNA probes is added until the array of specifically bound DNA probes is complete.

A test sample is then analyzed for the presence of target DNA molecules by determining which of the DNA capture probes hybridize, with complementary DNA in the test sample (*e.g.*, a PCR amplified gene of interest). An electronic charge is also used to move and concentrate target molecules to one or more test sites on the microchip. The electronic concentration of sample DNA at each test site promotes rapid hybridization of sample DNA with complementary capture probes (hybridization may occur in minutes). To remove any unbound or nonspecifically bound DNA from each site, the polarity or charge of the site is reversed to negative, thereby forcing any unbound or nonspecifically

bound DNA back into solution away from the capture probes. A laser-based fluorescence scanner is used to detect binding,

In still further embodiments, an array technology based upon the segregation of fluids on a flat surface (chip) by differences in surface tension (ProtoGene, Palo Alto, CA) is utilized (*See e.g.*, U.S. Patent Nos. 6,001,311; 5,985,551; and 5,474,796; each of which is herein incorporated by reference). Protogene's technology is based on the fact that fluids can be segregated on a flat surface by differences in surface tension that have been imparted by chemical coatings. Once so segregated, oligonucleotide probes are synthesized directly on the chip by ink-jet printing of reagents. The array with its reaction sites defined by surface tension is mounted on a X/Y translation stage under a set of four piezoelectric nozzles, one for each of the four standard DNA bases. The translation stage moves along each of the rows of the array and the appropriate reagent is delivered to each of the reaction site. For example, the A amidite is delivered only to the sites where amidite A is to be coupled during that synthesis step and so on. Common reagents and washes are delivered by flooding the entire surface and then removing them by spinning.

DNA probes unique for the SNP or mutation of interest are affixed to the chip using Protogene's technology. The chip is then contacted with the PCR-amplified genes of interest. Following hybridization, unbound DNA is removed and hybridization is detected using any suitable method (*e.g.*, by fluorescence de-quenching of an incorporated fluorescent group).

In yet other embodiments, a "bead array" is used for the detection of polymorphisms (Illumina, San Diego, CA; *See e.g.*, PCT Publications WO 99/67641 and WO 00/39587, each of which is herein incorporated by reference). Illumina uses a BEAD ARRAY technology that combines fiber optic bundles and beads that self-assemble into an array. Each fiber optic bundle contains thousands to millions of individual fibers depending on the diameter of the bundle. The beads are coated with an oligonucleotide specific for the detection of a given SNP or mutation. Batches of beads are combined to form a pool specific to the array. To perform an assay, the BEAD

ARRAY is contacted with a prepared subject sample (e.g., DNA). Hybridization is detected using any suitable method.

c. Enzymatic Detection of Hybridization

5 In some embodiments of the present invention, hybridization is detected by enzymatic cleavage of specific structures (INVADER assay, Third Wave Technologies; *See e.g.*, U.S. Patent Nos. 5,846,717, 6,090,543; 6,001,567; 5,985,557; and 5,994,069; each of which is herein incorporated by reference). The INVADER assay detects specific DNA and RNA sequences by using structure-specific enzymes to cleave a complex
10 formed by the hybridization of overlapping oligonucleotide probes. Elevated temperature and an excess of one of the probes enable multiple probes to be cleaved for each target sequence present without temperature cycling. These cleaved probes then direct cleavage of a second labeled probe. The secondary probe oligonucleotide can be 5'-end labeled with a fluorescent dye that is quenched by a second dye or other quenching moiety.
15 Upon cleavage, the de-quenched dye-labeled product may be detected using a standard fluorescence plate reader, or an instrument configured to collect fluorescence data during the course of the reaction (*i.e.*, a "real-time" fluorescence detector, such as an ABI 7700 Sequence Detection System, Applied Biosystems, Foster City, CA).

The INVADER assay detects specific mutations and SNPs in unamplified
20 genomic DNA. In an embodiment of the INVADER assay used for detecting SNPs in genomic DNA, two oligonucleotides (a primary probe specific either for a SNP/mutation or wild type sequence, and an INVADER oligonucleotide) hybridize in tandem to the genomic DNA to form an overlapping structure. A structure-specific nuclease enzyme recognizes this overlapping structure and cleaves the primary probe. In a secondary
25 reaction, cleaved primary probe combines with a fluorescence-labeled secondary probe to create another overlapping structure that is cleaved by the enzyme. The initial and secondary reactions can run concurrently in the same vessel. Cleavage of the secondary probe is detected by using a fluorescence detector, as described above. The signal of the test sample may be compared to known positive and negative controls.

In some embodiments, hybridization of a bound probe is detected using a TAQMAN assay (PE Biosystems, Foster City, CA; *See e.g.*, U.S. Patent Nos. 5,962,233 and 5,538,848, each of which is herein incorporated by reference). The assay is performed during a PCR reaction. The TAQMAN assay exploits the 5'-3' exonuclease activity of DNA polymerases such as AMPLITAQ DNA polymerase. A probe, specific for a given allele or mutation, is included in the PCR reaction. The probe consists of an oligonucleotide with a 5'-reporter dye (*e.g.*, a fluorescent dye) and a 3'-quencher dye. During PCR, if the probe is bound to its target, the 5'-3' nucleolytic activity of the AMPLITAQ polymerase cleaves the probe between the reporter and the quencher dye. The separation of the reporter dye from the quencher dye results in an increase of fluorescence. The signal accumulates with each cycle of PCR and can be monitored with a fluorimeter.

In still further embodiments, polymorphisms are detected using the SNP-IT primer extension assay (Orchid Biosciences, Princeton, NJ; *See e.g.*, U.S. Patent Nos. 5,952,174 and 5,919,626, each of which is herein incorporated by reference). In this assay, SNPs are identified by using a specially synthesized DNA primer and a DNA polymerase to selectively extend the DNA chain by one base at the suspected SNP location. DNA in the region of interest is amplified and denatured. Polymerase reactions are then performed using miniaturized systems called microfluidics. Detection is accomplished by adding a label to the nucleotide suspected of being at the SNP or mutation location. Incorporation of the label into the DNA can be detected by any suitable method (*e.g.*, if the nucleotide contains a biotin label, detection is via a fluorescently labeled antibody specific for biotin).

5. Other Detection Assays

Additional detection assays that are produced and utilized using the systems and methods of the present invention include, but are not limited to, enzyme mismatch cleavage methods (*e.g.*, Variagenics, U.S. Pat. Nos. 6,110,684, 5,958,692, 5,851,770, herein incorporated by reference in their entireties); polymerase chain reaction; branched

hybridization methods (e.g., Chiron, U.S. Pat. Nos. 5,849,481, 5,710,264, 5,124,246, and 5,624,802, herein incorporated by reference in their entireties); rolling circle replication (e.g., U.S. Pat. Nos. 6,210,884 and 6,183,960, herein incorporated by reference in their entireties); NASBA (e.g., U.S. Pat. No. 5,409,818, herein incorporated by reference in its entirety); molecular beacon technology (e.g., U.S. Pat. No. 6,150,097, herein incorporated by reference in its entirety); E-sensor technology (Motorola, U.S. Pat. Nos. 6,248,229, 6,221,583, 6,013,170, and 6,063,573, herein incorporated by reference in their entireties); cycling probe technology (e.g., U.S. Pat. Nos. 5,403,711, 5,011,769, and 5,660,988, herein incorporated by reference in their entireties); Dade Behring signal amplification methods (e.g., U.S. Pat. Nos. 6,121,001, 6,110,677, 5,914,230, 5,882,867, and 5,792,614, herein incorporated by reference in their entireties); ligase chain reaction (Barnay Proc. Natl. Acad. Sci USA 88, 189-93 (1991)); and sandwich hybridization methods (e.g., U.S. Pat. No. 5,288,609, herein incorporated by reference in its entirety).

6. Mass Spectroscopy Assay

In some embodiments, a MassARRAY system (Sequenom, San Diego, CA.) is used to detect variant sequences (*See e.g.*, U.S. Patent Nos. 6,043,031; 5,777,324; and 5,605,798; each of which is herein incorporated by reference). DNA is isolated from blood samples using standard procedures. Next, specific DNA regions containing the mutation or SNP of interest, about 200 base pairs in length, are amplified by PCR. The amplified fragments are then attached by one strand to a solid surface and the non-immobilized strands are removed by standard denaturation and washing. The remaining immobilized single strand then serves as a template for automated enzymatic reactions that produce genotype specific diagnostic products.

Very small quantities of the enzymatic products, typically five to ten nanoliters, are then transferred to a SpectroCHIP array for subsequent automated analysis with the SpectroREADER mass spectrometer. Each spot is preloaded with light absorbing crystals that form a matrix with the dispensed diagnostic product. The MassARRAY system uses MALDI-TOF (Matrix Assisted Laser Desorption Ionization - Time of Flight) mass spectrometry. In a process known as desorption, the matrix is hit with a pulse from

a laser beam. Energy from the laser beam is transferred to the matrix and it is vaporized resulting in a small amount of the diagnostic product being expelled into a flight tube. As the diagnostic product is charged when an electrical field pulse is subsequently applied to the tube they are launched down the flight tube towards a detector. The time between
5 application of the electrical field pulse and collision of the diagnostic product with the detector is referred to as the time of flight. This is a very precise measure of the product's molecular weight, as a molecule's mass correlates directly with time of flight with smaller molecules flying faster than larger molecules. The entire assay is completed in less than one thousandth of a second, enabling samples to be analyzed in a total of 3-5 second
10 including repetitive data collection. The SpectroTYPER software then calculates, records, compares and reports the genotypes at the rate of three seconds per sample.

In some embodiments, the present invention provides an oligonucleotide comprising a DME related sequence, or a complement of a DME-related sequence. In preferred embodiments, an oligonucleotide of the present invention comprises a sequence
15 or a complement of a sequence selected from the group consisting SEQ ID NOs. 1-3360 and 3361-7669, or a substantially similar sequence.

In some embodiments, an oligonucleotide probe or oligonucleotide primer is created so the 5' terminus, 3' terminus or central base contains the genetic polymorphism site. In some preferred embodiments, an oligonucleotide is created comprising at least 13
20 contiguous bases of a sequence selected from SEQ ID NOs 1 through 3360 and 3361-7669, or the complement thereto, and further comprising the 21st nucleotide of the sequence selected from SEQ ID NOs 1 through 3360 and 3361-7669, or the complement thereto.

In some embodiments, an oligonucleotide of the present invention flanks or is
25 adjacent to a polymorphic site, such that the presence of the polymorphism can be detected by modification of the oligonucleotide in a manner dependent on the presence or absence of the polymorphism.

In some embodiments, the present invention provides kits comprising one or more of the components necessary for practicing the present invention. For example, the
30 present invention provides kits for storing or delivering the enzymes of the present

with a deleted base. In Sequence No. 674, n is VNTR and (cctgy)x, where x is an integer between 1 and 50, indicates a repeated sequence. The bases with numbers in parentheses indicate the number of times they are repeated. For example, "(T) 9-12" in Sequence No. 1552 (ABCB11 No. 55 in Table 1) indicates T is repeated 9 to 12 times.

5 Here, "position" indicates the position of the SNP genome. The position of SNPs in the 5' flanking region, intron region and 3' flanking region are intron base sequences counted as a single number starting at the exon-intron junction. The position of SNPs in the exon region are exon base sequences counted as a single number starting at the exon-intron junction. Also, (+) or no symbol indicates a number counted in the 3' upstream
10 direction and (-) indicates a number counted in the 5' downstream direction. The number in the "number" column indicates the position of the SNP in the gene maps of the various genes (FIG 9 through FIG 141 and FIG 144 through 312).

The sequence represented by the SEQ ID Nos. 1-3360 and 3361-7669 can readily be associated with the corresponding gene, chromosome, and chromosomal position.

15 Each of the genes shown in Table 1 correlates to a corresponding Figure in the present application. The Figures show a map of the gene with positional identifiers for each of the polymorphisms. The Figures also provide an accession number that correlates to public genome databases, allowing the genetic context of the polymorphism and the gene to be understood. Using the information in Table 1, the Figures, and public genome
20 databases, one skilled in the art is able to identify flanking sequences. This allows, for example, the development of PCR primers that flank the polymorphism. Considerations for PCR primer design are known in the art for both single PCR reactions and multiplex reactions (See e.g., Henegariu et al., BioTechniques 23:504-511 [1997] and PCR Applications, edited by Innis, Gelfand, and Sninsky, Academic Press, San Diego, CA
25 1999), each of which is herein incorporated by references in its entirety). Examples of primers that find use in the amplification of sequences containing polymorphisms, as well as amplification conditions, are found at the IMS-JST JSNP database website (See, submissions from Laboratory for Genotyping, The SNP Research Center, The Institute of Physical and Chemical Research (RIKEN)).

One example of information generated using SEQ ID Nos. 1-3360 and 3361-7669 and information in publicly available databases is provided in Figure 143. The first column in this figure shows that 3360 entries are made, corresponding to the first 3360 entries found in Table 1. The second column, entitled "GENE" provides a gene name abbreviation, while the next column provides a long gene name. The next columns show the chromosome (CHROM), a reference mRNA accession number (REF. MRNA), a locus link database accession number (L-LINK), an OMIM database accession number (OMIM_ID) which allows disease association information to be readily obtained, the exon count for the gene (EXONS), and the number of polymorphisms in the gene (NO GENE).

Creating an Oligonucleotide Probe or Oligonucleotide Primer

In some embodiments, an oligonucleotide used as a primer and/or probe in the detection method of the present invention serves as the template of the base sequences (Sequence No. 1 through 3360 and 3361 through 7669) shown in Table 1 if, for example, a SNP is to be detected. The primer/probe can be designed so it is synthesized as the base sequence itself or as a portion of the base sequence. In preferred embodiments, the SNP is included in the base sequence of the primer/probe (and denoted in capital letters in the base sequence column of Table 1). The primers/probes may also be complementary to the non-mutant sequence.

The SNP in the following example is designed so it is on the 3' or 5' end of the base sequence. It is designed to be within four bases of the 3' or 5' end, and ideally within two bases of the end. The SNP can also be in the center of the oligonucleotide base sequence. Here, "center" means the number of the bases from the SNP base to the 5' end is substantially equal to the number of bases from the SNP base to the 3' end. If there is an odd number of bases in the oligonucleotide, the central region should be essentially five bases in length, preferably three bases in length, and ideally one base in length. In a base sequence with 41 bases, for example, the central region should be bases 19 through 23, preferably bases 20 through 22, and ideally base 21. If there is an even number of bases, the central region should be four bases and ideally two bases. In a base sequence

of 40 bases, for example, the central region should be bases 19 through 22 and ideally base 20.

If the polymorphism consists of a plurality of bases, in some embodiments, the probe/primer is designed so the full polymorphism sequence is contained in the probe/primer. In some preferred embodiments, it is designed so one of the bases 1 through 4 on the 5' end or 3' end complementing the primer DNA corresponds to the base at the very end of the polymorphism bases. (This is called the "corresponding base"; ideally, it is the base at the 5' or 3' end). For example, in the INVADER assay, if a probe and INVADER oligonucleotide are prepared to detect a genetic polymorphism (CAGAGGCT) in No. 12 of NDUFA7 in Table 1 (Sequence No. 828), the position of the corresponding base in the probe in FIG 4a (a "T" base in the figure) is designed to become "C" at the far left of sequence CAGAGGCT, and the N base in the INVADER oligonucleotide shown in FIG 4b is designed to replace the "C" at the far left of CAGAGGCT with A, T, C or G). Conversely, if designed so the position of the corresponding base in the INVADER oligonucleotide is the far right "T" in CAGAGGCT, the "N" base is such that the corresponding base in the probe is "T." Further, the corresponding base of the INVADER oligonucleotide and the allele probe can be set anywhere in the CAGAGGCT sequence.

In preferred embodiments, the length of the base sequence is at least 13 bases, preferably between 13 and 60 bases, more preferably between 15 and 40 bases, and ideally between 18 and 30 bases. These oligonucleotide base sequences can be used as probes, as forward (sense) primers or as reverse (anti-sense) primers to detect target genes.

These oligonucleotides can link regions hybridized with genome DNA in tandem to unhybridized regions. The linking order can be upstream or downstream. The hybridized regions in these oligonucleotides can be designed from base sequence data containing the SNP described in Table 1, and created so the sequence containing the region hybridized with genome DNA closest to the 5' or 3' end is the SNP. These oligonucleotides can be used as probes to detect SNP using the INVADER assay.

The primer used in some embodiments of the present invention is designed to determine the functional change caused by the SNPs in the base sequences in Table 1, to determine whether the change is effective or ineffective, and to determine the existence of side effects. It is designed to include the SNP in the PCR-amplified base sequence. In some preferred embodiments, the primer should have at least 15 base sequences, preferably between 15 and 30 base sequences, and ideally between 18 and 24 base sequences. The template DNA regions in the primer base sequence should contain 500 bp or less amplified fragments, preferably between 100 and 300 bp fragments, and ideally between 100 and 150 bp fragments.

The oligonucleotide probes and primers designed in this manner can be synthesized chemically using any method commonly known in the art. For example, the oligonucleotides can be synthesized using a commercially available chemical synthesis device. The production of probes can be conducted automatically by adding fluorescent tags (e.g., FAM, VIC, Cy3) or other labels.

These oligonucleotides can be included in genetic polymorphism detection kits along with polymerase (e.g., Taq polymerase), a buffering solution (e.g., a Tris buffering solution), dNTP, fluorescent dyes (e.g., VIC, FAM), or other desired kit components.

Detection

In some embodiments, the oligonucleotides prepared in the examples above are used as primers/probes, and the genes or a portion thereof (template DNA) encoding the drug metabolizing enzyme is amplified using DNA polymerase. A primer/probe prepared in this manner can be hybridized with template DNA and used to detect DNA with the target genetic polymorphism. The DNA used as the template can be prepared using any method commonly known in the art. Examples include cesium chloride density gradient ultra centrifugation method, the SDS solvency method or the phenol chloroform extraction method.

1 **Detection Using PCR**

The amplification can be performed using a polymerase chain reaction (PCR). The DNA polymerase can be LA Taq DNA polymerase (Takara), Ex Taq polymerase (Takara), AMPLITAQ Gold polymerase (Applied Biosystems), AMPLITAQ (Applied Biosystems) or Pfu DNA polymerase (Stratagene), as well as other polymerases.

An illustrative example of amplification conditions is provided below. The present invention is not limited to the conditions provided in this example. In preferred embodiments, each cycle in the transforming phase should last between 10 and 40 seconds at 85°C to 105°C and preferably 20 and 30 seconds at 94°C, each cycle in the annealing phase should last 30 seconds to 1 minute at 50°C to 72°C and preferably 20 seconds to 1 minute at 60°C, and each cycle in the elongation phase should last 1 minute to 4 minutes between 65°C and 75°C and preferably 2 minutes to 3 minutes at 72°C. There should be 30 to 40 cycles, although fewer or more cycles are contemplated. In order to completely transform the template DNA and the primer, each cycle in the transforming phase should last 1 minute to 5 minutes at 95°C before the amplifying cycle. If AMPLITAQ GOLD polymerase manufactured by Applied Biosystems is used, it should last from 8 minutes to 15 minutes and ideally from 10 minutes to 12 minutes. In order to completely elongate the amplified DNA, the elongation phase should last between 1 minute and 10 minutes at 72°C after the amplification cycle. If the amplified product is not immediately detected, it should be processed again at 4°C to make sure the amplification was not irregular. In this way, the gene encoding the drug metabolizing enzyme is amplified.

After amplification, gel electrophoresis is performed on the amplified product, the amplified product is stained using ethidium bromide or SYBR Green, and one, two or three bands are detected in the amplified product (DNA fragments) to determine the portion (DNA fragment) of the drug metabolizing enzyme containing the genetic polymorphism in the gene encoding the drug metabolizing enzyme. Polyacrylamide gel electrophoresis or capillary electrophoresis can be performed instead of aerogel electrophoresis. PCR can be performed using a primer tagged with a fluorescent dye to detect the amplified product. A detection method that does not require electrophoresis

can also be used, such as bonding the amplified product in solid phase to a microplate and detecting the amplified product using a fluorescent or enzymatic reaction.

2. Detection Using the TAQMAN PCR Method

5 In the TAQMAN PCR method, the PCR reaction is performed using a fluorescent dye-tagged allele-specific oligo and Taq DNA polymerase. The allele-specific oligo used in the TAQMAN PCR method (TAQMAN probe) can be designed based on the SNP data. The 5' end of the TAQMAN probe is tagged using a fluorescent reporter dye R such as FAM or VIC, and the 3' end is tagged using a quencher Q (light-quenching
10 substance). (See FIG 1.). Here, the fluorescent light energy absorbed by the quencher is not detected. Because the 3' end of the TAQMAN probe is phosphorylated, there is no elongation reaction from the TAQMAN probe in the PCR reaction (FIG 1). However, a PCR reaction is performed on the TAQMAN probe with TaqDNA polymerase and a primer designed to amplify the region containing the SNP. The following reaction
15 occurs.

First, the TAQMAN probe is hybridized in a specific sequence of template DNA (FIG 2a) and an elongation reaction is simultaneously performed from the PCR primer (FIG 2b). Because the Taq DNA polymerase has 5' nuclease activity, the hybridized TAQMAN probe is severed as the PCR primer elongation reaction continues. When the
20 TAQMAN probe is severed, the quencher has no effect on the fluorescent dye, and the fluorescent light is detected (FIG 2c).

For example, suppose there is an A allele (Allele 1) and a G allele (Allele 2) at the SNP position as shown in FIG 3. Allele 1 is tagged by a specific TAQMAN probe with FAM and Allele 2 is tagged by a specific TAQMAN probe with VIC (see FIG 3). Two
25 different allele-specific oligos are added to the PCR drug, and TAQMAN PCR is performed on the detected template. The fluorescence detector then detects the fluorescent intensity of the FAM and VIC. When the SNP position in the allele and the position corresponding to the SNP in the TAQMAN probe are complementary, the probe is hybridized with the allele, the fluorescent dye in the probe is severed by the Taq

polymerase, the effect of the quencher is eliminated, and the intensity of the fluorescence is detected.

If the template is homozygous for Allele 1, strong FAM fluorescence is detected and hardly any VIC fluorescence is detected. If the template is heterozygous for Allele 1
5 and Allele 2, both FAM and VIC fluorescence are detected.

3. SNP Detection Using the INVADER assay

In the INVADER assay, an allele-specific oligo and the template are hybridized to detect the SNP. In the INVADER assay, two different non-tagged oligos and one
10 fluorescent dye-tagged oligo are used. One of the two non-tagged oligos is known as the probe. In some embodiments, the probe has a region hybridized to the genome DNA (template DNA) and a region (called a flap) that is not hybridized with the genome DNA, and that has a sequence unrelated to the sequence of the genomic DNA. The hybridized region has base sequences corresponding to the SNP (FIG 4a). The flap sequence is
15 complementary to a FRET probe (described below). The other of the two non-tagged oligos is called the INVADER oligonucleotide. This oligonucleotide is designed so that it is hybridized in complementary fashion from the SNP position towards the 3' end of the genome DNA (FIG 4b). In some preferred embodiments, the sequence corresponding to the SNP position can be any base (denoted by N in FIG 4b). When the template DNA
20 genome is hybridized with the two probes, the base (N) from the INVADER oligonucleotide is inserted in the SNP position (FIG 4c) forming a cleavage structure at the SNP position.

In some embodiments, the fluorescent dye-tagged oligonucleotide is a sequence completely unrelated to the alleles. This probe is a FRET (fluorescence resonance energy
25 transfer) probe (FIG 5). The fluorescent dye R tags the base (reporter) at the 5' end of the FRET probe. A quencher Q absorbs the fluorescence. Here, the quencher absorbs the fluorescent light and the light is not detected. A specific region (Region 1) is designed on the 5' end of the FRET probe (reporter base) to face the 3' end from Region 1 (This region is Region 2). As a result, Region 1 and Region 2 form a complementary duplex

(FIG 5). The 3'-region from the regions forming the complementary duplex can be hybridized with the flap of the allele probe to form a complementary chain (FIG 5).

In the INVADER assay, a cleavage agent (e.g., CLEAVASE enzyme, Third Wave Technologies, Madison, WI) is used, which is an enzyme (5' nuclease) with specific
5 endonuclease activity for identifying and cleaving a specific DNA structure. When the genome DNA, the probe and the INVADER oligonucleotide form a cleavage structure at the SNP position, the cleavage agent severs 3' of the SNP position on the allele probe. The section with three bases forming a flap with the 5' end is identified as shown in FIG 4c, and the flap is severed. The structure with the SNP position is identified by the
10 cleavage agent (FIG 6a), the probe is severed at the flap position, and the flap is separated (FIG 6b). Next, the released flap from the probe bonds with the FRET probe in complementary fashion to form a duplex (FIG 6c). The cleavage agent identifies this structure and cleaves the section with the fluorescent dye. The cleaved fluorescent dye is no longer affected by the quencher and fluorescent light becomes detectable (FIG 6d). If
15 the SNP position does not match the sequence corresponding to the SNP in the allele probe as shown in FIG 7, the specific DNA structure is not identified by the cleavage agent, the probe is not severed, and fluorescent light is not detected.

When the SNP is T/C, for example, a T INVADER oligonucleotide, a T probe, a FRET probe with FAM bonded to the reporter for the T SNP, a C INVADER
20 oligonucleotide, a C probe and a FRET probe with VIC bonded to the reporter for the C SNP are prepared. These are combined and SNP detection is performed. If there is a T/T homo, FAM fluorescence is generated. If there is a C/C homo, VIC fluorescence is detected. If there is a T/C hetero, both FAM and VIC fluorescence are detected. Because the FAM and VIC fluorescence wavelengths are different, both can be readily identified.

Detection Using the SniPer Method

In order to detect SNP using the SniPer method, an allele identifier is amplified using RCA. The genome DNA template is a straight chain, and a probe is hybridized with the genome DNA. When there is a complementary match between the probe
30 sequence and the genome DNA template sequence and a complementary chain forms, a

ligation reaction on the genome DNA forms a ring. As a result, RCA continues on cyclic DNA. If the end of the probe does not match the genome DNA, the RCA reaction does not occur because there is no ligation and no ring. In the SniPer method, therefore, a single chain probe is designed to anneal the genome DNA and create a ring. This single chain probe is called a padlock probe. The severed end of the padlock probe is the sequence corresponding to the target SNP. The padlock probe and the genome DNA mix and a ligation reaction occurs. If the severed end of the padlock probe and the SNP section of the genome DNA are complementary, the severed end of the padlock probe connects and forms a ring during the ligation reaction. If they are not complementary, a ring does not form. Therefore, only a padlock probe corresponding to the target SNP forms a ring and is amplified by the DNA polymerase. The presence of amplification is used to detect the SNP. A synthetic oligonucleotide with a hairpin structure and a fluorescent dye and quencher on both ends can be used in the detection process.

Detection Using the MALDI-TOF/MS Method

In the matrix assisted laser desorption-time of flight/mass spectroscopy (MALDI-TOF/MS) method, SNP typing is performed using a mass spectrometer. A preferred embodiment of this method has the following steps.

(i) PCR Amplification and Refinement of DNA Fragments Containing SNP

After making sure the base at the SNP location and the PCR primer do not overlap, the DNA fragment is amplified, exonuclease or alkali phosphatase processing is performed on the amplified product, the dNTP is removed, and the amplified fragment is refined.

(ii) Primer Extension Reaction (Thermal Cycle) and Refinement

A primer ten or more times the template in the region identified as the PCR product is added, a thermal cycle reaction is performed, and a primer elongation reaction is performed. The primer used here is designed so the 3' end is next to the base corresponding to the SNP position. The primer length should be 15 to 30 bases, ideally 20 to 25 bases. If there is a multiplex reaction, a sequence that is not complementary to

the template is added to the 5' end. There should be 20 to 30 (ideally 25) thermal cycles at two different temperatures. These should be 85 to 105°C (ideally 94°C) and 35 to 40°C (ideally 37°C).

The reaction product is then refined using a refining kit so it can be used in the mass spectrometer.

(iii) Mass Spectroscopy Using a Mass Spectrometer

The elongated and refined reaction product is applied to the mass spectrometer, and a quality of the target product is measured. In other words, the refined product is mixed with the matrix and 0.5 to 1.0 mL spots are formed on the MALDI plate. After drying the plate, the substance is irradiated by a laser beam and a spectrogram is produced.

Detection Using the Base Sequence Determining Method

In the present invention, a polymorphism can be detected using an elongation reaction on a single base. In other words, four different types of dideoxynucleotides identified by different fluorescent compounds are added to reaction systems including the gene to be detected and a single base elongation reaction is performed. Here, the base to be elongated is the polymorphism. Two reactions are performed; one to stop the DNA synthesis and another to identify the 3' end of the DNA molecule with fluorescence.

Electrophoresis is performed on four different reaction solutions with the same lanes and capillaries for the sequencing gel. The sequence is determined by detecting the differences in the fluorescent dyes identifying the DNA bands using a fluorescence detector. The oligonucleotides with one base elongated have the elongation confirmed using different types of fluorescent dyes in a fluorescence detector and mass spectrometer. Instead of fluorescent-tagged dideoxynucleotides, the primer can be identified using fluorescence used with non-tagged dideoxynucleotides.

Drug Evaluation

Using information obtained by the methods of the present invention, the efficacy and stability of the drug metabolized by the drug metabolizing enzyme can be evaluated.

For example, in some embodiments, the drug can be evaluated using a typing system. In other words, the frequency of expressed and unexpressed alleles (e.g., toxic alleles that cause undesired side effects) can be compared using any one of the detection methods mentioned above. Once they have been compared, markers can be selected to indicate, for example, a toxic expression where the allele frequency differs. In statistical analysis, this is usually set as x2. However, this is different in other methods such as the Fisher method. The active components (altered and metabolized drug components) in the drug will be reflected in blood and tissue concentrations. All of the genetic polymorphisms can be checked against the causes of the toxic effects to isolate specific correlating genetic polymorphisms. The substances corresponding to the probes or primers used to analyze all of the genetic polymorphisms are prepared beforehand on reaction plates, cards or glass plates, and unprepared human genome DNA is added and reacted to determine the allele pattern. If there are genetic polymorphisms correlating with toxicity or other phenotypes, then human side-effects can be expected or predicted. The same is true of drug effectiveness. Because the genetic polymorphisms correlating to effectiveness and side-effects differ depending on the drug, typing performed using genetic polymorphisms can be performed to anticipate effectiveness and side-effects.

Differences in allele frequency can be determined in certain instances by comparing the frequency of genetic polymorphisms to effectiveness/ineffectiveness or the presence/absence of side-effects. If, for example, an SNP analysis is performed on persons with a toxic reaction (side-effect) to Drug A, the results may show a 90% of the people have T/T (e.g., detected based on the intensity of fluorescent FAM light). The same results may show 10% of people with no toxic reaction have a T/T and 90% have a C/C. As a result of the SNP analysis, the evaluation may be not to administer Drug A to persons with T/T.

Drug Screening

In the present invention, the genetic polymorphism data obtained as described above is compared to genetic polymorphism data from genes encoding certain drug metabolizing enzymes to indicate the safety and effectiveness of drugs metabolized by

these drug metabolizing enzymes. Therefore, the genetic polymorphism data obtained using the method of the present invention can be used to determine the likely effectiveness of certain drug therapies and to select the appropriate drug.

The evaluation methods described above can be used. Genetic polymorphisms with correlations to side-effects and effectiveness are said to be influenced by the activation, transfer and translation of certain enzymes. The cause and effect relationship with the side-effect or effectiveness expression mechanism may be indirect. The metabolization of drugs is being studied by pharmaceutical companies in laboratory and clinical testing. If there are genetic polymorphisms in enzyme genes correlating with severe side-effects, they can be removed and used under different conditions. The same is true of effectiveness. Drugs can be screened, therefore, using side-effects and effectiveness data. A wide variety of conditions and diseases (See e.g., Physician's Desk Reference) benefit from analysis using the systems and methods of the present invention.

In some embodiments of the present invention, a sample is taken from a subject (e.g., by a drug company) and sent to a laboratory for analysis using a detection assay. The laboratory results (e.g., detection assay test result data) is returned to the party providing the sample such that an appropriate decision can be made, including, but not limited to, development or administration of a drug to a subject.

In clinical testing (Tests I through III), the frequency of the expression of genetic polymorphisms can be studied in volunteers exhibiting certain side-effects and volunteers not exhibiting the same side-effects to a drug. In this way, novel genetic polymorphisms correlating with side-effects and effectiveness can be detected. This information can be used to screen drugs. Exemplary drugs and drug-related data and other information that find use in or with the present invention, including but are not limited to the methods and databases described herein, are described in the PHYSICIANS' DESK REFERENCE (PDR). (e.g., 2002 Edition, Medical Economics Company, Inc., Montvale, NJ). The PDR is expressly incorporated by reference herein as if fully set forth.

EXPERIMENTAL EXAMPLES

The following examples are provided in order to demonstrate and further illustrate certain preferred embodiments and aspects of the present invention and are not to be construed as limiting the scope thereof.

5

Example 1 Obtaining SNP Data

(1) DNA Extraction

10 Blood was extracted from 48 unrelated people in the presence of EDTA. The DNA was extracted in the following way based on the method in the Genome Analysis Manual (Yusuke Nakamura ed., Springer-Verlag Tokyo).

Ten milliliters of blood was transferred to a 50 ml test tube and centrifuged for five minutes at room temperature and 3000 rpm. After the supernatant (blood serum) had
15 been removed using a pipette, 30 ml of RBC-dissolving buffer (10 mM NH_4HCO_3 , 144 mM NH_3Cl) was added. After mixing until there was no sediment, it was allowed to stand for 20 minutes at room temperature. After being centrifuged for five minutes at room temperature and 3000 rpm, the supernatant (blood serum) was again removed using a pipette to obtain white blood cells. Another 30 ml of RBC-dissolving buffer was added and the process was repeated twice. Then, 4 ml of proteinase K buffer [50 mM Tris-HCl (pH 7.4), 100 mM NaCl, 1 mM EDTA (pH 8.0)] was added to the white blood cells, 200 ml of SDS was added, 200 ml of 10 mg/ml proteinase K was added, and the solution was
20 tumble-mixed. The solution was then allowed to stand overnight at 37°C. The next day, 4 ml of phenol was added, and the solution was slowly tumble-mixed for four hours using a Taitec T-50 Rotator. After being centrifuged for 10 minutes at room temperature and 3000 rpm, the supernatant was removed using a new tube. Then, 4 ml of phenol-chloroform-isoamylalcohol (volume ratio 25:24:1) was added, the solution was tumble-mixed for two hours in the manner described above, and the solution was centrifuged. The supernatant was removed using a new tube, 4 ml of chloroform-isoamylalcohol
25 (volume ratio 24:1) was added, and the solution was tumble-mixed. Fibrous white
30

precipitate (DNA) was removed using a 2 ml tube, 1 ml of 70% ethanol was added, and the solution was tumble-mixed. The DNA was transferred to a new tube, dried and dissolved in 500 ml of TE solution [10 mM Tris-HCl (pH 4.7), 1 mM EDTA (pH 7.4)] to obtain a genome DNA sample.

(2) PCR

A genome sequence was obtained from the GenBank DNA Database. After removing the repeating sequences using the RepMask computer program, the PCR primer was set so there would be approximately 1 kb of PCR product. The genome DNA from 48 unrelated people was prepared at the same concentration. After mixing the same amount of DNA from three people in a single tube, 60 ng was used in the PCR. The PCR was Ex-Taq (Takara 2.5 U) and performed using the GeneAmp PCR System 9700 (PE Applied Biosystems). After reacting for two hours at 94°C, denaturing was performed for 30 seconds at 96°C, annealing was performed for 30 seconds at 55°C or 60°C, and elongation was performed for one minute at 72°C in each cycle. There were 35 cycles.

(3) Sequence

After refining the PCR product using ArrayIt (Telechem), the sequence reaction was performed using the BigDye Terminator RR Mix (PE Applied Biosystems). After reacting for two hours at 96°C, denaturing was performed for 20 seconds at 96°C, annealing was performed for 30 seconds at 50°C, and elongation was performed for 4 minutes at 60°C in each cycle using the GeneAmp PCR System 9700 (PE Applied Biosystems). There were 25 cycles. After the sequencing reaction, the sequencing was analyzed using the ABI Prism 3700 DNA Analyzer.

(4) SNP Detection

An analysis was performed on the SNP detection using the PolyPhred computer program (Nickerson et al., 1997, Nucleic Acid Res., 25, 2745-2751).

(5) Results

The SNP results shown in Table 1 were obtained. The analyzed drug metabolizing enzyme, the abbreviation of the enzyme, the databank (GenBank) accession number, the structure of the gene for the drug metabolizing enzyme, and the position of the SNPs are shown in FIG 9 through FIG 141 and FIG 144 through 312. In FIG 9

through FIG 141 and FIG 144 through 312, the exons are blank boxes or black lines in the genes denoted by the horizontal lines. The position of the SNPs is denoted above the genes with solid lines and numbers.

5

Example 2

Typing

Typing was performed on two different groups of patients using the INVADER assay. In FIG 142, the x-axis (Allele 1) indicates the intensity of the FAM fluorescent light corresponding to T, and the x-axis (Allele 2) indicates the intensity of the VIC fluorescent light corresponding to C. The slanted line indicates the SNP pattern for T/T, the black circles denote the pattern for C/C, and the white circles denote the pattern for T/C. The black squares indicate the background values. The x marks indicate where the detection failed. The group of patients in the graph for panel A (top) had many C/C SNP patterns and the group of patients in the graph for panel B (bottom) had many T/T SNP patterns.

15

Example 3

SNP Detection

20

Genome DNA was extracted from five unrelated people using the method described in Example 1, and the SNPs in three different drug metabolizing enzyme genes (EPHX1, ABCB2, AANAT) were detected using the INVADER assay method. The INVADER oligonucleotides and probes were designed using base sequence No. 3 (Sequence No. 49) and No. 17 (Sequence No. 63) in the case of EPHX1, base sequence No. 4 (Sequence No. 4) and No. 11 (Sequence No. 11) in the case of ABCB2, and base sequence No. 3 (Sequence No. 561) in the case of AANAT. The positions of the SNPs are shown in Table 1.

25

30 The results are shown in Table 2.

Table 2

Drug Metabolizing Enzyme Gene	EPHX1		ABCB2		AANAT
	No. 3	No. 17	No. 4	No. 11	No. 3
	Seq. No. 49	Seq. No. 63	Seq. No. 4	Seq. No. 11	Seq. No. 561
SNP	(T/G)	(A/G)	(G/T)	(G/A)	(T/A)
Subject I	T/T	A/G	T/T	G/A	T/T
Subject II	T/T	A/A	G/G	G/G	T/A
Subject III	T/G	A/A	G/G	A/A	T/T
Subject IV	G/G	A/G	G/T	G/G	T/T
Subject V	T/G	A/G	G/T	G/A	T/A

As shown in Table 2, the SNPs in the drug metabolizing genes of patients can be detected and the patterns determined using the method of the present invention.

Example 4

Correlation between SNP genotypes and optimal amounts of a medicament for treatment validity and safety

In this example, validity and safety of medicaments were investigated using SNP analysis.

Thiopurine S-methyltransferase (TPMT) is an enzyme that transfers a methyl group to a sulfur atom attached to a purine ring, and is one of the major enzymes for metabolizing drugs such as the anti-cancer agents 6-mercaptopurine and 6-thioguanine, and thiopurine derivatives such as the immunosuppressive agent azathioprine. This example shows a correlation between optimal amounts of azathioprine and various combinations of the alleles at the 868th SNP of intron 3 of TPMT (Seki, *et al.*, J Hum Genet 45(5):299 [2000], incorporated by reference herein in its entirety; Accession No. AB045146.1) (G or T alleles) and the 2682nd SNP of intron 3 (C or A alleles)(Table 3 and Table 4).

Table 3

868	2682	High	Low
TT	AA	2	0
TT	AT	3	0
TT	TT	1	0
GT	AA	0	2
GT	AT	1	7
GT	TT	4	1
GG	AA	1	0
GG	AT	0	1
GG	TT	1	0

Optimal amounts of azathioprine were determined by adopting suppression of rejection after renal transplantation as an index. A group of patients in which the validity of treatment with 100 mg/day of azathioprine was confirmed was designated as a high dose group, and a group of patients in which side effects developed with treatment of 100 mg/day, but in which validity was confirmed with a treatment of 50 mg/day was designated as a low dose group. Table 3 indicates the number of patients having each combination of alleles, with the columns labeled “High” and “Low” representing the numbers of patients of each genotype in the high dose and the low dose groups, respectively. Side effects include leukopenia, anthema, angiitis, nausea/vomiting, anorexia, diarrhea, malaise, myalgia, arthralgia, fever, chill, and dizziness. More serious side effects include, for example, blood disorders, shock-like symptoms, infectious diseases, and hepatic disorders, and renal disorders.

Investigation of a correlation between the high dose and low dose groups and the two types of SNPs indicated above revealed that when G is present in at least one allele at the 868th SNP of intron 3 (G/G homozygous or G/T heterozygous) and A is present in at least one allele at the 2682nd SNP of intron 3 (A/A homozygous or A/T heterozygous),

side effects were developed with 100 mg/day and 50 mg/day was an optimal amount for 10 out of 12 patients (low dose group), while 100 mg/day was an optimal amount for 11 out of 12 patients with other allele combinations (high dose group) (Table 4).

Investigation of this combination of two SNP loci in patients enables prediction of

- 5 optimal amounts of azathioprine for treatment prior to the administration of the drug, for improved validity and safety. These results indicate that the validity and safety of medicaments can be predicted using analysis of SNPs associated with medicament metabolic enzymes, *e.g.*, as described in this specification and including but not limited to the DME-associated SNPs listed in Table 1. As used in this example only, the term
- 10 "optimal amount" refers to the best dosage selected from the tested amounts of 50 mg/day or 100/mg per day. It will be appreciated by those skilled in the art that a study testing additional amounts of a medicament (*e.g.*, a study in which amounts are varied in smaller increments, such as 40, 50, 60, 70, 80, 90, etc. mg/day) would provide additional information regarding ranges of amounts giving optimal performance for patients having
- 15 a particular genotype, and that optimal amounts of this or any other medicament are not limited to the particular amounts of 50 or 100 mg/day tested in this example.

Table 4

Genotype	Optimal amount	
	100 mg/day	50 mg/day
G as the 868 th SNP and A as the 2682 nd	2	10
Other combinations	11	1

(Fisher exact test: $p=0.0003$)

Sequence Listing Free Text

- SEQ ID NO:39: n indicates t (Position 21).
- 5 SEQ ID NO:64: n indicates c (Position 21).
- SEQ ID NO:580: n indicates a or deletion (Position 21).
- SEQ ID NO:634: n indicates a or deletion (Position 21).
- SEQ ID NO:656: n indicates a or deletion (Position 21).
- SEQ ID NO:658: n indicates c or deletion (Position 21).
- 10 SEQ ID NO:671: n indicates a or deletion (Position 21).
- SEQ ID NO:672: n indicates g or deletion (Position 21).
- SEQ ID NO:673: n indicates c or deletion (Position 21).
- SEQ ID NO:674: n indicates (cctgy)x or deletion (Position 21).
- SEQ ID NO:676: n indicates gaa or deletion (Position 21).
- 15 SEQ ID NO:677: n indicates ag or deletion (Position 21).
- SEQ ID NO:785: n indicates ta. (Position 21).
- SEQ ID NO:797: n indicates acac. (Position 21).
- SEQ ID NO:806: n indicates gatttggtatccag. (Position 21).
- SEQ ID NO:808: n indicates ag or deletion (Position 21).
- 20 SEQ ID NO:809: n indicates ta or deletion (Position 21).
- SEQ ID NO:815: n indicates t (Position 21).
- SEQ ID NO:828: n indicates cagagct (Position 21).
- SEQ ID NO:830: n indicates ca or deletion (Position 21).
- SEQ ID NO:831: n indicates ag or deletion (Position 21).
- 25 SEQ ID NO:843: n indicates gtaaa (Position 21).
- SEQ ID NO:845: n indicates a (Position 21).
- SEQ ID NO:888: n indicates tc (Position 21).
- SEQ ID NO:890: n indicates t or deletion (Position 21).
- SEQ ID NO:913: n indicates t or deletion (Position 21).
- 30 SEQ ID NO:932: n indicates t or deletion (Position 21).

SEQ ID NO:933: n indicates t or deletion (Position 21).

SEQ ID NO:955: n indicates at or deletion (Position 21).

SEQ ID NO:956: n indicates a or deletion (Position 21).

SEQ ID NO:957: n indicates c or deletion (Position 21).

5 SEQ ID NO:987: n indicates c (Position 21).

SEQ ID NO:999: n indicates gtt or deletion (Position 21).

SEQ ID NO:1164: n indicates at (Position 21).

SEQ ID NO:1166: n indicates c or deletion (Position 21).

SEQ ID NO:1167: n indicates t or deletion (Position 21).

10 SEQ ID NO:1168: n indicates t or deletion (Position 21).

SEQ ID NO:1169: n indicates g (Position 21).

SEQ ID NO:1171 n indicates c (Position 21).

SEQ ID NO:1173: n indicates t (Position 21).

SEQ ID NO:1175: n indicates c or deletion (Position 21).

15 SEQ ID NO:1200: n indicates a or deletion (Position 21).

SEQ ID NO:1204: n indicates a (Position 21).

SEQ ID NO:1207: n indicates tt (Position 21).

SEQ ID NO:1210: n indicates at (Position 21).

SEQ ID NO:1245: n indicates t (Position 21).

20 SEQ ID NO:1248: n indicates t or deletion (Position 21).

SEQ ID NO:1249: n indicates t (Position 21).

SEQ ID NO:1251: n indicates a or deletion (Position 21).

SEQ ID NO:1252: n indicates tgt or deletion (Position 21).

SEQ ID NO:1260: n indicates t or deletion (Position 21).

25 SEQ ID NO:1309: n indicates a or deletion (Position 21).

SEQ ID NO:1389: n indicates g or deletion (Position 21).:

SEQ ID NO:1411: n indicates a or deletion (Position 21).

SEQ ID NO:1417: n indicates aaag (Position 21).

SEQ ID NO:1424: n indicates gtg or deletion (Position 21).

30 SEQ ID NO:1426: n indicates gg or tgggtgggtgga (Position 21).

- SEQ ID NO:1429: n indicates at or deletion (Position 21).
 SEQ ID NO:1436: n indicates a (Position 21).
 SEQ ID NO:1453: n indicates c or deletion (Position 21).
 SEQ ID NO:1456: n indicates gg (Position 21).
 5 SEQ ID NO:1465: n indicates gtc or deletion (Position 21).
 SEQ ID NO:1487: n indicates t or deletion (Position 21).
 SEQ ID NO:1494: n indicates tt (Position 21).
 SEQ ID NO:1497: n indicates t repeated 9 to 12 times (Position 21).
 SEQ ID NO:1499: n indicates a or deletion (Position 21).
 10 SEQ ID NO:1501: n indicates a repeated 10 to 13 times (Position 21).
 SEQ ID NO:1504: n indicates ct or deletion (Position 21).
 SEQ ID NO:1507: n indicates cagatcttctcagctaatttagaaatgt (Position 21).
 SEQ ID NO:1533: n indicates a or deletion (Position 21).
 SEQ ID NO:1540: n indicates c (Position 21).
 15 SEQ ID NO:1545: n indicates t (Position 21).
 SEQ ID NO:1552: n indicates t repeated 9 to 12 times (Position 21).
 SEQ ID NO:1555: n indicates t (Position 21).
 SEQ ID NO:1557: n indicates aaaaaaagaaaa (Position 21).
 SEQ ID NO:1558: n indicates aaaaaaaaaa (Position 21).
 20 SEQ ID NO:1559: n indicates aaaaaaaaaa (Position 21).
 SEQ ID NO:1563: n indicates t or deletion (Position 21).
 SEQ ID NO:1572: n indicates c (Position 21).
 SEQ ID NO:1574: n indicates a or deletion (Position 21).
 SEQ ID NO:1575: n indicates c or deletion (Position 21).
 25 SEQ ID NO:1596: n indicates cct or deletion (Position 21).
 SEQ ID NO:1598: n indicates tc (Position 21).
 SEQ ID NO:1616: n indicates ca or deletion (Position 21).
 SEQ ID NO:1638: n indicates g (Position 21).
 SEQ ID NO:1661: n indicates t or deletion (Position 21).
 30 SEQ ID NO:1690: n indicates gccag (Position 21).

- SEQ ID NO:1718: n indicates t (Position 21).
- SEQ ID NO:1723: n indicates c or deletion (Position 21).
- SEQ ID NO:1729: n indicates tc or deletion (Position 21).
- SEQ ID NO:1740: n indicates ct or deletion (Position 21).
- 5 SEQ ID NO:1771: n indicates a (Position 21).
- SEQ ID NO:1781: n indicates a or deletion (Position 21).
- SEQ ID NO:1787: n indicates t or deletion (Position 21).
- SEQ ID NO:1791: n indicates t or deletion (Position 21).
- SEQ ID NO:1792: n indicates g or deletion (Position 21).
- 10 SEQ ID NO:1800: n indicates t or deletion (Position 21).
- SEQ ID NO:1801: n indicates t or deletion (Position 21).
- SEQ ID NO:1802: n indicates a or deletion (Position 21).
- SEQ ID NO:1815: n indicates a or deletion (Position 21).
- SEQ ID NO:1819: n indicates ca or deletion (Position 21).
- 15 SEQ ID NO:1820: n indicates t or deletion (Position 21).
- SEQ ID NO:1824: n indicates t or deletion (Position 21).
- SEQ ID NO:1829: n indicates t or deletion (Position 21).
- SEQ ID NO:1830: n indicates c or deletion (Position 21).
- SEQ ID NO:1838: n indicates a or deletion (Position 21).
- 20 SEQ ID NO:1840: n indicates t or deletion (Position 21).
- SEQ ID NO:1847: n indicates gatt or deletion (Position 21).
- SEQ ID NO:1848: n indicates t (Position 21).
- SEQ ID NO:1853: n indicates t or deletion (Position 21).
- SEQ ID NO:1854: n indicates gt (Position 21).
- 25 SEQ ID NO:1857: n indicates a or deletion (Position 21).
- SEQ ID NO:1858: n indicates a or deletion (Position 21).
- SEQ ID NO:1862: n indicates t or deletion (Position 21).
- SEQ ID NO:1865: n indicates at or deletion (Position 21).
- SEQ ID NO:1871: n indicates a or deletion (Position 21).
- 30 SEQ ID NO:1874: n indicates t or deletion (Position 21).

- SEQ ID NO:1877: n indicates at or deletion (Position 21).
 SEQ ID NO:1878: n indicates a or deletion (Position 21).
 SEQ ID NO:1879: n indicates t repeated 12 to 14 times (Position 21).
 SEQ ID NO:1882: n indicates t or deletion (Position 21).
 5 SEQ ID NO:1884: n indicates cac or deletion (Position 21).
 SEQ ID NO:1891: n indicates cca (Position 21).
 SEQ ID NO:1919: n indicates t or deletion (Position 21).
 SEQ ID NO:1949: n indicates c or deletion (Position 21).
 SEQ ID NO:1957: n indicates aaaa or deletion (Position 21).
 10 SEQ ID NO:1970: n indicates c or deletion (Position 21).
 SEQ ID NO:1980: n indicates t repeated 7 to 9 times (Position 21).
 SEQ ID NO:1981: n indicates a or deletion (Position 21).
 SEQ ID NO:1993: n indicates taac or deletion (Position 21).
 SEQ ID NO:1994: n indicates ctcttt (Position 21).
 15 SEQ ID NO:1995: n indicates ct (Position 21).
 SEQ ID NO:2002: n indicates a or deletion (Position 21).
 SEQ ID NO:2005: n indicates t or deletion (Position 21).
 SEQ ID NO:2008: n indicates g or deletion (Position 21).
 SEQ ID NO:2011: n indicates aattagaa or deletion (Position 21).
 20 SEQ ID NO:2012: n indicates tttaaaa or tttaa (Position 21).
 SEQ ID NO:2015: n indicates t or deletion (Position 21).
 SEQ ID NO:2020: n indicates t or deletion (Position 21).
 SEQ ID NO:2024: n indicates g or deletion (Position 21).
 SEQ ID NO:2025: n indicates t or deletion (Position 21).
 25 SEQ ID NO:2030: n indicates aaa or deletion (Position 21).
 SEQ ID NO:2031: n indicates a or deletion (Position 21).
 SEQ ID NO:2042: n indicates c (Position 21).
 SEQ ID NO:2072: n indicates a or deletion (Position 21).
 SEQ ID NO:2074: n indicates a or deletion (Position 21).
 30 SEQ ID NO:2243: n indicates tca repeated 14 to 16 times (Position 21).

- SEQ ID NO:2244: n indicates a repeated 8 to 10 times (Position 21).
SEQ ID NO:2245: n indicates cacagtcac or deletion (Position 21).
SEQ ID NO:2246: n indicates tt or deletion (Position 21).
SEQ ID NO:2247: n indicates a repeated 10 to 12 times (Position 21).
5 SEQ ID NO:2248: n indicates c or deletion (Position 21).
SEQ ID NO:2249: n indicates a repeated 16 to 18 times (Position 21).
SEQ ID NO:2250: n indicates g (Position 21).
SEQ ID NO:2252: n indicates c or deletion (Position 21).
SEQ ID NO:2253: n indicates t or deletion (Position 21).
10 SEQ ID NO:2254: n indicates a or deletion (Position 21).
SEQ ID NO:2255: n indicates tg (Position 21).
SEQ ID NO:2257: n indicates t repeated 10 to 13 (Position 21).
SEQ ID NO:2258: n indicates gt repeated 11 to 13 times (Position 21).
SEQ ID NO:2259: n indicates a or deletion (Position 21).
15 SEQ ID NO:2260: n indicates g or deletion (Position 21).
SEQ ID NO:2261: n indicates g or deletion (Position 21).
SEQ ID NO:2262: n indicates t repeated 9 to 11 times (Position 21).
SEQ ID NO:2263: n indicates g (Position 21).
SEQ ID NO:2265: n indicates tt or deletion (Position 21).
20 SEQ ID NO:2266: n indicates a repeated 7 to 9 times (Position 21).
SEQ ID NO:2267: n indicates t repeated 9 to 11 times (Position 21).
SEQ ID NO:2268: n indicates a repeated 9 to 10 times (Position 21).
SEQ ID NO:2269: n indicates gt or deletion (Position 21).
SEQ ID NO:2270: n indicates a or deletion (Position 21).
25 SEQ ID NO:2271: n indicates t (Position 21).
SEQ ID NO:2273: n indicates a or deletion (Position 21).
SEQ ID NO:2274: n indicates ct or deletion (Position 21).
SEQ ID NO:2275: n indicates g or deletion (Position 21).
SEQ ID NO:2276: n indicates a or deletion (Position 21).
30 SEQ ID NO:2277: n indicates a or deletion (Position 21).

SEQ ID NO:2279: n indicates c or deletion (Position 21).

SEQ ID NO:2280: n indicates aaag or deletion (Position 21).

SEQ ID NO:2348: n indicates t repeated 22 to 26 times (Position 21).

- 5 SEQ ID NO:2349: n indicates g repeated 8 to 10 times (Position 21).

SEQ ID NO:2350: n indicates c repeated 6 to 7 times (Position 21).

SEQ ID NO:2351: n indicates a repeated 12 to 14 times (Position 21).

SEQ ID NO:2427: n indicates caccaggcagcagactctgatgaggaggggagggg (Position 21).

SEQ ID NO:2429: n indicates g (Position 21).

- 10 SEQ ID NO:2474: n indicates tcac or deletion (Position 21).

SEQ ID NO:2475: n indicates t or deletion (Position 21).

SEQ ID NO:2476: n indicates t repeated 9 to 11 times (Position 21).

SEQ ID NO:2477: n indicates a repeated 7 to 8 times (Position 21).

SEQ ID NO:2495: n indicates t repeated 13 to 16 times (Position 21).

- 15 SEQ ID NO:2496: n indicates t repeated 9 to 10 times (Position 21).

SEQ ID NO:2497: n indicates t repeated 14 to 16 times (Position 21).

SEQ ID NO:2498: n indicates t repeated 13 to 17 times (Position 21).

SEQ ID NO:2499: n indicates t (Position 21).

SEQ ID NO:2501: n indicates a repeated 8 to 9 times (Position 21).

- 20 SEQ ID NO:2502: n indicates t repeated 8 to 9 times (Position 21).

SEQ ID NO:2503: n indicates gcagtattactgtagt or deletion (Position 21).

SEQ ID NO:2504: n indicates t repeated 13 to 14 times (Position 21).

SEQ ID NO:2505: n indicates t repeated 9 to 10 times (Position 21).

SEQ ID NO:2506: n indicates t repeated 10 to 11 times (Position 21).

- 25 SEQ ID NO:2524: n indicates t or deletion (Position 21).

SEQ ID NO:2525: n indicates t repeated 12 to 15 times (Position 21).

SEQ ID NO:2586: n indicates a or deletion (Position 21).

SEQ ID NO:2587: n indicates at or deletion (Position 21).

SEQ ID NO:2594: n indicates t or deletion (Position 21).

- 30 SEQ ID NO:2595: n indicates ttc or deletion (Position 21).

- SEQ ID NO:2606: n indicates ctt (Position 21).
- SEQ ID NO:2651: n indicates c repeated 9 to 11 times (Position 21).
- SEQ ID NO:2652: n indicates a repeated 15 to 21 times (Position 21).
- SEQ ID NO:2653: n indicates ggggtggcggggtggg or deletion (Position 21).
- 5 SEQ ID NO:2654: n indicates t or deletion (Position 21).
- SEQ ID NO:2655: n indicates a (Position 21).
- SEQ ID NO:2657: n indicates a or deletion (Position 21).
- SEQ ID NO:2658: n indicates t repeated 10 to 12 times (Position 21).
- SEQ ID NO:2659: n indicates tt (Position 21).
- 10 SEQ ID NO:2661: n indicates tcctccttgaagctgacgt or deletion (Position 21).
- SEQ ID NO:2662: n indicates ca repeated 12 to 18 times (Position 21).
- SEQ ID NO:2685: n indicates a repeated 18 to 20 times (Position 21).
- SEQ ID NO:2686: n indicates aa (Position 21).
- SEQ ID NO:2688: n indicates t or deletion (Position 21).
- 15 SEQ ID NO:2689: n indicates t repeated 9 to 13 times (Position 21).
- SEQ ID NO:2690: n indicates aa or deletion (Position 21).
- SEQ ID NO:2691: n indicates ttgaca or gtccaatat (Position 21).
- SEQ ID NO:2692: n indicates cta or deletion (Position 21).
- SEQ ID NO:2693: n indicates t repeated 9 to 10 times (Position 21).
- 20 SEQ ID NO:2694: n indicates gagatgttggtggtcacat (Position 21).
- SEQ ID NO:2696: n indicates cc or deletion (Position 21).
- SEQ ID NO:2697: n indicates act or deletion (Position 21).
- SEQ ID NO:2755: n indicates tat or deletion (Position 21).
- SEQ ID NO:2756: n indicates ac repeated 14 to 17 times (Position 21).
- 25 SEQ ID NO:2757: n indicates a repeated 16 to 27 times (Position 21).
- SEQ ID NO:2758: n indicates t or deletion (Position 21).
- SEQ ID NO:2759: n indicates a repeated 8 to 10 times (Position 21).
- SEQ ID NO:2760: n indicates gt repeated 9 to 11 times (Position 21).
- SEQ ID NO:2761: n indicates aa or deletion (Position 21).
- 30 SEQ ID NO:2762: n indicates t or deletion (Position 21).

- SEQ ID NO:2763: n indicates ac repeated 8 to 12 times (Position 21).
 SEQ ID NO:2764: n indicates a or deletion (Position 21).
 SEQ ID NO:2810: n indicates a (Position 21).
 SEQ ID NO:2812: n indicates aa or deletion (Position 21).
 5 SEQ ID NO:2813: n indicates ca or deletion (Position 21).
 SEQ ID NO:2814: n indicates t or deletion (Position 21).
 SEQ ID NO:2815: n indicates tgtgtg or deletion (Position 21).
 SEQ ID NO:2912: n indicates a (Position 21).
 SEQ ID NO:2914: n indicates g (Position 21).
 10 SEQ ID NO:2916: n indicates actt or deletion (Position 21).
 SEQ ID NO:2917: n indicates ttta or deletion (Position 21).
 SEQ ID NO:2918: n indicates a repeated 11 to 13 times (Position 21).
 SEQ ID NO:2919: n indicates t repeated 8 to 10 times (Position 21).
 SEQ ID NO:2920: n indicates a repeated 12 to 14 times (Position 21).
 15 SEQ ID NO:2921: n indicates cttgta or deletion (Position 21).
 SEQ ID NO:2922: n indicates a repeated 9 to 10 times (Position 21).
 SEQ ID NO:2923: n indicates ctt or deletion (Position 21).
 SEQ ID NO:2924: n indicates ctt (Position 21).
 SEQ ID NO:2926: n indicates a or deletion (Position 21).
 20 SEQ ID NO:2927: n indicates a repeated 9 to 11 times (Position 21).
 SEQ ID NO:2928: n indicates tgt or deletion (Position 21).
 SEQ ID NO:2929: n indicates a repeated 24 to 27 times (Position 21).
 SEQ ID NO:2930: n indicates ta repeated 10 to 21 times (Position 21).
 SEQ ID NO:2931: n indicates a repeated 8 to 10 times (Position 21).
 25 SEQ ID NO:2932: n indicates a repeated 11 to 13 times (Position 21).
 SEQ ID NO:2933: n indicates a repeated 8 to 10 times (Position 21).
 SEQ ID NO:2999: n indicates tatc or deletion (Position 21).
 SEQ ID NO:3000: n indicates atattcacttggtatctg or deletion (Position 21).
 SEQ ID NO:3001: n indicates ttta or deletion (Position 21).
 30 SEQ ID NO:3002: n indicates t (Position 21).

- SEQ ID NO:3004: n indicates g or deletion (Position 21).
- SEQ ID NO:3005: n indicates a or deletion (Position 21).
- SEQ ID NO:3006: n indicates a repeated 9 to 11 times (Position 21).
- SEQ ID NO:3007: n indicates g or deletion (Position 21).
- 5 SEQ ID NO:3008: n indicates at repeated 4 to 5 times (Position 21).
- SEQ ID NO:3009: n indicates t repeated 7 to 8 times (Position 21).
- SEQ ID NO:3010: n indicates t repeated 19 to 23 times (Position 21).
- SEQ ID NO:3011: n indicates t or deletion (Position 21).
- SEQ ID NO:3012: n indicates tgat or deletion (Position 21).
- 10 SEQ ID NO:3013: n indicates t repeated 8 to 10 times (Position 21).
- SEQ ID NO:3014: n indicates a or deletion (Position 21).
- SEQ ID NO:3021: n indicates a repeated 13 to 15 times (Position 21).
- SEQ ID NO:3022: n indicates t repeated 12 to 15 times (Position 21).
- SEQ ID NO:3042: n indicates g (Position 21).
- 15 SEQ ID NO:3044: n indicates a or deletion (Position 21).
- SEQ ID NO:3046: n indicates g or deletion (Position 21).
- SEQ ID NO:3047: n indicates t repeated 11 to 13 times (Position 21).
- SEQ ID NO:3049: n indicates a or deletion (Position 21).
- SEQ ID NO:3051: n indicates t repeated 9 to 11 times (Position 21).
- 20 SEQ ID NO:3054: n indicates t or deletion (Position 21).
- SEQ ID NO:3056: n indicates t or deletion (Position 21).
- SEQ ID NO:3060: n indicates t or deletion (Position 21).
- SEQ ID NO:3065: n indicates aaga (Position 21).
- SEQ ID NO:3069: n indicates aaaa or deletion (Position 21).
- 25 SEQ ID NO:3073: n indicates t repeated 9 to 11 times (Position 21).
- SEQ ID NO:3081: n indicates a or deletion (Position 21).
- SEQ ID NO:3103: n indicates t repeated 11 to 13 times (Position 21).
- SEQ ID NO:3119: n indicates acta (Position 21).
- SEQ ID NO:3125: n indicates gtg or deletion (Position 21).
- 30 SEQ ID NO:3130: n indicates t repeated 11 to 12 times (Position 21).

SEQ ID NO:3140: n indicates tta or deletion (Position 21).

SEQ ID NO:3154: n indicates g (Position 21).

SEQ ID NO:3156: n indicates a (Position 21).

SEQ ID NO:3158: n indicates cct or deletion (Position 21).

5 SEQ ID NO:3169: n indicates gga or deletion (Position 21).

SEQ ID NO:3179: n indicates t repeated 12 to 14 times (Position 21).

SEQ ID NO:3184: n indicates t repeated 16 to 17 times (Position 21).

SEQ ID NO:3196: n indicates g (Position 21).

SEQ ID NO:3273: n indicates ag (Position 21).

10 SEQ ID NO:3306: n indicates g (Position 21).

SEQ ID NO:3310: n indicates c (Position 21).

SEQ ID NO:3315: n indicates ct or deletion (Position 21).

SEQ ID NO:3317: n indicates gc or deletion (Position 21).

SEQ ID NO:3352: n indicates t repeated 9 to 11 times (Position 21).

15 SEQ ID NO:3355: n indicates a (Position 21).

SEQ ID NO:3358: n indicates t or deletion (Position 21).

SEQ ID NO: 3510² n represents at or deletion (Location 21).

SEQ ID NO: 3512² n represents c or deletion (Location 21).

SEQ ID NO: 3513² n represents t or deletion (Location 21).

20 SEQ ID NO:3514² n represents t or deletion (Location 21).

SEQ ID NO:3515² n represents g or deletion (Location 21).

SEQ ID NO:3517² n represents c or deletion (Location 21).

SEQ ID NO:3519² n represents t or deletion (Location 21).

SEQ ID NO:3521² n represents c or deletion (Location 21).

25 SEQ ID NO:3649² n represents 14 to 16 repeats of tca (from Location 21).

SEQ ID NO:3650² n represents 8 to 10 repeats of a (from Location 21).

SEQ ID NO:3651² n represents cacagtcac or deletion (Location 21).

SEQ ID NO:3652² n represents tt or deletion (Location 21).

SEQ ID NO:3653² n represents 10 to 12 repeats of a (from Location 21).

- SEQ ID NO:3654² n represents c or deletion (Location 21).
- SEQ ID NO:3655² n represents 16 to 18 repeats of a (from Location 21).
- SEQ ID NO:3656² n represents g or deletion (Location 21).
- SEQ ID NO:3658² n represents c or deletion (Location 21).
- 5 SEQ ID NO:3659² n represents t or deletion (Location 21).
- SEQ ID NO:3660² n represents a or deletion (Location 21).
- SEQ ID NO:3661² n represents tg or deletion (Location 21).
- SEQ ID NO:3663² n represents 10 to 13 repeats of t (from Location 21).
- SEQ ID NO:3664² n represents 11 to 13 repeats of gt (from Location 21).
- 10 SEQ ID NO:3665² n represents a or deletion (Location 21).
- SEQ ID NO:3666² n represents g or deletion (Location 21).
- SEQ ID NO:3667² n represents g or deletion (Location 21).
- SEQ ID NO:3668² n represents 9 to 11 repeats of t (from Location 21).
- SEQ ID NO:3669² n represents g or deletion (Location 21).
- 15 SEQ ID NO:3671² n represents tt or deletion (Location 21).
- SEQ ID NO:3672² n represents 7 to 9 repeats of a (from Location 21).
- SEQ ID NO:3673² n represents 9 to 11 repeats of t (from Location 21).
- SEQ ID NO:3674² n represents 9 to 10 repeats of a (from Location 21).
- SEQ ID NO:3675² n represents gt or deletion (Location 21).
- 20 SEQ ID NO:3676² n represents a or deletion (Location 21).
- SEQ ID NO:3677² n represents t or deletion (Location 21).
- SEQ ID NO:3679² n represents a or deletion (Location 21).
- SEQ ID NO:3680² n represents ct or deletion (Location 21).
- SEQ ID NO:3681² n represents g or deletion (Location 21).
- 25 SEQ ID NO:3682² n represents a or deletion (Location 21).
- SEQ ID NO:3683² n represents a or deletion (Location 21).
- SEQ ID NO:3684² n represents a or deletion (Location 21).

	SEQ ID NO:3685	n represents c or deletion (Location 21).
	SEQ ID NO:3686	n represents aaag or deletion (Location 21).
	SEQ ID NO:3751	n represents 22 to 26 repeats of t (from Location 21).
	SEQ ID NO:3752	n represents 8 to 10 repeats of g (from Location 21).
5	SEQ ID NO:3753	n represents 6 to 7 repeats of c (from Location 21).
	SEQ ID NO:3754	n represents 12 to 14 repeats of a (from Location 21).
	SEQ ID NO:3833	n represents tt or deletion (Location 21).
	SEQ ID NO:3834	n represents 9 to 11 repeats of a (from Location 21).
	SEQ ID NO:3835	n represents 8 to 12 repeats of a (from Location 21).
10	SEQ ID NO:3836	n represents t or deletion (Location 21).
	SEQ ID NO:3837	n represents t or deletion (Location 21).
	SEQ ID NO:3838	n represents t or deletion (Location 21).
	SEQ ID NO:3839	n represents a or deletion (Location 21).
	SEQ ID NO:3840	n represents t or deletion (Location 21).
15	SEQ ID NO:3841	n represents t or deletion (Location 21).
	SEQ ID NO:3842	n represents 11 to 15 repeats of t (from Location 21).
	SEQ ID NO:3843	n represents cat or deletion (Location 21).
	SEQ ID NO:3844	n represents t or deletion (Location 21).
	SEQ ID NO:3845	n represents a or deletion (Location 21).
20	SEQ ID NO:3846	n represents a or deletion (Location 21).
	SEQ ID NO:3847	n represents t or deletion (Location 21).
	SEQ ID NO:3848	n represents a or deletion (Location 21).
	SEQ ID NO:3857	n represents g or deletion (Location 21).
	SEQ ID NO:3879	n represents a or deletion (Location 21).
25	SEQ ID NO:3885	n represents aaag or deletion (Location 21).
	SEQ ID NO:3915	n represents t or deletion (Location 21).
	SEQ ID NO:3918	n represents a or deletion (Location 21).

	SEQ ID NO:3926	n represents at or deletion (Location 21).
	SEQ ID NO:3933	n represents a or deletion (Location 21).
	SEQ ID NO:3950	n represents c or deletion (Location 21).
	SEQ ID NO:3953	n represents gg or deletion (Location 21).
5	SEQ ID NO:3962	n represents gtc or deletion (Location 21).
	SEQ ID NO:3984	n represents t or deletion (Location 21).
	SEQ ID NO:3991	n represents tt or deletion (Location 21).
	SEQ ID NO:3994	n represents 9 to 12 repeats of t (from Location 21).
	SEQ ID NO:3996	n represents a or deletion (Location 21).
10	SEQ ID NO:3998	n represents 10 to 13 repeats of a (from Location 21).
	SEQ ID NO:4001	n represents ct or deletion (Location 21).
	SEQ ID NO:4004	n represents cagatcttcttcagctaatttagaaatgt or deletion (Location 21).
	SEQ ID NO:4030	n represents a or deletion (Location 21).
15	SEQ ID NO:4037	n represents c or deletion (Location 21).
	SEQ ID NO:4042	n represents t or deletion (Location 21).
	SEQ ID NO:4049	n represents 9 to 12 repeats of t (from Location 21).
	SEQ ID NO:4052	n represents t or deletion (Location 21).
	SEQ ID NO:4054	n represents g (a) ⁴ , a (a) ⁴ or a (Location 21).
20	SEQ ID NO:4058	n represents t or deletion (Location 21).
	SEQ ID NO:4067	n represents c or deletion (Location 21).
	SEQ ID NO:4069	n represents a or deletion (Location 21).
	SEQ ID NO:4070	n represents c or deletion (Location 21).
	SEQ ID NO:4077	n represents g or deletion (Location 21).
25	SEQ ID NO:4079	n represents 18 to 20 repeats of t (from Location 21).
	SEQ ID NO:4084	n represents 11 to 13 repeats of a (from Location 21).
	SEQ ID NO:4085	n represents gaaa or deletion (Location 21).

- SEQ ID NO:4089 n represents 10 to 12 repeats of a (from Location 21).
- SEQ ID NO:4092 n represents c or deletion (Location 21).
- SEQ ID NO:4102 n represents ca or deletion (Location 21).
- SEQ ID NO:4109 n represents at or deletion (Location 21).
- 5 SEQ ID NO:4113 n represents ctt or deletion (Location 21).
- SEQ ID NO:4115 n represents g or deletion (Location 21).
- SEQ ID NO:4117 n represents ggggct or deletion (Location 21).
- SEQ ID NO:4121 n represents 19 to 22 repeats of t (from Location 21).
- SEQ ID NO:4126 n represents 6 to 7 repeats of t (from Location 21).
- 10 SEQ ID NO:4129 n represents 11 to 13 repeats of t (from Location 21).
- SEQ ID NO:4173 n represents 7 to 8 repeats of c (from Location 21).
- SEQ ID NO:4175 n represents 10 to 12 repeats of a (from Location 21).
- SEQ ID NO:4183 n represents c or deletion (Location 21).
- SEQ ID NO:4188 n represents aaga or deletion (Location 21).
- 15 SEQ ID NO:4190 n represents 9 to 11 repeats of a (from Location 21).
- SEQ ID NO:4193 n represents ct or deletion (Location 21).
- SEQ ID NO:4198 n represents 8 to 9 repeats of t (from Location 21).
- SEQ ID NO:4218 n represents g or deletion (Location 21).
- SEQ ID NO:4224 n represents cttt or deletion (Location 21).
- 20 SEQ ID NO:4229 n represents t or deletion (Location 21).
- SEQ ID NO:4234 n represents c or deletion (Location 21).
- SEQ ID NO:4235 n represents a or deletion (Location 21).
- SEQ ID NO:4238 n represents gtt or deletion (Location 21).
- SEQ ID NO:4239 n represents t or deletion (Location 21).
- 25 SEQ ID NO:4259 n represents at or deletion (Location 21).
- SEQ ID NO:4273 n represents g or deletion (Location 21).
- SEQ ID NO:4280 n represents 15 to 17 repeats of a (from Location 21).

- SEQ ID NO:4294 n represents t or deletion (Location 21).
- SEQ ID NO:4298 n represents t or deletion (Location 21).
- SEQ ID NO:4310 n represents t or deletion (Location 21).
- SEQ ID NO:4314 n represents a or deletion (Location 21).
- 5 SEQ ID NO:4315 n represents 13 to 15 repeats of t (from Location 21).
- SEQ ID NO:4316 n represents 12 to 13 repeats of a (from Location 21).
- SEQ ID NO:4317 n represents t or deletion (Location 21).
- SEQ ID NO:4319 n represents t or deletion (Location 21).
- SEQ ID NO:4320 n represents 13 to 15 repeats of a (from Location 21).
- 10 SEQ ID NO:4325 n represents a or deletion (Location 21).
- SEQ ID NO:4331 n represents 5 to 11 repeats of t (from Location 21).
- SEQ ID NO:4333 n represents 8 to 9 repeats of t (from Location 21).
- SEQ ID NO:4334 n represents t or deletion (Location 21).
- SEQ ID NO:4345 n represents 9 to 10 repeats of t (from Location 21).
- 15 SEQ ID NO:4348 n represents 10 to 11 repeats of a (from Location 21).
- SEQ ID NO:4354 n represents a or deletion (Location 21).
- SEQ ID NO:4361 n represents a or deletion (Location 21).
- SEQ ID NO:4372 n represents ct or deletion (Location 21).
- SEQ ID NO:4391 n represents t or deletion (Location 21).
- 20 SEQ ID NO:4397 n represents a or deletion (Location 21).
- SEQ ID NO:4398 n represents at or deletion (Location 21).
- SEQ ID NO:4408 n represents tgtcaaaggaaggacacg or deletion (Location 21).
- SEQ ID NO:4414 n represents 6 to 8 repeats of tc (from Location 21).
- SEQ ID NO:4416 n represents c or deletion (Location 21).
- 25 SEQ ID NO:4419 n represents t or deletion (Location 21).
- SEQ ID NO:4424 n represents t or deletion (Location 21).
- SEQ ID NO:4425 n represents c or deletion (Location 21).

SEQ ID NO:4590 n represents ct or deletion (Location 21).

- SEQ ID NO:4597 n represents a or deletion (Location 21).
- SEQ ID NO:4600 n represents t or deletion (Location 21).
- SEQ ID NO:4603 n represents g or deletion (Location 21).
- SEQ ID NO:4606 n represents aattagaa or deletion (Location 21).
- 5 SEQ ID NO:4607 n represents tttaaaa or ttttaa (Location 21).
- SEQ ID NO:4610 n represents t or deletion (Location 21).
- SEQ ID NO:4615 n represents t or deletion (Location 21).
- SEQ ID NO:4627 n represents c or deletion (Location 21).
- SEQ ID NO:4652 n represents 11 to 14 repeats of t (from Location 21).
- 10 SEQ ID NO:4653 n represents t or deletion (Location 21).
- SEQ ID NO:4654 n represents 10 to 13 repeats of t (from Location 21).
- SEQ ID NO:4655 n represents t or deletion (Location 21).
- SEQ ID NO:4657 n represents t or deletion (Location 21).
- SEQ ID NO:4658 n represents ta or deletion (Location 21).
- 15 SEQ ID NO:4660 n represents 13 to 15 repeats of t (from Location 21).
- SEQ ID NO:4661 n represents c or deletion (Location 21).
- SEQ ID NO:4662 n represents 17 to 20 repeats of a (from Location 21).
- SEQ ID NO:4663 n represents 11 to 13 repeats of t (from Location 21).
- SEQ ID NO:4664 n represents 8 to 9 repeats of t (from Location 21).
- 20 SEQ ID NO:4665 n represents 10 to 11 repeats of a (from Location 21).
- SEQ ID NO:4666 n represents 16 to 19 repeats of a (from Location 21).
- SEQ ID NO:4758 n represents g or deletion (Location 21).
- SEQ ID NO:4760 n represents 6 to 7 repeats of a (from Location 21).
- SEQ ID NO:4761 n represents c or deletion (Location 21).
- 25 SEQ ID NO:4763 n represents tcctcaggg or deletion (Location 21).
- SEQ ID NO:4764 n represents 8 to 10 repeats of cgc (from Location 21).
- SEQ ID NO:4765 n represents 10 to 12 repeats of a (from Location 21).

SEQ ID NO:4766 n represents caccaggcagcagactctgatgaggaggggaggggg or deletion (Location 21).

SEQ ID NO:4768 n represents g or deletion (Location 21).

SEQ ID NO:4808 n represents tcac or deletion (Location 21).

5 SEQ ID NO:4809 n represents t or deletion (Location 21).

SEQ ID NO:4810 n represents 9 to 11 repeats of t (from Location 21).

SEQ ID NO:4811 n represents 7 to 8 repeats of a (from Location 21).

SEQ ID NO:4847 n represents agg or deletion (Location 21).

SEQ ID NO:4848 n represents taacatt or deletion (Location 21).

10 SEQ ID NO:4849 n represents 10 to 12 repeats of a (from Location 21).

SEQ ID NO:4850 n represents 15 to 17 repeats of t (from Location 21).

SEQ ID NO:4851 n represents 11 to 13 repeats of a (from Location 21).

SEQ ID NO:4877 n represents 11 to 13 repeats of t (from Location 21).

SEQ ID NO:4878 n represents t or deletion (Location 21).

15 SEQ ID NO:4879 n represents t or deletion (Location 21).

SEQ ID NO:4880 n represents 10 to 12 repeats of a (from Location 21).

SEQ ID NO:4881 n represents t or deletion (Location 21)

SEQ ID NO:4883 n represents 7 to 9 repeats of c (from Location 21).

SEQ ID NO:4884 n represents a or deletion (Location 21)

20 SEQ ID NO:4891 n represents 13 to 16 repeats of t (from Location 21).

SEQ ID NO:4892 n represents 9 to 10 repeats of t (from Location 21).

SEQ ID NO:4893 n represents 14 to 16 repeats of t (from Location 21).

SEQ ID NO:4894 n represents 13 to 17 repeats of t (from Location 21).

SEQ ID NO:4895 n represents t or deletion (Location 21).

25 SEQ ID NO:4897 n represents 8 to 9 repeats of a (from Location 21).

SEQ ID NO:4898 n represents 8 to 9 repeats of t (from Location 21).

SEQ ID NO:4899 n represents gcagtattactgtagt or deletion (Location 21).

- SEQ ID NO:4900 n represents 13 to 14 repeats of t (from Location 21).
- SEQ ID NO:4901 n represents 9 to 10 repeats of t (from Location 21).
- SEQ ID NO:4902 n represents 10 to 11 repeats of t (from Location 21).
- SEQ ID NO:4907 n represents 10 to 14 repeats of a (from Location 21).
- 5 SEQ ID NO:4908 n represents 13 to 15 repeats of a (from Location 21).
- SEQ ID NO:4909 n represents a or deletion (Location 21).
- SEQ ID NO:4910 n represents t or deletion (Location 21).
- SEQ ID NO:4918 n represents 13 to 15 repeats of a (from Location 21).
- SEQ ID NO:4919 n represents 12 to 15 repeats of a (from Location 21).
- 10 SEQ ID NO:4936 n represents g or deletion (Location 21).
- SEQ ID NO:4938 n represents aa or deletion (Location 21).
- SEQ ID NO:4983 n represents a or deletion (Location 21).
- SEQ ID NO:4985 n represents aa or deletion (Location 21).
- SEQ ID NO:4986 n represents ca or deletion (Location 21).
- 15 SEQ ID NO:4987 n represents t or deletion (Location 21).
- SEQ ID NO:4988 n represents tgtgtg or deletion (Location 21).
- SEQ ID NO:5076 n represents a or deletion (Location 21).
- SEQ ID NO:5078 n represents g or deletion (Location 21).
- SEQ ID NO:5080 n represents actt or deletion (Location 21).
- 20 SEQ ID NO:5081 n represents ttta or deletion (Location 21).
- SEQ ID NO:5082 n represents 11 to 13 repeats of a (from Location 21).
- SEQ ID NO:5083 n represents 8 to 10 repeats of t (from Location 21).
- SEQ ID NO:5084 n represents 12 to 14 repeats of a (from Location 21).
- SEQ ID NO:5085 n represents cttgta or deletion (Location 21).
- 25 SEQ ID NO:5086 n represents 9 to 10 repeats of a (from Location 21).
- SEQ ID NO:5087 n represents ctt or deletion (Location 21).
- SEQ ID NO:5088 n represents ctt or deletion (Location 21).

- SEQ ID NO:5090 n represents a or deletion (Location 21).
- SEQ ID NO:5091 n represents 9 to 11 repeats of a (from Location 21)
- SEQ ID NO:5092 n represents tgt or deletion (Location 21).
- SEQ ID NO:5093 n represents 24 to 27 repeats of a (from Location 21)
- 5 SEQ ID NO:5094 n represents 10 to 21 repeats of ta (from Location 21)
- SEQ ID NO:5095 n represents 8 to 10 repeats of a (from Location 21)
- SEQ ID NO:5096 n represents 11 to 13 repeats of a (from Location 21)
- SEQ ID NO:5097 n represents 8 to 10 repeats of a (from Location 21)
- SEQ ID NO:5155 n represents ctat or deletion (Location 21).
- 10 SEQ ID NO:5156 n represents attacttggtatctg or deletion (Location 21).
- SEQ ID NO:5157 n represents ttta or deletion (Location 21).
- SEQ ID NO:5158 n represents t or deletion (Location 21).
- SEQ ID NO:5160 n represents g or deletion (Location 21).
- SEQ ID NO:5161 n represents a or deletion (Location 21).
- 15 SEQ ID NO:5162 n represents 9 to 11 repeats of a (from Location 21).
- SEQ ID NO:5163 n represents g or deletion (Location 21).
- SEQ ID NO:5164 n represents 4 to 5 repeats of at (from Location 21).
- SEQ ID NO:5165 n represents 7 to 8 repeats of t (from Location 21).
- SEQ ID NO:5166 n represents 19 to 23 repeats of t (from Location 21).
- 20 SEQ ID NO:5167 n represents t or deletion (Location 21).
- SEQ ID NO:5168 n represents tgat or deletion (Location 21).
- SEQ ID NO:5169 n represents 8 to 10 repeats of t (from Location 21).
- SEQ ID NO:5170 n represents a or deletion (Location 21).
- SEQ ID NO:5187 n represents gtg or deletion (Location 21).
- 25 SEQ ID NO:5189 n represents gg or tgggtgggtgga (Location 21).
- SEQ ID NO:5209 n represents acaaca or deletion (Location 21).
- SEQ ID NO:5210 n represents 11 to 13 repeats of t (from Location 21).

- SEQ ID NO:5410⁵ n represents at or deletion (Location 21).
- SEQ ID NO:5436⁵ n represents tgt or deletion (Location 21).
- SEQ ID NO:5445⁵ n represents t or deletion (Location 21).
- SEQ ID NO:5550⁵ n represents t or deletion (Location 21).
- 5 SEQ ID NO:5556⁵ n represents g or deletion (Location 21).
- SEQ ID NO:5557⁵ n represents 11 to 13 repeats of t (from Location 21).
- SEQ ID NO:5559⁵ n represents a or deletion (Location 21).
- SEQ ID NO:5561⁵ n represents 9 to 11 repeats of t (from Location 21).
- SEQ ID NO:5564⁵ n represents t or deletion (Location 21).
- 10 SEQ ID NO:5566⁵ n represents t or deletion (Location 21).
- SEQ ID NO:5570⁵ n represents t or deletion (Location 21).
- SEQ ID NO:5575⁵ n represents aaga or deletion (Location 21).
- SEQ ID NO:5579⁵ n represents aaaa or deletion (Location 21).
- SEQ ID NO:5583⁵ n represents 9 to 11 repeats of t (from Location 21).
- 15 SEQ ID NO:5591⁵ n represents a or deletion (Location 21).
- SEQ ID NO:5614⁵ n represents 11 to 13 repeats of t (from Location 21).
- SEQ ID NO:5630⁵ n represents acta or deletion (Location 21).
- SEQ ID NO:5636⁵ n represents gtg or deletion (Location 21).
- SEQ ID NO:5641⁵ n represents 11 to 12 repeats of t (from Location 21).
- 20 SEQ ID NO:5651⁵ n represents tta or deletion (Location 21).
- SEQ ID NO:5665⁵ n represents g or deletion (Location 21).
- SEQ ID NO:5667⁵ n represents a or deletion (Location 21).
- SEQ ID NO:5669⁵ n represents cct or deletion (Location 21).
- SEQ ID NO:5680⁵ n represents gga or deletion (Location 21).
- 25 SEQ ID NO:5690⁵ n represents 12 to 14 repeats of t (from Location 21).
- SEQ ID NO:5695⁵ n represents 16 to 17 repeats of t (from Location 21).
- SEQ ID NO:5707⁵ n represents g or deletion (Location 21).

- SEQ ID NO:5996 n represents a or deletion (Location 21).
- SEQ ID NO:6001 n represents aatt or deletion (Location 21).
- SEQ ID NO:6003 n represents t or deletion (Location 21).
- SEQ ID NO:6009 n represents g or deletion (Location 21).
- 5 SEQ ID NO:6021 n represents at or deletion (Location 21).
- SEQ ID NO:6027 n represents 4 to 5 repeats of caaaa (from Location 21).
- SEQ ID NO:6036 n represents 9 to 10 repeats of a (from Location 21).
- SEQ ID NO:6041 n represents a or deletion (Location 21).
- SEQ ID NO:6047 n represents t or deletion (Location 21).
- 10 SEQ ID NO:6051 n represents t or deletion (Location 21).
- SEQ ID NO:6052 n represents g or deletion (Location 21).
- SEQ ID NO:6060 n represents t or deletion (Location 21).
- SEQ ID NO:6061 n represents t or deletion (Location 21).
- SEQ ID NO:6062 n represents a or deletion (Location 21).
- 15 SEQ ID NO:6072 n represents gaa or deletion (Location 21).
- SEQ ID NO:6073 n represents ag or deletion (Location 21).
- SEQ ID NO:6089 n represents 9 to 11 repeats of t (from Location 21).
- SEQ ID NO:6090 n represents a or deletion (Location 21).
- SEQ ID NO:6091 n represents t or deletion (Location 21).
- 20 SEQ ID NO:6173 n represents tat or deletion (Location 21).
- SEQ ID NO:6174 n represents 14 to 17 repeats of ac (from Location 21).
- SEQ ID NO:6175 n represents 16 to 27 repeats of a (from Location 21).
- SEQ ID NO:6176 n represents t or deletion (Location 21).
- SEQ ID NO:6177 n represents 8 to 10 repeats of a (from Location 21).
- 25 SEQ ID NO:6178 n represents 9 to 11 repeats of gt (from Location 21).
- SEQ ID NO:6179 n represents aa or deletion (Location 21).
- SEQ ID NO:6180 n represents t or deletion (Location 21).

- SEQ ID NO:6181 n represents 8 to 12 repeats of ac (from Location 21).
- SEQ ID NO:6182 n represents a or deletion (Location 21).
- SEQ ID NO:6202 n represents agg or deletion (Location 21).
- SEQ ID NO:6204 n represents 11 to 15 repeats of a (from Location 21).
- 5 SEQ ID NO:6205 n represents 11 to 14 repeats of a (from Location 21).
- SEQ ID NO:6208 n represents gt or deletion (Location 21).
- SEQ ID NO:6224 n represents ta or deletion (Location 21).
- SEQ ID NO:6307 n represents 16 to 19 repeats of a (from Location 21).
- SEQ ID NO:6308 n represents aa or deletion (Location 21).
- 10 SEQ ID NO:6310 n represents t or deletion (Location 21).
- SEQ ID NO:6311 n represents 10 to 12 repeats of t (from Location 21).
- SEQ ID NO:6312 n represents aa or deletion (Location 21).
- SEQ ID NO:6313 n represents ttgacagtccaatat, ttgaca, gtccaatat or deletion (Location 21).
- 15 SEQ ID NO:6314 n represents cta or deletion (Location 21).
- SEQ ID NO:6315 n represents a or deletion (Location 21).
- SEQ ID NO:6317 n represents 9 to 11 repeats of t (From Location 21).
- SEQ ID NO:6318 n represents c or deletion (Location 21).
- SEQ ID NO:6320 n represents gagatgtgtggctcacat or deletion (Location 21).
- 20 SEQ ID NO:6322 n represents cc or deletion (Location 21).
- SEQ ID NO:6323 n represents act or deletion (Location 21).
- SEQ ID NO:6405 n represents a or deletion (Location 21).
- SEQ ID NO:6415 n represents 8 to 11 repeats of t (from Location 21).
- SEQ ID NO:6416 n represents 10 to 13 repeats of t (from Location 21).
- 25 SEQ ID NO:6472 n represents g or deletion (Location 21).
- SEQ ID NO:6473 n represents c or deletion (Location 21).
- SEQ ID NO:6554 n represents t or deletion (Location 21).

SEQ ID NO:6555 n represents 12 to 15 repeats of t (from Location 21).

SEQ ID NO:6609 n represents a or deletion (Location 21).

SEQ ID NO:6610 n represents at or deletion (Location 21).

SEQ ID NO:6725 n represents 16 repeats of cctgc or 16 repeats of cctgt (from

5 Location 21).

SEQ ID NO:6726 n represents t or deletion (Location 21).

SEQ ID NO:6728 n represents c or deletion (Location 21).

SEQ ID NO:6739 n represents acac or deletion (Location 21).

SEQ ID NO:6748 n represents gatttggtatccag or deletion (Location 21).

10 SEQ ID NO:6750 n represents ag or deletion (Location 21).

SEQ ID NO:6751 n represents ta or deletion (Location 21).

SEQ ID NO:6757 n represents t or deletion (Location 21).

SEQ ID NO:6759 n represents 12 to 14 repeats of gt from Location 21).

SEQ ID NO:6771 n represents cagagct or deletion (Location 21).

15 SEQ ID NO:6772 n represents ct or deletion (Location 21).

SEQ ID NO:6773 n represents ag or deletion (Location 21).

SEQ ID NO:6785 n represents gtaaa or deletion (Location 21).

SEQ ID NO:6786 n represents aaaaa or deletion (Location 21).

SEQ ID NO:6787 n represents a or deletion (Location 21).

20 SEQ ID NO:6828 n represents tc or deletion (Location 21).

SEQ ID NO:6830 n represents t or deletion (Location 21).

SEQ ID NO:6831 n represents t or deletion (Location 21).

SEQ ID NO:6832 n represents gaagaaactgtgacagttt or deletion (Location 21).

SEQ ID NO:6833 n represents cct or deletion (Location 21).

25 SEQ ID NO:6834 n represents ttct or deletion (Location 21).

SEQ ID NO:6835 n represents ttcttttaaattg or deletion (Location 21).

SEQ ID NO:6837 n represents ttcaggccttt or deletion (Location 21).

- SEQ ID NO:6839 n represents ggcctg or deletion (Location 21).
- SEQ ID NO:6841 n represents a or deletion (Location 21).
- SEQ ID NO:6870 n represents 9 to 11 repeats of c (from Location 21).
- SEQ ID NO:6871 n represents 15 to 21 repeats of a (from Location 21).
- 5 SEQ ID NO:6872 n represents ggggtggcggggtggg or deletion (Location 21).
- SEQ ID NO:6873 n represents t or deletion (Location 21).
- SEQ ID NO:6874 n represents a or deletion (Location 21).
- SEQ ID NO:6876 n represents a or deletion (Location 21).
- SEQ ID NO:6877 n represents 10 to 12 repeats of t (from Location 21).
- 10 SEQ ID NO:6878 n represents tt or deletion (Location 21).
- SEQ ID NO:6880 n represents tcctcctgaagctgacgt or deletion (Location 21).
- SEQ ID NO:6881 n represents 12 to 18 repeats of ca (from Location 21).
- SEQ ID NO:6894 n represents gtt or deletion (Location 21).
- SEQ ID NO:6897 n represents ga or deletion (Location 21).
- 15 SEQ ID NO:6921 n represents t or deletion (Location 21).
- SEQ ID NO:6940 n represents t or deletion (Location 21).
- SEQ ID NO:6941 n represents t or deletion (Location 21).
- SEQ ID NO:6942 n represents t or deletion (Location 21).
- SEQ ID NO:6965 n represents at or deletion (Location 21).
- 20 SEQ ID NO:6966 n represents a or deletion (Location 21).
- SEQ ID NO:6967 n represents c or deletion (Location 21).
- SEQ ID NO:6997 n represents c or deletion (Location 21).
- SEQ ID NO:7005 n represents t or deletion (Location 21).
- SEQ ID NO:7006 n represents ttc or deletion (Location 21).
- 25 SEQ ID NO:7017 n represents ctt or deletion (Location 21).
- SEQ ID NO:7049 n represents 8 to 9 repeats of a (from Location 21).
- SEQ ID NO:7053 n represents 10 to 12 repeats of t (from Location 21).

SEQ ID NO:7461 n represents 4 to 6 repeats of c (from Location 21).

SEQ ID NO:7483 n represents ggcgaggcggcgcgc or deletion (Location 21).

SEQ ID NO:7485 n represents ata or deletion (Location 21).

SEQ ID NO:7488 n represents 11 to 12 repeats of t (from Location 21).

5 SEQ ID NO:7489 n represents 12 to 14 repeats of t (from Location 21).

SEQ ID NO:7493 n represents 9 to 10 repeats of t (from Location 21).

SEQ ID NO:7495 n represents 6 to 7 repeats of ta (from Location 21).

SEQ ID NO:7497 n represents tgtatacgtatacatatatacatatatacatatata or deletion (Location 21).

10 SEQ ID NO:7503 n represents attt or deletion (Location 21).

SEQ ID NO:7510 n represents cct or deletion (Location 21).

SEQ ID NO:7519 n represents tggtt or deletion (Location 21).

SEQ ID NO:7520 n represents a or deletion (Location 21).

SEQ ID NO:7531 n represents 9 to 10 repeats of t (from Location 21).

15 SEQ ID NO:7538 n represents a or deletion (Location 21).

SEQ ID NO:7566 n represents a or deletion (Location 21).

SEQ ID NO:7615 n represents a or deletion (Location 21).

SEQ ID NO:7649 n represents gtg or deletion (Location 21).

SEQ ID NO:7651 n represents gg or tgggtgggtgga (Location 21).

20 SEQ ID NO:7667 n represents ct or deletion (Location 21).

All publications and patents mentioned in the above specification are herein incorporated by reference. Various modifications and variations of the described method and system of the invention will be apparent to those skilled in the art without departing from the scope and spirit of the invention. Although the invention has been described in connection with specific preferred embodiments, it should be understood that the invention as claimed should not be unduly limited to such specific

